SATENT COOPERATION TRE 'Y

From the INTERNATIONAL BUREAU

PCT

NOTIFICATION OF ELECTION

(PCT Rule 61.2)

To:

Commissioner
US Department of Commerce
United States Patent and Trademark
Office, PCT
2011 South Clark Place Room
CP2/5C24
Arlington, VA 22202

ETATS-UNIS D'AMERIQUE in its capacity as elected Office

Date of mailing (day/month/year) 27 June 2001 (27.06.01)

International application No. PCT/BE00/00077

International filing date (day/month/year) 03 July 2000 (03.07.00)

Applicant's or agent's file reference

JAN-002-PCT

Priority date (day/month/year) 01 July 1999 (01.07.99)

Applicant

CONTRERAS, Roland, Henri et al

1.	The designated Office is hereby notified of its election made:				
	X in the demand filed with the International Preliminary Examining Authority on:				
	22 January 2001 (22.01.01)			
	in a notice effecting later election filed with the International Bureau	on:			
2.	The election X was				
	was not				
	made before the expiration of 19 months . Rule 32.2(b).	2 applies, within the time limit under			

The International Bureau of WIPO 34, chemin des Colombettes 1211 Geneva 20, Switzerland

Authorized officer

Pascal Piriou

Telephone No.: (41-22) 338.83.38

Facsimile No.: (41-22) 740.14.35



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(19) World Intellectual Property Organization International Bureau



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PCT

(10) International Publication Number WO 01/02550 A2

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C12N 15/00

(26) Publication Language:

English

(30) Priority Data: 99870141.1

1 July 1999 (01.07.1999) EP

- (71) Applicant (for all designated States except US): JANSSEN PHARMACEUTICA N.V. [BE/BE]; Turn-houtseweg 30, B-2340 Beerse (BE).
- (72) Inventors; and
- (75) Inventors/Applicants (for US only): CONTRERAS, Roland, Henri [BE/BE]; Molenstraat 53, B-9820 Schelderode (BE). DE BACKER, Marianne, Denise [BE/BE]; Janssen Pharmaceutica N.V., Turnhoutseweg 30, B-2340 Beerse (BE). LUYTEN, Walter, Herman, Maria, Louis [BE/BE]; Janssen Pharmaceutica N.V., Turnhoutseweg 30, B-2340 Beerse (BE). MALCORPS, Isabelle, Karin, Luc [BE/BE]; Begijnenstraat 18, B-2980 Zoersel (BE). NELISSEN, Bart, Jozef, Maria [BE/BE]; Janssen Pharmaceutica N.V, Turnhoutseweg 30, B-2340

Beerse (BE). REEKMANS, Rieka, Josephina [BE/BE]; Wijnbergstraat 190, B-8560 Wevelgem (BE).

- (74) Agent: COIGNEZ, Koen; De Clercq, Brants & Partners cv, E. Gevaertdreef 10 a, B-9830 Sint-Martens-Latem (BE).
- (81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID. IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.
- (84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:

 Without international search report and to be republished upon receipt of that report.

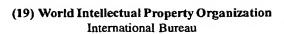
For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.



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(54) Title: CELL DEATH RELATED DRUG TARGETS IN YEAST AND FUNGI

(57) Abstract: The invention describes the use of nucleic acids and polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi for the preparation of a medicament for treating diseases associated with yeast or fungi or for the treatment of proliferative disorders or for preventing apoptosis in certain diseases. Methods are provided to identify compounds which selectively modulate the expression or functionality of said polypeptides in the same or a parallel pathway. Also provided are compounds as well as pharmaceutical compositions, medicaments and vaccines. The invention also comprises new nucleic acid sequences, probes and primers derived thereof, expression vectors and host cells transformed with said vectors, polypeptides and antibodies raised against said polypeptides.





(43) International Publication Date 11 January 2001 (11.01.2001)

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English

(10) International Publication Number WO 01/02550 A3

- (51) International Patent Classification⁷: C12Q 1/68, C12N 15/81, A61P 31/04, 31/10, C07K 14/395, 14/40, 16/14
- (21) International Application Number: PCT/BE00/00077
- (22) International Filing Date: 3 July 2000 (03.07.2000)
- (25) Filing Language:
- (26) Publication Language: English
- (30) Priority Data: 99870141.1 1 July 1999 (01.07.1999) EF
- (71) Applicant (for all designated States except US): JANSSEN PHARMACEUTICA N.V. [BE/BE]; Turn-houtseweg 30, B-2340 Beerse (BE).
- (72) Inventors; and
- (75) Inventors/Applicants (for US only): CONTRERAS, Roland, Henri [BE/BE]; Molenstraat 53, B-9820 Schelderode (BE). DE BACKER, Marianne, Denise [BE/BE]; Janssen Pharmaceutica N.V., Turnhoutseweg 30, B-2340 Beerse (BE). LUYTEN, Walter, Herman, Maria, Louis [BE/BE]; Janssen Pharmaceutica N.V., Turnhoutseweg 30, B-2340 Beerse (BE). MALCORPS, Isabelle, Karin, Luc [BE/BE]; Begijnenstraat 18, B-2980 Zoersel (BE). NELISSEN, Bart, Jozef, Maria [BE/BE]; Janssen Pharmaceutica N.V, Turnhoutseweg 30, B-2340

Beerse (BE). REEKMANS, Rieka, Josephina [BE/BE]; Wijnbergstraat 190, B-8560 Wevelgem (BE).

- (74) Agent: COIGNEZ, Koen; De Clercq, Brants [entity:amp]
 Partners cv, E. Gevaertdreef 10 a, B-9830 Sint-MartensLatem (BE).
- (81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.
- (84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:

- with international search report
- (88) Date of publication of the international search report: 15 November 2001

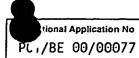
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A3

(54) Title: CELL DEATH RELATED DRUG TARGETS IN YEAST AND FUNGI

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A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12Q1/68 C12N15/81
C07K14/40 C07K16/14

A61P31/04

A61P31/10

C07K14/395

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

 $\label{lem:minimum} \begin{tabular}{ll} Minimum documentation searched (classification system followed by classification symbols) \\ IPC 7 C12N \end{tabular}$

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

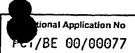
Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUM	ENTS CONSIDERED TO BE RELEVANT	
Category °	Citation of document, with indication. where appropriate, of the relevant passages	Relevant to claim No.
Х	DATABASE TREMBL [Online] EMBL database Heidelberg ac: p89096, 1 May 1997 (1997-05-01) KOBAYASHI O. ET AL.: "The region of Flo1 protein responsible for sugar recognition." XP002135238 abstract	1-16,34, 38,39, 44-55
X	DATABASE SWISS PROT [Online] ac: p39561, 1 February 1995 (1995-02-01) BUSSEY H. ET AL.: "gene: YAR061W" XP002135239 hypotetical 7.6 kD protein in FL01-PH011 intergenic region. abstract	1-16,34, 38,39, 44-55

X Further documents are listed in the continuation of box C.	Patent family members are listed in annex.		
 Special categories of cited documents: "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier document but published on or after the international filling date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filling date but later than the priority date claimed 	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art. "&" document member of the same patent family		
Date of the actual completion of the international search	Date of mailing of the international search report		
7 June 2001	2 8. 8. 01		
Name and mailing address of the ISA European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Authorized officer Panzica, G		

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INTERATIONAL SEARCH REPORT

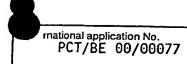


		_L
	ation) DCCUMENTS CONSIDERED TO BE RELEVANT	
Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
x	LIGR M. ET AL.: "Mammal Bax triggers apoptotic changes in Yeast" FEBS LETTERS, vol. 438, 1998, page 61-65 XP000857722 AMSTERDAM NL the whole document	1-16,34, 38,39, 44-55
×	US 5 882 874 A (FISHER PAUL B) 16 March 1999 (1999-03-16)	1-16,34, 38,39, 44-55
	the whole document	14-33
x	US 5 700 644 A (ARIAZI ERIC A ET AL) 23 December 1997 (1997-12-23)	1-16,34, 38,39, 44-55
Ì	the whole document	
Y	RESEARCH GENETICS: HTTP://WWW.APPS.RESGEN.COM/YEAST_ORF/YEAST_ORF_LOC_MAIN.HTLM,1998, XP002134776 The whole document	1-16,34, 38,39, 44-55
Y	WO 95 28497 A (JOLLA CANCER RES FOUND) 26 October 1995 (1995-10-26)	1-16,34, 38,39, 44-55
	abstract page 21, line 12 - line 31 example 1	44-55
(GB 2 326 413 A (NOVARTIS AG) 23 December 1998 (1998-12-23)	1-16,34, 38,39, 44-55
	abstract examples 1-9	
	MADEO FRANK ET AL: "A yeast mutant showing diagnostic markers of early and late apoptosis." JOURNAL OF CELL BIOLOGY, vol. 139, no. 3, 3 November 1997 (1997-11-03), pages 729-734, XP002168669 ISSN: 0021-9525 abstract	1-6,34, 38,39, 44-55
	MARZO ISABEL ET AL: "Bax and adenine nucleotide translocator cooperate in the mitochondrial control of apoptosis." SCIENCE (WASHINGTON D C), vol. 281, no. 5385, 1998, pages 2027-2031, XP000982449 ISSN: 0036-8075 abstract	1-16,34, 38,39, 44-55
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	ation) DUCUMENTS CONSIDERED TO BE RELEVANT	
Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	MATSUYAMA S ET AL: "THE MITOCHONDRIAL FOF1-ATPASE PROTON PUMP IS REQUIRED FOR FUNCTION OF THE PROAPOPTOTIC PROTEIN BAX IN YEAST AND MAMMALIAN CELLS" MOLECULAR CELL,CAMBRIDGE, MA,US, vol. 1, February 1998 (1998-02), pages 327-336, XP000987219 ISSN: 1097-2765 the whole document	1-16,34, 38,39, 44-55
A	XU QUNLI ET AL: "Methods of assaying Bcl-2 and Bax family proteins in yeast." METHODS (ORLANDO), vol. 17, no. 4, April 1999 (1999-04), pages 292-304, XP002168670 ISSN: 1046-2023 the whole document	1-16,34, 38,39, 44-55
1	SUN J ET AL: "SCREENING FOR BCL-2 HOMOLOGUES IN ASPERGILLUS NIDULANS" FASEB JOURNAL, FED. OF AMERICAN SOC. FOR EXPERIMENTAL BIOLOGY, BETHESDA, MD, US, vol. 11, 1997, page A425 XP000982451 ISSN: 0892-6638 abstract	1-16,34, 38,39, 44-55
	TAO W ET AL: "IDENTIFICATION OF YEAST PROTEINS THAT BIND SPECIFICALLY TO BCL-2" FASEB JOURNAL, FED. OF AMERICAN SOC. FOR EXPERIMENTAL BIOLOGY, BETHESDA, MD,US, vol. 11, 1997, page A1240 XP000982452 ISSN: 0892-6638 the whole document	1-16,34, 38,39, 44-55
	TAO W ET AL: "MODULATION OF CELL DEATH IN YEAST BY THE BCL-2 FAMILY OF PROTEINS" JOURNAL OF BIOLOGICAL CHEMISTRY, AMERICAN SOCIETY OF BIOLOGICAL CHEMISTS, BALTIMORE, MD,US, vol. 272, no. 24, 13 June 1997 (1997-06-13), pages 15547-15552, XP000982450 ISSN: 0021-9258 the whole document	1-16,34, 38,39, 44-55





Box I O	bservations where certain claims were found unsearchable (Continuation of item 1 f first sheet)
This Interna	ational Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:
1. Cla	aims Nos.: cause they relate to subject matter not required to be searched by this Authority, namely:
bed	aims Nos.: cause they relate to parts of the International Application that do not comply with the prescribed requirements to such extent that no meaningful International Search can be carried out, specifically:
bec	ims Nos.: cause they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).
Box II Ob	servations where unity of invention is lacking (Continuation of item 2 of first sheet)
This Internati	ional Searching Authority found multiple inventions in this international application, as follows:
1. As a sear	all required additional search fees were timely paid by the applicant, this International Search Report covers all chable claims.
2. As a of ar	Il searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment ny additional fee.
3. As o	nly some of the required additional search fees were timely paid by the applicant, this International Search Report rs only those claims for which fees were paid, specifically claims Nos.:
	equired additional search fees were timely paid by the applicant. Consequently, this International Search Report is cted to the invention first mentioned in the claims; it is covered by claims Nos.: 16,34,38,39,44-55 (in part)
Remark on Pr	The additional search fees were accompanied by the applicant's protest. No protest accompanied the payment of additional search fees.



FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

1. Claims: 1-16, 34, 38, 39, 44-55 (in part)

Invention 1:

Nucleic acid as set forth in Seq.Id.No.1 and protein sequence as set forth in Seq.Id.No.2 of the sequence listing, their methods of production and uses in medical preparations against disorders caused by Fungi or Yeast.

2. Claims: 1-55 in part

Inventions 2 to 228:

Same as for invention 1 but in relation to each group of nucleic acid sequence and its relative aminoacid sequence:

Invention 2: Seq.Id.Nos. 3 and 4,

. . .

Invention 228: Seq.d.Nos. 455 and 456.

INT: ANATIONAL SEARCH REPORT lation on patent family members

·tional	Application No
PCT/BE	00/00077

Patent document cited in search report		Publication date		atent family nember(s)	Publication date
US 5882874	Α	16-03-1999	AU	2881799 A	15-09-1999
US 5700644	Α	23-12-1997	NONE		
w0 9528497	A	26-10-1995	AU EP US	2290195 A 0759090 A 5702897 A	10-11-1995 26-02-1997 30-12-1997
GB 2326413	Α	23-12-1998	NONE		

WIPO

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(PCT Article 36 and Rule 70)

INTERNATIONAL PRELIMINARY EXAMINATION REPORT

Applicant's o	r agent's file reference			- N-PF-	
		FOR FURTHER A	CTION	See Notifica Preliminary	ation of Transmittal of International Examination Report (Form PCT/IPEA/416)
International	application No.	International filing date	(day/month	'year)	Priority date (day/month/year)
PCT/BE00	/00077	03/07/2000			01/07/1999
	International Patent Classification (IPC) or national classification and IPC C12N15/00				
Applicant					
JANSSEN	PHARMACEUTICA N.V.	et al.			
 This international preliminary examination report has been prepared by this International Preliminary Examining Authority and is transmitted to the applicant according to Article 36. 					
2. This RE	PORT consists of a total of	10 sheets, including th	is cover s	heet.	
bee (se	This report is also accompanied by ANNEXES, i.e. sheets of the description, claims and/or drawings which have been amended and are the basis for this report and/or sheets containing rectifications made before this Authority (see Rule 70.16 and Section 607 of the Administrative Instructions under the PCT).				
	Innexes consist of a total of	3 sheets.			
	ort contains indications relat	ing to the following iten	ns:	·	
1	Basis of the report				i
11	☐ Priority				
III	Non-establishment of op	inion with regard to no	velty, inve	ntive step ar	nd industrial applicability
IV	Lack of unity of inventior	า			-
· V	Reasoned statement und citations and explanation	der Article 35(2) with re ns suporting such state	egard to no ment	velty, inven	tive step or industrial applicability;
VI	Certain documents cited				:
	Certain defects in the int				
VIII	Certain observations on	the international applic	ation		
Date of submis	sion of the demand		Date of co	mpletion of thi	is report

22/01/2001 25.09.2001 Name and mailing address of the international Authorized officer preliminary examining authority: European Patent Office D-80298 Munich Nichogiannopoulou, A Tel. +49 89 2399 - 0 Tx: 523656 epmu d Fax: +49 89 2399 - 4465 Telephone No. +49 89 2399 8054

INTERNATIONAL PRELIMINARY EXAMINATION REPORT

International application No. PCT/BE00/00077

 Basis of the report 	I.	Basis	of the	report
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	th ar	e receiving Office in	ments of the international applic response to an invitation under to this report since they do not o	Article 14 are	e referred to in this rep	ort as "originally filed"	
	1-	41	as originally filed				
	CI	aims, No.:					
	1-:	55	as originally filed				
	Dr	awings, sheets:					
	29	161-21/161,23/161-2 /161-56/161, /161-161/161	27/161,	as originally	filed		
		/161,28/161, /161	as received on	23/11/2000	with letter of	22/11/2000	
	Se	quence listing part	t of the description, pages:				
	1-5	570, filed with the let	ter of 24.10.2000				
2.	Wi lan	With regard to the language , all the elements marked above were available or furnished to this Authority in the language in which the international application was filed, unless otherwise indicated under this item.					
	The	ese elements were a	available or furnished to this Aut	hority in the fo	ollowing language: ,	which is:	
		the language of a	translation furnished for the purp	poses of the i	nternational search (ur	nder Rule 23.1(b)).	
		the language of pu	ublication of the international app	olication (unde	er Rule 48.3(b)).	. ,,	
		the language of a 55.2 and/or 55.3).	translation furnished for the purp	ooses of inter	national preliminary ex	amination (under Rule	
• 3.	Wit	h regard to any nuc ernational preliminar	eleotide and/or amino acid seq y examination was carried out o	uence disclos n the basis of	sed in the internationa the sequence listing:	I application, the	
		contained in the in	ternational application in written	form.			
			the international application in c		able form		
	\boxtimes		ently to this Authority in written t		45.5 15.111.		
	\boxtimes		ently to this Authority in comput		erm.		
	Ø	The statement that	t the subsequently furnished wri	tten sequence		eyond the disclosure in	



	Ø	The statement that the listing has been furn	ne information recorded in computer readable form is identical to the written sequence shed.			
4.	The	amendments have re	esulted in the cancellation of:			
		the description,	pages:			
		the claims,	Nos.:			
		the drawings,	sheets:			
5.			established as if (some of) the amendments had not been made, since they have been ond the disclosure as filed (Rule 70.2(c)):			
		(Any replacement sh report.)	eet containing such amendments must be referred to under item 1 and annexed to this			
6.		litional observations, i separate sheet	necessary:			
111	. Nor	n-establishment of o	pinion with regard to novelty, inventive step and industrial applicability			
1.		The questions whether the claimed invention appears to be novel, to involve an inventive step (to be non-obvious), or to be industrially applicable have not been examined in respect of:				
		the entire internation	al application.			
	Ø	claims Nos. 1-16, 34,	38, 39, 44, 45, all partially, 17-33, 35-37, 40-43 all completely.			
be	ecaus	e:				
	×		application, or the said claims Nos. 44, 45 relate to the following subject matter which sternational preliminary examination (<i>specify</i>):			
			s or drawings (indicate particular elements below) or said claims Nos. are so unclear inion could be formed (specify):			
	×	the claims, or said cla meaningful opinion co	nims Nos. 11-14, 16, 40-43 are so inadequately supported by the description that no buld be formed.			
			h report has been established for the said claims Nos. 1-16, 34, 38, 39, 44-55 all , 40-43 all completely.			
2.	and/		preliminary examination cannot be carried out due to the failure of the nucleotide ce listing to comply with the standard provided for in Annex C of the Administrative			
		the written form has r	ot been furnished or does not comply with the standard.			

International application No. PCT/BE00/00077

		the computer readable form has not been furnished or does not comply with the standard.				
IV	. Lac	ck of unity of invention				
1.	In r	In response to the invitation to restrict or pay additional fees the applicant has:				
		restricted the claims.				
		paid additional fees.				
		paid additional fees und	der prot	est.		
		neither restricted nor pa	aid addi	tional fee	s.	
2.		This Authority found that the requirement of unity of invention is not complied and chose, according to Rule 68.1, not to invite the applicant to restrict or pay additional fees.				
3.	This	nis Authority considers that the requirement of unity of invention in accordance with Rules 13.1, 13.2 and 13.3 is				
		complied with.				
	Ø	not complied with for th see separate sheet	e follow	ing reaso	ns:	
4.	Con	nsequently, the following parts of the international application were the subject of international preliminary amination in establishing this report:				
		all parts.				
	☒	the parts relating to claims Nos. 1-16, 34, 38, 39, 44-55.				
	cita	asoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; ations and explanations supporting such statement				
1. Statement						
		elty (N)	Yes: No:	Claims Claims	1-16, 34, 38, 39, 44-55	
		ntive step (IS)	Yes: No:	Claims Claims	1-16, 34, 38, 39, 44-55	
	Industrial applicability (IA)		Yes: No:	Claims Claims	1-16, 34, 38, 39, 44-55	

VII. Certain defects in the international application

2. Citations and explanations see separate sheet

INTERNATIONAL PRELIMINARY EXAMINATION REPORT

International application No. PCT/BE00/00077

The following defects in the form or contents of the international application have been noted: see separate sheet

VIII. Certain observations on the international application

The following observations on the clarity of the claims, description, and drawings or on the question whether the claims are fully supported by the description, are made: see separate sheet

Re Item I

Basis of the report

The amendments to the drawings filed with the letter of 22.11.2000 are formally 1. allowable under Article 34(2)(b) PCT because they are the corrections of obvious errors under Rule 91.1 and do not introduce subject-matter extending beyond the content of the application as filed.

Re Item III

Non-establishment of opinion with regard to novelty, inventive step and industrial applicability

- 1. No meaningful examination could be performed for claims 1-16, 34, 38, 39, 44-55 all partially and 17-33, 35-37, 40-43 all completely, for the following reasons:
- 1.1. Rule 66. 1.(e) (PCT):

No complete international search report has been established for claims 1-16, 34, 38, 39, 44-55 all partially and 17-33, 35-37, 40-43 (see Form PCT/ISA/210 issued on 28/08/2001). Accordingly, said claims need not be the subject of international preliminary examination.

1.2. Articles 5 and 6 PCT:

Claims 11-14, 16 and 40-43 do not comply with the requirements of Articles 5 and 6 (PCT). Said claims relate to compounds identifiable by the claimed methods without giving a true technical characterisation of such compounds. Moreover no such compounds are disclosed in the present application. In consequence the scope of said claims is ambiguous and vague and their subject-matter is neither sufficiently disclosed nor supported. These deficiencies render a meaningful examination of the claimed subject-matter impossible.

2. Claims 44 and 45 -as far as they concern in vivo methods- relate to subject-matter considered by this Authority to be covered by the provisions of Rule 67.1(iv) PCT. Consequently, no opinion will be formulated with respect to the industrial applicability of the subject-matter of these claims (Article 34(4)(a)(i) PCT).

Re Item IV

Lack of unity of invention

- The present application lacks unity as required by Article 3(4)(iii) PCT and Rule 13 1. PCT. Rule 13.1 PCT states that for unity of invention to be present, all subject-matter should be linked by a single general inventive concept. Each of the 228 groups of inventions listed on Form PCT/ISA/206 issued on 28.06.2001 constitutes a separate, distinct invention for the following reason. The common concept linking these 228 groups is that they are all allegedly involved in a Bax-induced apoptotic pathway in yeast. Bax induction of apoptotic pathways in yeast has already been known from the prior art. D3 teaches that Bax induces an apoptotic cascade in yeast and discloses genes involved in a pathway leading to apoptosis and their use for killing yeast. Since no other "special" technical feature (Rule 13.2 PCT) could be identified to provide a linking concept between the four groups, each must be considered as a separate invention.
 - N.B. The use of the term "invention" here in no way implies recognition of an inventive step for the subject-matter of any group.

Re Item V

Reasoned statement under Article 35(2) with regard to novelty, inventive step or

industrial applicability; citations and explanations supporting such statement

- 1. Reference is made to the following documents:
 - D1: DATABASE TREMBL [Online] EMBL database Heidelberg ac: p89096, 1 May 1997 (1997-05-01) KOBAYASHI O. ET AL.: 'The region of Flo1 protein responsible for sugar recognition.' XP002135238
 - D2: DATABASE SWISS PROT [Online] ac: p39561, 1 February 1995 (1995-02-01) BUSSEY H. ET AL.: 'gene: YAR061W' XP002135239
 - D3: LIGR M. ET AL.: 'Mammal Bax triggers apoptotic changes in Yeast' FEBS LETTERS, vol. 438, 1998, page 61-65 XP000857722 AMSTERDAM NL

2. Novelty (Article 33(2) PCT)

The present application discloses sequences involved in the molecular pathways leading to apoptosis in yeast. The claimed sequences were obtained by differential display screening of Bax induced mRNAs on arrays of yeast ORFs. The use of such sequences in pharmacy is alleged. There is no indication of a function of the claimed cDNAs.

D1 and D2 are database entries that are identical to SEQ ID Nos:1 and 2 of the present application. D3 discloses that Bax induces apoptotic pathways in yeast, D1-D3 are thus detrimental to the novelty and inventive step of claims 1-16, 34, 38, 39 and 44-45.

Inventive step (Article 33(3) PCT) 3.

Due to the fact that no function has been established for the claimed sequences. these do not appear to be associated with any known technical effect. Accordingly, the only underlying technical problem that can be recognised is the provision of sequences somehow associated with the apoptotic pathway in yeast. To establish inventive activity,

the provision of a sequence must be justified by the technical purpose, i.e. by a

hitherto unknown or unexpected technical effect, caused by those technical features which distinguish the claimed molecules from numerous other ones. Due to the absence of any disclosed function or technical effect, the provision of the present sequences amounts to nothing more than an arbitrary selection. Consequently, the claimed molecules as well as compositions, vectors, host cells kits and methods relating to them (claims 1-16, 34, 38, 39 and 44-45) are considered to lack an inventive step, pursuant to Article 33(3) PCT.

4. Industrial applicability (Article 33(4) PCT)

In so far as the present specification is completely silent with regard to the function of the claimed sequences, the possible fields of application for the claimed protein and polynucleotides suggested in the specification are merely speculative. Thus it is questionable whether the claimed subject-matter actually meets the requirements set forth in Article 33(4) PCT.

Re Item VII

Certain defects in the international application

1. Contrary to the requirements of Rule 5.1(ii) PCT, documents D1-D3 are not identified in the description and the relevant background art disclosed therein is not briefly discussed.

Re Item VIII

Certain observations on the international application

- The claimed use of the disclosed sequences for the preparation of a medicament for 1. treating diseases associated with yeast or fungi is neither disclosed in nor supported by the application as filed. Such use is purely hypothetical and amounts to little more than an unsubstantiated desideratum. Accordingly, claims 1-4, 15, 44-48 do not fulfill the requirements of Articles 5 and 6 EPC.
- 2. In this context it should also be noted that even the relation of the disclosed sequences with apoptosis is purely hypothetical: Bax-induced or Bax-regulated expression or over-expression of genes and apoptotic pathways are related but not overlapping concepts. There is no evidence that every Bax regulated sequence is involved in apoptosis, even if such involvement were sufficient to justify speculations on a medical use.
- 3. Furthermore, present claims 1 and 2 do not satisfy the provisions of Article 6 PCT in that the term "functional equivalents" and "functional fragment" is unclear. A functional equivalent of a sequence involved in an apoptotic pathway in yeast is any sequence somehow involved in an apoptotic pathway in yeast. Claims to such an equivalent would have to be additionally defined in terms of its sequence for the purposes of Article 6 PCT.

CELL DEATH RELATED DRUG TARGETS IN YEAST AND FUNGI

The present invention relates to the identification of genes and proteins encoded thereof from yeast and fungi whose expression is modulated upon programmed cell death and which genes, proteins or functional fragments and equivalents thereof may be used as selective targets for drugs to treat infections caused by or associated with yeast and fungi or for the treatment of proliferative disorders or for the prevention of apoptosis in certain diseases.

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Invasive fungal infections (e.g. Candida spp, Aspergillus spp., Fusarium spp., Zygomycetes spp.) (Walsh, 1992) have emerged during the past two decades as important pathogens causing formidable morbidity and mortality in an increasingly diverse and progressively expanding population of immunocompromised patients. Those with the acquired immune deficiency syndrome (AIDS) constitute the most rapidly growing group of patients at risk for life-threatening mycosis. But fungal infections have also increased in frequency in several populations of other susceptible hosts, including very-low-birth-weight infants, cancer patients receiving chemotherapy, organ transplant recipients, burn patients and surgical patients with complications.

These fungal infections are not limited to humans and other mammals, but are also important in plants where they can cause diseases or cause the production of unwanted compounds (e.g. Fusarium spp., Aspergillus spp., Botritis spp., Cladosporium spp.).

Although recent advances in antifungal chemotherapy have had an impact on these mycoses, expanding populations of immunocompromised patients will require newer approaches to antifungal therapy. The discovery of novel antifungal agents is thus an essential element of any new antifungal therapy.

Classical approaches for identifying anti-fungal compounds have relied almost exclusively on inhibition of fungal or yeast growth as an endpoint. Libraries of natural products, semi-synthetic, or synthetic chemicals are screened for their ability to kill or arrest growth of the target pathogen or a related nonpathogenic model organism. These tests are cumbersome and provide no information about a compound's mechanism of action. The promising lead compounds that emerge from such screens must then be tested for possibl host-toxicity and detailed mechanism of action studies must subsequently be conducted to identify the aff cted molecular targ t.

Cells from multicellular organisms can commit suicid in response to specific signals or injury by an intrinsic program of cell death. Apoptosis is a form of programmed cell death which leads to elimination of unnec ssary or damaged cells. To

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survive, all cells from multicellular organisms depend on the constant repression of this suicide program by signals from other cells (Raff, 1992). It has been assumed that such an altruistic form of cell survival arose with multicellularity and would have been counterselected in unicellular organisms. Recent findings indicate, however, that a similar process of cell survival also operates in single-celled eukaryotes.

It has been found that expression of the mammalian *Bax* gene triggers cell death in *Saccharomyces cerevisiae* and the fission yeast *Schizosaccharomyces pombe* with morphological changes similar to apoptosis (Jürgensmeier *et al.*, 1997). However, the mechanism of *Bax* lethality in *S. cerevisiae* remains unclear.

Since it has been discovered that the mammalian *Bax* gene triggers apoptotic changes in yeast (Ligr *et al.*, 1998), this can be an indication that the molecular pathways eventually leading to programmed cell death may also be partially present in yeast cells and other unicellular eukaryotes.

It is an aim of the present invention to provide nucleic acid as well as polypeptide sequences which represent potential molecular targets for the identification of new compounds which can be used in alleviating diseases or conditions associated with yeast or fungi infections.

It is a further aim of the present invention to provide uses of these nucleic acid and amino acid molecules for the preparation of a medicament for treating diseases associated with yeast or fungi.

It is also an aim of the invention to provide pharmaceutical compositions and vaccines comprising these nucleic acids or polypeptides.

It is also an aim of the present invention to provide vectors comprising these nucleic acids, as well as host cells transfected or transformed with said vectors.

It is also an aim of the invention to provide antibodies against these polypeptides, which can be used as such, or in a composition as a medicine for treating diseases associated with yeast and fungi.

It is another aim of the invention to provide methods to selectively identify compounds capable of inhibiting or activating expression of such polypeptides in yeast or fungi infections. The nucleic acid and polypeptide molecules alternatively can be incorporated into an assay or kit to identify these compounds.

It is also an aim of the invention to provide a method of preventing infection with yeast or fungi.

It is also an aim of the inv ntion to provide probes and primers deriv d from the nucleic acid sequences of the invention.

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All the aims of the present invention have been met by the embodiments as set out below.

The present inventors identified a range of specific nucleotide sequences which are involved in the molecular pathways eventually leading to programmed cell death. The present inventors were able to identify via macro array screening a range of genes involved in a pathway eventually leading to programmed cell death in the yeast *Saccharomyces cerevisiae*. As explained in Example 2, genes showing a difference of a factor 5 or more in expression as a result of *Bax*-induced cell death, were identified as differentially expressed candidate genes. Some of these genes are clearly down-regulated in a *Bax*-expressing strain, while other genes show an upregulated expression (Table 1). Example 3 describes a further experiment wherein the results of differential expression were analysed using the PathwaysTM software and differentially expressed nucleic acid sequence were identified.

According to a first embodiment, the invention relates to the use of a nucleic acid molecule encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which nucleic acid sequence is selected from:

- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 20 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 25 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 30 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484, or encoding a functional equivalent, derivative or biopr cursor of said protein;
- 35 (b) a nucleic acid molecul encoding a protein having an amino acid sequence which is more than 70% similar, preferably mor than 75% or 80% similar, mor

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preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 5 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 10 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 15 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484; (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 20 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 25 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 30 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 35 484;

- (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 5 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 10 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 15 445, 447, 449, 451, 453 or 455;
- (e) a nucleic acid sequence which is more than 70% identical, preferably more than 75 or 80% identical, more preferably more than 85%, or 90% or 95% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 20 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 25 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 30 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453 or 455;
 - (f) a nucleic acid sequence encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e); and
- 35 (g) the complem nt of any of the nucl ic acids quences as specified in a) to f),

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for the preparation of a medicament for treating diseases associated with yeast or fungi.

Sequence similarity searches were performed using the BLAST software package version 2. Identity and similarity percentages were calculated using BLOSUM62 as a scoring matrix.

As known in the art, "similarity" between two polypeptides is determined by comparing the amino acid sequence and its conserved amino acid substitutes of one polypeptide to the sequence of a second polypeptide. Moreover, also known in the art is "identity" which means the degree of sequence relatedness between two polypeptide or two polynucleotide sequences as determined by the identity of the match between two strings of such sequences. Both identity and similarity can be readily calculated. While there exist a number of methods to measure identity and similarity between two polynucleotide or polypeptide sequences, the terms "identity" and "similarity" are well known to skilled artisans (Carillo and Lipton, 1988). Methods commonly employed to determine identity or similarity between two sequences include, but are not limited to, those disclosed in "Guide to Huge Computers (Bishop, 1994) and Carillo and Lipton (1988). Preferred methods to determine identity are designed to give the largest match between the two sequences tested. Methods to determine identity and similarity are codified in computer programs. Preferred computer program methods to determine identity and similarity between two sequences include, but are not limited to, GCG program package (Devereux et al., 1984), BLASTP, BLASTN and FASTA (Altschul et al, 1990).

The nucleic acid sequences to be used according to this aspect of the invention from *Saccharomyces cerevisiae* are defined in SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 457, 459, 461, 463, 465, 467, 469, 471 and 473.

The invention also relates to nucleic acid sequences from *Candida albicans*, as repres nted by the SEQ ID NOs 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371,

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373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 475, 477, 479, 481, and 483.

The expression "a pathway eventually leading to programmed cell death" refers to a sequence of steps ultimately leading to cell death and which can be triggered at various steps in this pathway by various agents, such as Bax, Bak, CED4, hydrogen peroxide, diamide and farnesol.

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The yeast or fungi according to the invention may be, but are not restricted to, pathogenic yeast or fungi. As such, yeast or fungi may cause infections in healthy individuals as well as in immunocompromised patients.

The expression "treating diseases associated with yeast and fungi" not only refers to diseases or infections caused by said organisms but also refers to allergic reactions caused by said organisms, such as the so-called "professional diseases" in, for instance, bakery and brewery and that are caused by yeast or fungi which are commonly known as "non-pathogenic".

The invention further relates to the use of nucleic acid sequence homologues of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 20 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 25 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 30 467, 469, 471, 473, 475, 477, 479, 481 or 483 but isolated from other yeast and fungi strains which are also involved in a pathway eventually leading to programmed cell death.

According to the invention, these sequenc s and their homologues in other yeast and fungi as well as the polypeptides which they encode represent novel molecular targets which can b incorporated into an assay to selectively identify compounds capabl of inhibiting or activating expr ssion of such polypeptides.

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Furthermore, the invention also relates to the potential use of said sequences in alleviating diseases or conditions associated with yeast or fungi infections, such as diseases caused by Candida spp., Aspergillus spp., Microsporum spp., Trichophyton spp., Fusarium spp., Zygomycetes spp., Botritis spp., Cladosporium spp., Malassezia spp., Epidermophyton floccosum, Blastomyces dermatitidis, Coccidioides immitis, Histoplasma capsulatum, Paracoccidioides brasiliensis, Cryptococcus neoformans, and Sporothrix schenckii.

According to another embodiment, the invention also relates to a nucleic acid sequence encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi selected from:

- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;
- (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, mor preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;

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- (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NO 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 475, 477, 479, 481 or 483;
- (e) a nucleic acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NO 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 475, 477, 479, 481 or 483; and,
- (f) a nucleic acid sequence encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e), and
- (g) the complement of any of the nucleic acid sequences as specified in a) to f).

According to a more specific embodiment, these nucleic acid sequences ar derived from Saccharomyces cerevisiae, Candida albicans or Aspergillus fumigatus.

A nucleic acid sequence according to the invention may comprise an mRNA sequence or alternatively a DNA sequence and preferably a cDNA sequence. A nucleic acid sequence according to the invention may also comprise any modified nucleotide known in the art.

The present invention further relates to a nucleic acid molecule capable of selectively hybridising to at least one of the nucleic acid molecules according to the invention, or the complement thereof.

The term "selectively hybridising" or "specifically hybridising means hybridising under conditions wherein sequences can be detected which are homologues of the sequences of the invention, but which are for instance derived from heterologous cells or organisms, and wherein said sequences do not hybridiz with known sequences. In a preferred embodiment, mammalian homologu s can be detected. It is well known to the p rson skilled in the art which methods for hybridisation can be used and which conditions ar necessary for selectively or specifically hybridising. Preferably, hybridization under high stringency conditions can be applied (Sambrook t al., 1989).

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As such, the present invention also relates to the use of the nucleic acid sequences of the invention for detecting homologues in heterologous organisms including but not limited to mammalian organisms.

The term "nucleic acid sequence" also includes the complementary sequence to any single stranded sequence given, or the antisense version thereof.

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The invention also relates to mRNA, DNA or cDNA versions of the nucleic acid molecules of the invention.

The present invention more particularly relates to an antisense molecule comprising a nucleic acid sequence capable of hybridizing to any of the above defined nucleic acid sequences.

Polynucleotides according to the invention may be inserted into vectors in an antisense orientation in order to provide for the production of antisense RNA. Antisens RNA or other antisense nucleic acids may also be produced by synthetic means.

The present invention also advantageously provides nucleic acid sequences of at least approximately 10 contiguous nucleotides of a nucleic acid according to the invention and preferably from 10 to 50 nucleotides. These sequences may, advantageously be used as probes or primers to initiate replication, or the like. Such nucleic acid sequences may be produced according to techniques well known in the art, such as by recombinant or synthetic means. The probes will hybridise specifically with any of the nucleic acid molecules of the invention. The primers will specifically amplify any of the nucleic acid molecules of the invention.

The probes or primers according to the invention may also be used in diagnostic kits or the like for detecting the presence of a nucleic acid according to the invention. These tests generally comprise contacting the probe with the sample under hybridising conditions and detecting the presence of any duplex or triplex formation between the probe and any nucleic acid in the sample.

According to the present invention these probes may be anchored to a solid support. Preferably, they are present on an array so that multiple probes can simultaneously hybridize to a single biological sample. The probes can be spotted onto the array or synthesized *in situ* on the array. (Lockhart *et al.*, 1996). A single array can contain more than 100, 500 or even 1,000 different probes in discrete locations. Such arrays can b used to screen for compounds interacting with said probes.

Advantageously, the nucleic acid sequences, according to the invention may be produced using recombinant or synthetic means, such as for example using PCR cloning mechanisms which generally involve making a pair of primers, which may be from approximately 10 to 50 nucleotid s to a region of the gene which is desired to be

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cloned, bringing the primers into contact with mRNA, cDNA, or genomic DNA from the yeast or fungal cell, performing a polymerase chain reaction under conditions which bring about amplification of the desired region, isolating the amplified region or fragment and recovering the amplified DNA. Generally, such techniques as defined herein are well known in the art, such as described in Sambrook *et al.* (1989). These techniques can be used to clone homologues of the nucleic acid sequences of the invention in other organisms.

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The nucleic acids or oligonucleotides according to the invention may carry a revealing label. Suitable labels include radioisotopes such as ³²P, ³³P or ³⁵S, enzym labels or other protein labels such as biotin or fluorescent markers. Such labels may be added to the nucleic acids or oligonucleotides of the invention and may be detected using techniques known in the art.

According to another embodiment of the invention, the nucleic acid sequences according to the invention as defined above may, advantageously, be included in a suitable expression vector which may be transformed, transfected or infected into a host cell. In such an expression vector the nucleic acid is operably linked to a control sequence, such as a suitable inducible promotor, or the like, to ensure expression of the proteins according to the invention in a suitable host cell. The expression vector may also comprise a reporter molecule. The expression vector may advantageously be a plasmid, cosmid, virus or other suitable vector which is known to those skilled in the art. The expression vector and the host cell defined herein also form part of the present invention. Preferably the host cell is a lower eukaryotic cell such as a yeast cell or a fungal cell. Yeast and fungal cells are particularly advantageous because they provide the necessary post-translational modifications to the expressed proteins of th invention, similar to those of the natural proteins from which they are derived. These modifications confer optimal conformation of said proteins, which when isolated may advantageously be used in kits, methods or the like.

The invention further relates to any nucleic acid as defined above for use as a medicament.

Nucleotide sequences according to the invention are particularly advantageous for providing selective therapeutic targets for treating yeast or fungi-associated infections. For example, an antisense nucleic acid capable of binding to the nucleic acid sequences according to the invention may be used to selectively inhibit expression of the corresponding polypeptides, leading to impaired growth or death of yeast and fungi with reductions of associated illnesses or diseas s.

According to another embodiment, the invention also relates to the use of a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi, said polypeptide being selected from:

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 5 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 10 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 15 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of 20 said protein;
- (b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 25 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 30 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 35 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432,

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- 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;
- (c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% 5 or 95% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 10 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 15 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 20 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484; and,
 - (d) a functional fragment of any of said proteins as defined in a) to c), for the preparation of a medicament for treating diseases associated with yeast or fundi.

The term "functional fragment" of a protein means a truncated version of the original protein or polypeptide referred to. The truncated protein sequence can vary widely in length; the minimum size being a sequence of sufficient size to provide a sequence with at least a comparable function and/or activity of the original sequence referred to, while the maximum size is not critical. In some applications, the maximum size usually is not substantially greater than that required to provide the desired activity and/or function(s) of the original sequence. A functional fragment can also relate to a subunit with similar function as said protein. Typically, the truncated amino acid sequence will rang from about 5 to about 60 amino acids in length. More typically, how ver, the sequence will be a maximum of about 50 amino acids in length, preferably a maximum of about 60 amino acids. It is usually desirable to select sequences of at 1 ast about 10, 12 or 15 amino acids.

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Functional fragments include those comprising an epitope which is specific or uniqu for the proteins according to the invention. Epitopes may be determined using, for example, peptide scanning techniques as described in Geysen *et al.* (1996). Preferred functional fragments have a length of at least, for example, 5, 10, 25, 50, 75, 100, 125, 150, 175 or 200 amino acids.

The polypeptides to be used according to this aspect of the invention from Saccharomyces cerevisiae, are represented by SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16. 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 10 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 15 278, 280, 282, 284, 458, 460, 462, 464, 466, 468, 470, 472 and 474. Also according to the invention is the use of the polypeptides from Candida albicans as represented by the SEQ ID NOs 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 20 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 476, 478, 480, 482 and 484.

The polypeptide or protein according to the invention may also include variants of any of the polypeptides of the invention as specified above having conservativ amino acid changes.

The nucleic acid molecules or the polypeptides of the invention may b provided in a pharmaceutically acceptable carrier, diluent or excipient therefor.

The present invention also relates to a vaccine for immunizing a mammal against infections caused by yeast and fungi comprising at least one (recombinant) nucleic acid molecule or at least one (recombinant) polypeptide of the invention in a pharmaceutically acceptable carrier.

Pharmaceutically acceptable carriers include any carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitabl carriers are typically larg, slowly metabolizing macromolecules such as prot ins, polysaccharides, polylactic acids, polyglycolic acids, polym ric amino acids,

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amino acid copolymers; and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

A "vaccine" is an immunogenic composition capable of eliciting protection against infections caused by yeast or fungi, whether partial or complete. A vaccine may also be useful for treatment of an individual, in which case it is called a therapeutic vaccine.

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Said vaccine compositions may include prophylactic as well as therapeutic vaccine compositions.

The term "therapeutic" refers to a composition capable of treating infections caused by yeast or fungi.

Some of the pathways leading to apoptosis are conserved between mammalian cells and yeast or fungi. Therefore, targets which are part of such a conserved pathway may be used to stimulate or inhibit the apoptosis in mammalian cells. E.g. stimulation of apoptosis is desirable in the treatment of tumor cells/tissues.

According to another embodiment, the present invention provides a method of identifying compounds which selectively inhibit, induce or interfere with the expression/production of the polypeptides encoded by the nucleotide sequences of the invention, or compounds which selectively inhibit, activate or interfere with the functionality of polypeptides expressed from the nucleotide sequences according to the invention, or which selectively inhibit, induce or interfere with the metabolic pathways in which these polypeptides are involved. Compounds may carry agonistic or antagonistic properties. The compounds to be screened may be of extracellular, intracellular, biologic or chemical origin.

Such a screening method may comprise the following steps (a) contacting a compound to be tested with cells having a mutation which results in overexpression or underexpression of at least one of the polypeptides as defined in claim 2, in addition to contacting wild type cells with said compound, (b) monitoring the growth, death rate or activity of said mutated cells compared to said wild type cells; wherein differential growth or activity of said mutated cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (c) alternatively monitoring the growth, death rate or activity of said mutated cells compared to mutated cells which were not contact d with the compound to be tested, wherein differential growth or activity of said mutated yeast of fungi cells is indicative of a lective action of said compound on a polypeptide in the same or a parallel pathway, (d) alternatively monitoring changes in morphologic and/or functional properties of components in said mutated cells caused by the addition of the compound to be tested.

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The term "cells" as used above relat s to any type of cells such as, but not limited to bacterial, yeast, fungal, plant or human cells.

Compounds found using this approach may additionally be tested on their efficiency in killing or inhibiting the growth of wild type cells in order to confirm their utility as medicament for treating wild type pathogenic strains/tumor cells.

According to the invention, the term "mutation" includes point mutations, deletions, insertions, duplications or any modification in the nucleic acid encoding said polypeptide, or at a different location in the genome of said cells, influencing the expression of said nucleic acid or polypeptide. In case point mutations occur, the number of nucleotides will be identical compared to the original sequence; only a change in nucleotide sequence can be observed. This stands in contrast with the other listed mutations where the number of the nucleotides will be different from the number observed in the wild type sequence and consequently will also reflect in a change of the nucleotide sequence.

Changes in morphologic and/or functional properties of cell components which can be monitored include for example morphological and molecular changes such as abnormal cell morphology, nuclear fragmentation, DNA breakage or changes in the expression of certain enzymes such as caspases, as well as monitoring changes in membrane potential or activity of mitochondria and release of cytochrome c from mitochondria. All these changes can be monitored on the whole cell which is contacted to the compound to be tested.

The invention also relates to a method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast and fungi or in metabolic pathways in which said polypeptides are involved, which method comprises (a) contacting a compound to be tested with yeast or fungal cells transformed, transfected or infected with an expression vector comprising an antisense sequence of at least one of the nucleic acid sequences as defined in claim 1, which expression results in underexpression of said polypeptide, in addition to contacting one or more wild type cells with said compound, (b) monitoring the growth, death rate or activity of said transformed, transfected or infected cells compared to said wild type cells; wherein diff rential growth or activity of said transformed, transfect d or infected yeast or fungal cells is indicativ of selective action of said compound on a polypeptide in the same or a parallel pathway, (c) alt rnatively monitoring the growth, death rate or activity of said transformed, transf cted or infected cells compar d to transformed, transf cted or infected cells which were not contacted with the compound to be tested, wherein

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differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (d) alternatively monitoring changes in morphologic and/or functional properties of components in said transformed, transfected or infected cells caused by the addition of the compound to be tested.

Alternative methods for identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast or fungi or in metabolic pathways in which said compounds are involved, may comprise the use of any other method known in the art resulting in gene activation, gene inactivation, gene modulation or gene silencing.

The invention also relates to a method of identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid molecule as defined in claim 1 joined in frame with a reporter gene and (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested. This enables to analyse the influence of the compound onto all/most aspects of transcriptional activation. Alternatively additional tests can routinely be performed to test the influence of the compound onto mRNA stability, translation and protein stability. All these aspects influence the concentration of corresponding proteins and consequently influence the effect of these on the metabolism of the cell.

The invention further relates to a method of identifying compounds which bind to or modulate the properties of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi, which method comprises (a) contacting a compound to be tested with at least one of the polypeptides as defined in claim 2, (b) detecting the complex formed between the compound to be tested and said polypeptide, (c) alternatively, examining the diminution/increase of complex formation between said polypeptide and a receptor/binding partner, caused by the addition of the compound being tested, (c) alternatively, examining the alteration in th functional activity of the polypeptide, caused by the addition of the compound being tested.

Detection of the complex formation can be performed using sev ral approaches. First, binding of a compound onto a polypeptide can be studied using classical binding tests: on of th binding partners, compound or polypeptide is lab led and interaction of both is measured. Most of these tests comprise following st ps:

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incubating both binding partners in conditions where binding is allowed, separation of free label from bound label present in the complex formed between both partners, and measuring the number of labeled complexes formed. Separation of free and bound label can be performed via filtration, centrifugation or other means as known by the person skilled in the art. Other techniques allow visualisation of complex formation without the need of such a separating step. For example, test systems using SPA (scincillation proximity assay) beads are based on the principle that radioactive ³H can only be measured when present in scincillation fluid. SPA beads contain scincillation fluid and can be coated with one of the binding partners. When this bead is approached and binds the other binding partner which is radioactively labeled, a signal will be detected allowing the complex to be visualised. Binding of the radioactive compound onto the scincillation bead is needed in order to result in a detectable signal; non-bound radioactive partners that stay free into the solution will not result in a detectable signal.

The protein or peptide fragments according to the invention employed in such a method may be for example in solution or coated on suspended beads as described above. Alternatively, these can be affixed to a solid support, borne on a cell or phage surface or located intracellularly.

When protein or peptide fragments are coated on solid supports, they can be tested for their binding affinity for large numbers of compounds. These can be used in different kinds of high throughput screenings in order to identify compounds having suitable binding affinity to the polypeptides according to the invention. Platform technologies or technologies based on SPR (see below) can be applied.

One may measure for example, the formation of complexes between the proteins of the invention and the compound being tested. Alternatively, one may examine the diminution or increase of complex formation between the protein according to the invention and a receptor/binding partner caused by the compound being tested.

Proteins which interact with the polypeptide of the invention may be identified by investigating protein-protein interactions using the two-hybrid vector system first proposed by Chien *et al.* (1991).

This technique is based on functional reconstitution in vivo of a transcription factor which activates a reporter gene. More particularly the technique comprises providing an appropriate host cell with a DNA construct comprising a reporter gene under the control of a promoter regulated by a transcription factor having a DNA binding domain and an activating domain, expressing in the host cell a first hybrid DNA sequence encoding a first fusion of a fragment or all of a nucleic acid sequence

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according to the invention and either said DNA binding domain or said activating domain of the transcription factor, expressing in the host at least one second hybrid DNA sequence, such as a library or the like, encoding putative binding proteins to be investigated together with the DNA binding or activating domain of the transcription factor which is not incorporated in the first fusion; detecting any binding of the proteins to be investigated with a protein according to the invention by detecting for the presence of any reporter gene product in the host cell; optionally isolating second hybrid DNA sequences encoding the binding protein.

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An example of such a technique utilizes the GAL4 protein in yeast, GAL4 is a transcriptional activator of galactose metabolism in yeast and has a separate domain for binding to activators upstream of the galactose metabolising genes as well as a protein-binding domain. Nucleotide vectors may be constructed, one of which comprises the nucleotide residues encoding the DNA binding domain of GAL4. These binding domain residues may be fused to a known protein encoding sequence, such as for example the nucleic acids according to the invention. The other vector comprises the residues encoding the protein-binding domain of GAL4. These residues are fused to residues encoding a test protein. Any interaction between polypeptides encoded by the nucleic acid according to the invention and the protein to be tested leads to transcriptional activation of a reporter molecule in a GAL-4 transcription deficient yeast cell into which the vectors have been transformed. Preferably, a reporter molecule such as B-galactosidase is activated upon restoration of transcription of the yeast galactose metabolism genes. Alternatively, other reporter proteins can be used such as EGFP (enhanced green fluorescent protein), or hEGFP. This latter has a decreased lifetime enabling the system to screen for compounds improving the interaction of studied binding partners.

The two-hybrid approach was first developed for yeast, and is an ideal screening system when looking for compounds active in killing yeast or fungi. Indeed, proteins expressed in this system will most probably carry the correct modifications as found in the pathogenic yeast strains. In addition, compounds active in this test system allow to screen and select compounds which are able to enter the cell, this selection is not possible when using *in vitro* test systems. When compounds are needed to target mammalian cells, modification of the studied proteins can b diff rent, changing the structure of corresponding prot ins. Moreover working with yeast might block certain compounds to enter the cell, which are normally able to traverse the mammalian cell m mbran. Consequently, working with mammalian two-hybrid syst m for this purpose

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will give already an immediate selection of the compounds that may enter mammalian cells.

Alternative in vitro methods can be used to investigate protein - protein interactions. Protein interaction analysis in vitro can shed light on their role in the intact cell by providing valuable information on specificity, affinity, and structure-function relation ship. Significant process in this respect has become with the advent, in the last few years, of commercially available biosensor technology. This allows to study macromolecular interactions in real-time, providing a wealth of high-quality data that can be used for kinetic analysis, affinity measurements, competition studies, etc. A major advantage of biosensor analysis is that there is no requirement for labeling on of the interacting components and then separating bound from free molecules- a fact that simplifies experimental procedures and provides more accurate measurements. The principle of surface plasmon resonance (SPR) is based on the detection of a change of the refractive index of the medium when a compound or protein binds to an immobilised partner molecule. For the SPR technology, one needs to load one of the interacting partners to the chip surface, followed by the superfusion of the second binding partner or more molecules. The second partner can be available as purified product, but alternatively a complex suspension containing this partner can also be used. Interaction of two or more compounds can be analysed, alternatively, compounds can be identified interfering or increasing this binding affinity towards each other.

SPR is not restricted to protein-protein interactions; any macromolecule with a suitable size will change the refractive index of the medium in contact with the biosensor surface and therefore give a signal. Studies have been done with protein-DNA interactions, as well as protein-lipid interactions. Moreover intact viruses, abd even cells, can also be injected over the biosensor surface, in order to analyse their binding to receptors, lectins, and so on.

Alternatively, NMR is also an excellent tool for a detailed study of protein-protein or DNA-protein interactions. Isotope edited or isotope filtered experiments whereby one compound is isotopically labeled with 15N or 13C are an ideal way to study these complexes. This method does not allow high throughput analysis of compounds interfering or enhancing molecular interactions. Nev rtheless, m dium or low throughput systems can b used to confirm results obtained by the high throughout assays or in cases wher none of the binding partners ar labeled. Other techniques which can be used to study interactions ar : overlay, ligand blotting, band-shift, co-

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immuno-precipitation, size exclusion chromatography and microcalorimetry (In. "Protein trageting Protocols" Ed. Clegg R.A. Humana Press, Totowa, New Yersey).

Compounds modulating pathways leading to apoptosis may change the activity of the polypeptide of the invention. Therefore screening tests may be setup looking for altered protein activity of the polypeptide of the invention. Based on the amino acid sequence a possible function of the polypeptide might be envisaged; activities can be confirmed and corresponding activity test can be started.

Alternatively additional tests can be performed to test the influence of the compound onto protein stability, post-translational modification, precursor processing and protein translocation. All these aspects influence the concentration and/or activity of corresponding proteins and consequently influence the effect of these onto the metabolism of the cell. Also here, medium or low throughput systems can be used to confirm results obtained by the high throughout assays.

In cases compounds need to be found to target tumor cells, screening assays will have to be used focused on the stimulation of the apoptotic pathway. This invention therefore also relates to in vitro and in vivo model systems comprising tumor tissue or cells expressing the polypeptides according to the invention which can be used to screen for therapeutic agents. In vivo modelsystems allow to test for compound efficacity but also the toxicity of these compounds can be tested. The compounds identified using any of the methods described in the invention not only include compounds which exert their effect in promoting cell death of yeast and fungi, but also include compounds which prevent or delay cell death. The latter compounds can be used to prevent or delay apoptosis of endogenic yeast or fungi in humans and other mammals which may be caused by pathogens or toxic environmental components.

According to a preferred aspect of the invention, the yeast or fungi according to any of the methods described, are chosen from *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Candida albicans*, or *Aspergillus fumigatus*.

The invention also relates to a compound identified using any of the methods of the invention.

Compounds identifiable or identified using a method according to the invention, may advantageously be used as a medicament. The invention also relates to a method for treating diseases associated with yeast or fungi comprising admixing a compound obtainable by a method of the invention with a suitable pharmaceutically acceptable carrier.

Th compounds of the invention can be used for the preparation of a medicament to treat diseases or conditions associated with yeast and fungi infections,

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for instance Candida spp., Aspergillus spp., Microsporum spp., Trichophyton spp., Fusarium spp., Zygomycetes spp., Botritis, spp., Cladosporium spp., Malassezia spp., Epidermophyton floccosum, Blastomyces dermatitidis, Coccidioides immitis, Histoplasma capsulatum, Paracoccidioides brasiliensis, Cryptococcus neoformans, and Sporothrix schenckii infections.

These compounds may also advantageously be included in a pharmaceutical composition together with a pharmaceutically acceptable carrier, diluent or excipient therefor.

A medicament according to the invention not only relates to fungistatic compounds for treating humans or mammals but also relates to fungicides for treating plants.

The invention also relates to genetically modified yeast or fungi in which modification results in the overexpression or underexpression of at least one of the nucleic acids or polypeptides of the invention, which overexpression or underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified yeast or fungi. These genetically modified organisms may have a positive effect on the endogenic flora of humans and other mammals. The genetically modified yeast or fungi can be included in a pharmaceutical composition or can be used for the preparation of a medicament for prophylactic or therapeutic use.

Also according to the invention is the use of a compound obtainable by a method of the invention for the preparation of a medicament for modifying the endogenic flora of humans and other mammals.

According to another embodiment, the invention also relates to an isolated protein which is involved in a pathway for programmed cell death of yeast or fungi selected from:

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482, or 484 or encoding a functional equivalent, derivative or bioprecursor of said prot in;
- (b) a protein having an amino acid sequence which is more than 70% similar, pr ferably more than 75% or 80% similar, more preferably more than 85%, 90 or 95% similar and most pr f rably more than 90% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304,

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306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482, or 484;

- (c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482, or 484; and.
- (d) a functional fragment of any of said proteins as defined in a) to c).

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According to the invention, the polypeptides as defined above may be used as a medicament.

Also encompassed within the present invention are antibodies, monoclonal or polyclonal, capable of specifically binding to one or more epitopes of the proteins of the invention. The term "specific binding" implies that there is substantially no cross-reaction of the antibody with other proteins.

The antibodies according to the invention may be produced according to techniques which are known to those skilled in the art. Monoclonal antibodies may be prepared using conventional hybridoma technology as described by Kohler and Milstein (1979). Polyclonal antibodies may also be prepared using conventional technology well known to those skilled in the art, and which comprises inoculating a host animal, such as a mouse, with a protein or epitope according to the invention and recovering the immune serum. The present invention also includes fragments of whole antibodies which maintain their binding activity, such as for example, Fv, F(ab') and F(ab')₂ fragments as well as single chain antibodies.

Antibodies according to the invention may also be used in a method of detecting the presenc of a polypeptide according to the invention, which method comprises reacting the antibody with a sample and identifying any protein bound to said antibody. A kit may also be provided for performing said method which comprises an antibody according to the invention and means for reacting the antibody with said sample.

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The antibodies according to the invention may be us d as a medicament or may be comprised in a pharmaceutical composition. According to a more specific embodiment, the antibodies may be used in the preparation of a medicament for treating diseases associated with yeast and fungi such as, but not restricted to, Candida albicans, Aspergillus spp., Fusarium spp., Botritis, spp., Cladosporium spp.

The invention also relates to a method of preventing infection with yeast or fungi, comprising administering a composition containing at least one polypeptide of the invention to a mammal in effective amount to stimulate the production of protective antibody or protective T-cell response.

According to another embodiment, the invention relates to a genetically modified mammalian cell or non-human organism in which modification results in the overexpression or underexpression of at least one of the nucleic acids of the invention or a human homologue thereof or at least one of the polypeptides of the invention or a human homologue thereof, which overexpression or underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified mammalian cell or in said genetically modified non-human organism.

Human homologues according to the invention can be obtained by selective hybridisation of the yeast and candida nucleic acid molecules of the invention against human genome or cDNA libraries according to methods well known in the art (Sambrook et al., 1989). Human polypeptide homologues are obtained from the corresponding human nucleic acid homologous nucleotide sequences.

The invention also relates to a method for identifying compounds for stimulating or inhibiting apoptosis comprising the use of at least one of the nucleic acid sequences of the invention or a human homologue thereof and/or at least one of the polypeptides of the invention or a human homologue thereof and/or a genetically modified mammalian cell or non-human organism as described in the invention.

The invention further relates to the compounds identifiable according to the above-described method and its use as a medicament.

The invention further relates to a method for preparing a pharmaceutical composition for treating proliferative disorders or for preventing apoptosis in certain diseases comprising admixing a compound according to claim 40 or 41 with a suitable pharmaceutically acceptable carri r.

The expression "proliferative disorders" or "proliferative dis ases" r fers to an abnormality within a patient or animal such as cancer. Normal cells start to proliferate du to a change in the coding or non-coding sequence of the DNA resulting in a swollen or distended tissue. Mutation may arise without obvious cause. An abnormal

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benign or malignant mass of tissue is formed that is not inflammatory. Cells of preexistent tissue start to divide unexpectedly and resulting cell mass possesses no physiologic function.

The expression "apoptosis" or "apoptosis-related diseases" includes diseases such as autoimmunity diseases, ischemia, diseases related with viral infections or neurodegenerations.

The invention also relates to the use of compounds obtainable by the above described methods for the preparation of a medicament for treating proliferative disorders or for preventing apoptosis in certain disorders.

According to another embodiment, the invention relates to the use of a nucleic acid molecule or a polypeptide described in the invention or human homologues thereof for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

The invention also relates to a pharmaceutical composition for use as a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases comprising a nucleic acid molecule of the invention or a human homologue thereof or a polypeptide of the invention or a human homologue thereof together with a pharmaceutically acceptable carrier diluent or excipient therefor.

The invention also relates to a vaccine for immunizing mammals against proliferative disorders or for preventing apoptosis in certain diseases comprising least one nucleic acid molecule of the invention or a human homologue thereof or at least one polypeptide of the invention or a human analogue thereof in a pharmaceutically acceptable carrier.

The invention also relates to the use of an antibody of the invention capable of binding to at least one of the polypeptides of the invention or a human homologu thereof for the preparation of a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

According to yet another embodiment, the invention relates to an expression vector comprising a human homologue of a nucleic acid sequence of the invention. Said expression vector may comprise an inducible promoter and may further comprise a sequence encoding a reporter molecule.

The invention also relates to a host cell transformed, transfect id or infected with any of the aboving described vectors.

According to another mbodiment the invention relates to a nucleic acid molecule comprising a human homologue of at least on of th nucl ic acid sequences described in the invention.

The invention also relates to an antisense molecule comprising a nucleic acid sequence capable of selectively hybridising to a nucleic acid molecule which is a human analogue of the invention.

The invention also relates to a polypeptide encoded by the nucleic acid molecule comprising said human homologues of the nucleic acids described in the invention.

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The invention, now being generally described, may be more clearly understood by reference to the following examples, which are included merely for purposes of illustration of certain aspects and embodiments of the present invention and are not intended to limit the invention. The contents of all references referred to in this text are hereby incorporated by reference.

FIGURE AND TABLE LEGENDS

- Figur 1. Saccharomyces cerevisiae sequences based on information obtained from the Saccharomyces Genome Database (SGD) (SEQ ID Nos 1 to 284)
- Figure 2. Candida albicans sequences (SEQ ID Nos 285 to 456).
- 5 Figure 3. Yeast genome macroarray containing a total of 6144 gene ORFs spotted on 2 nylon membrane filters. The filters are cut in the upper right corner for orientation and the DNA is on the labelled side of the filter. Each filter contains 2 fields and each field is divided into 8 grids, organised in 24 rows and 8 columns.
- The spots represent the genome wide expression profile without (A) and with (B) Bax modulated expression (Example 2).
 - Figure 4. Results from a second experiment analogous and analysed as described in the examples section (Example 3).
- 15 Table 1. Genes modulated by Bax expression in S. cerevisiae. This list includes all the genes for which mRNA levels changed more than fivefold in a first experiment (see Example 2). The factor by which the transcript level was affected, is expressed as the Qt value. A Qt value higher than 1 indicates upregulation while a Qt value lower than 1 indicates a downregulation. For instance, a Qt of 0.5 indicates a two-fold lower transcript level of a particular mRNA due to Bax expression in S. cerevisiae. Upregulation or downregulation of a specific mRNA is stated when Qt had a value of at least five or at most 0,21, respectively.
- 25 <u>Table 2.</u> Genes modulated by *Bax* expression in *S. cerevisiae*. This list includes all the genes for which mRNA levels changed significantly in a second experiment (see Example 3). In this experiment, the Qt values were calculated using the Pathways Software (Research Genetics).

EXAMPLES

Exampl 1. Differ ntial gene xpr ssion analysis upon Bax-induced cell death Materials and media

Bacterial strain *Escherichia coli* MC1061 (Casadaban and Cohen, 1980) was used for the construction and the amplification of plasmids. Yeast strains were grown under normal conditions on standard media (Sherman *et al.*, 1979). The *Saccharomyces cereviseae* strain INVSc1 (Invitrogen®) was transformed by means of the lithium acetate method (Schiestl and Gietz, 1989) with YIpUTyL or_YIpUTYLMuBax, after linearisation in the Ty δ element (Zhu, 1986).

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Cloning of mouse BAX cDNA

Mouse *Bax* cDNA, encoding the mouse Bax-α protein, was cloned by Pfu DNA polymerase (Stratagene®) chain reaction amplification (PCR) from an EL4/13.18 thymoma cDNA library (BCCMTM/LMBP-LIB15) by making use of the primers:

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5'-ATGGACGGGTCCGGGAGCAG-3' and

5'-TCAGCCCATCTTCTTCCAGATGGTGAG-3'.

The resulting PCR product was cloned in a *Hin*cll-openend pUC19 according to standard procedures (Sambrook J. *et al.*, 1989).

20 Plasmid constructions

The 2μ ori and the *URA3* marker gene were removed from pUT332 (Gatignol *et al.*, 1990) by successive digestions with *Cla*I and *Bgl*II. A *Bam*HI-*Hin*dIII GAL1 promoter fragment was ligated into the *Bgl*II-*Hin*dIII-opened plasmid._A *Xba*I-*Fsp*I FLP terminator fragment was inserted into this *Xba*I-*Hin*dIII(blunted)-opened plasmid so that the plasmid YIpUT was obtained. Insertion of a blunted *Eco*RI-*Bsa*AI Ty δ element in the *Kpn*I-*Aat*II-opened and blunted YIpUT resulted in the plasmid YIpUTy. Subsequent insertion of the *LEU2* marker gene, as a blunted *Bsa*AI-*Bsr*GI fragment, in the *Bam*HI-opened and blunted YIpUTy resulted in the plasmid YIpUTyL.

Mouse *Bax* cDNA was excised from pUC19 by digestion with *Xba*I and *Hin*dIII and subcloned into the *Xba*I-*Hin*dIII-opened plasmid YIpUTyL, obtaining the final expression plasmid YIpUTyLMuBax.

The plasmid YlpUTyLMuBax has been deposited in th BCCM[™]/LMBP culture collection as p5CTyGALmBax with accession number 3871 under r stricted use.

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Gen Filters

The Yeast GeneFiltersTM were purchased from Research Genetics Inc. (Huntsville, AL, USA).

The Yeast GeneFiltersTM are hybridization ready nylon membranes containing a total of 6144 gene ORFs (Open Reading Frames) individually amplified by PCR and spotted on 2 nylon membrane filters (Filter I and II). The filters are cut in the upper right corner and the DNA is on the labeled side of the filter.

Filter I contains 3072 ORFs organized into two fields (fields 1 and 2). Each field contains 1536 ORFs divided into 8 grids (A, B, C, D, E, F, G and H). The grids ar organized in 24 rows and 8 columns.

Filter II contains 3072 ORFs organized in two fields (field 3 and 4). Fields 3 and 4 are organized in the same way as fields 1 and 2.

The Yeast ORF target

The yeast filters consist of over 6000 PCR products corresponding to 6144 yeast ORFs derived from the SGD. The PCR reactions used ORF specific primer pairs designed to amplify the entire open reading frame. The primers were generated from unique sequences containing the start codon ATG and termination codon (kindly provided by M. Cherry at Stanford Genome Center). Thus the PCR product contains the complete open reading frame including the start and stop codons. These products were purified and resuspended at 50 nanograms per microliter in a colored solution to allow the printing to be monitored. A robotic device was used to spot approximately 1/10 of a microliter of the denatured PCR product solution on a positively charged nylon membrane. The DNA was then UV cross-linked to the membrane.

Results

Induction of Bax-expression in yeast cells

S. cerevsiae cells (strain INVSc1) were transformed with the expression plasmid YIpUTyLMuBax or the parental plasmid YIpUTyL as a negative control. Alternative yeast strains (such as W303-1A (Thomas and Rothstein, 1989)) with equivalent properties are known in the art and can also be used.

The Ty δ element of both plasmids allowed a stable multi-copy integration in th genome of the yeast cell. Southern analysis of the cells containing YIpUTyLMuBax reveal d the integration of 5 GAL1-controlled Bax-cass ttes near Ty elements.

The yeast cells containing YIpUTyLMuBax and the yeast cells containing YIpUTyL were grown overnight in in 10 ml minimal glucose-containing medium. The precultures were then further diluted to an OD₆₀₀ of 0,2 in 100 ml minimal glucose-containing medium and grown until an OD₆₀₀ of 1 was reached. Subsequently, the yeast cells containing YIpUTyL were washed and a dilution thereof was transferred into 100 ml galactose-containing medium and incubated for 15 hours. After this additional period the cultures reached an OD₆₀₀ of 1. The yeast cells containing YipUTyLMuBax were also washed and transferred into 100 ml galactose-containing medium and incubated for 15 hours.

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RNA isolation

Total RNA was isolated using RNApureTM Reagent (Genhunter Corporation Nashville, TN, USA) according to the GenHunter protocol. 1.5 10⁹ cells were concentrated in a microcentrifuge tube and 1ml RNApureTM Reagent was added together with 1 g of glass pearls. The yeast cells were broken by thorough mixing during five 2-minutes periods, and placed on ice in-between to avoid RNA digestion. Chloroform (150 μl) was added to the lysate and centrifuged for 10 min at 4°C and at 15000 rpm. The supernatant was transferred to a new tube and the RNA was precipitated with an equal volume of isopropanol. After 10 min incubation on ice, the RNA was pelleted by centrifugation and the pellet was washed with 70% ice-cold ethanol. The dried RNA pellet was resuspended in 50 μl RNAse free dH₂O.

First strand cDNA synthesis in the presence of α -33P dCTP

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Probes with high specific activity were prepared by first strand cDNA synthesis using total RNA isolated from INVSc1 YIpUTyLMuBax or INVSc1 YIpUTyL yeast cells and incorporation of α -³³P dCTP as follows: 2 μ I (1 μ g/mI) of Oligo dT was added to 20 μ g of total RNA in a maximal volume of 8 μ I RNase-free dH₂O and incubated at 70°C for 10 min. After cooling down on ice for 1 min, the following components were added:

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6 µl 5x concentrated First Strand Buffer (GIBCO-BRL)

1 µl 0,1 M DTT

1 μl RNas Block (40 units/μl) (Stratagene)

1,5 μ l 20 mM dXTP-solution (X = A, G and T) (Pharmacia)

1,5 µl SuperScript™ Revers Transcriptase (200 units/µl) (GIBCO-BRL)

35 10 μ l α -³³P dCTP (10mCi/ml, 3000 Ci/mmol) (Amersham)

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and incubated for 2 h at 37°C during which first strand cDNA synthesis took place.

Unincorporated label was separated from the probe on a Sephadex G-50 column (Pharmacia). The radioactivity incorporated in the probe was measured by liquid scintillation. The specific activity of the probes was 3 or 5 10⁸ cpm/µg for both the INVSc1YIpUTyL and the INVSc1YIpUTyLMuBax probe.

Additionally, the length of first strand cDNA probes was controlled on an alkaline 2% agarose gel using standard electrophoresis techniques, and resulted in the detection, via stimulated phosphorescence autoradiography, of the bulk of the fragments around 500 bp.

Hybridisation with the S. cerevisiae Yeast GeneFilters™ and signal detection

The Yeast GeneFiltersTM were successively hybridised with the α -³³P dCTP labelled cDNA probes using the MicroHybTM solution provided by the manufacturer (Research Genetics Inc., Huntsville, AL, USA). This solution was applied as well in the prehybridisation step as during hybridisation. The MicroHyb solution contains formamide to allow hybridisation to occur at lower temperatures.

The hybridisation experiment was performed essentially as follows: during prehybridisation, the Yeast GeneFiltersTM were placed in a hybridisation flask (35x250 mm) filled with 5 or 10 ml MicroHybTM solution (42°C) containing 5 µl polydA (0,5 or 1 µg/ml) and incubated for 24 hours at 42°C whilst rotating (10 rpm). After disposal of the prehybridisation solution, the denatured (3 min at 100°C) cDNA was added in 5 ml prewarmed MicroHyb solution and again incubated overnight at 42°C whilst rotating. Following two wash steps of 20 min in wash buffer (2x SSC, 1% SDS) at 50°C, a third wash step was performed in a second wash buffer (0,5x SSC, 1% SDS) for an additional 15 min at room temperature. The Yeast GeneFiltersTM were placed in a PhosphorImagerTM cassette with storage phosphorscreen. After 4 days of development the screen was developed and scanned using the PhosphorImagerTM 455 SI from Molecular Dynamics. The results of these can be seen in Figure 3.

In-between the hybridisation experiments, the filters were stripped off by incubation in 500 ml of a 0,5% SDS solution (prewarmed to near boiling temperatur) during at least 1 hour at room temperature.

Quantification of the hybridisation signals was done using the ImageQuantTM 4.1 software tool from Molecular Dynamics (Sunnyvale, CA). The quantification was performed per grid of the Yeast GeneFiltersTM, and by drawing a roster of 24 columns and 8 rows onto each grid of each filter. As such, each rectangle of the roster corresponds to a spot on the Yeast GeneFiltersTM. Subsequently, from each grid a volume-report (quantification) was drawn up and the data were transferred to a MicrosoftTM Excel sheet. Also for each grid a correction factor was calculated. Signals neighboring big and dark spots were separately quantified. For each grid, a background level was calculated.

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Statistical processing of quantification results

The statistical processing of the results was accomplished in MicrosoftTM Excel. For each grid, the following statistical functions were separately defined:

- 1. The frequency of occurrence of the values in a precisely defined intensity range(data range), established between 1000 and 61000, split up in intervals of 5000.
 - 2. The frequency in terms of percentage.
 - 3. The cumulated frequency in terms of percentage.

These numeric values were used for the graphical display of the cumulated frequency in terms of percentage.

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Subsequently, the results of the two experiments (hybridization with cDNA from YIpUTyL containing INVSc1 cells and hybridization with cDNA from YIpUTyLMuBax containing INVSc1 cells) were integrated by determination of a second range of statistical functions:

- 1. The average of the values of the two experiments for each spot on the filter.
- 2. The standard deviation on this average. This is a measure for the distribution of the values around this average.
- 3. The standard deviation in terms of percentage.

The quotient of the values of the second experiment (Bax expression) against the values from the first experiment (control) was determined. This immediately ave the factor by which the expression of a specific gene is changed upon Bax induction.

In order to process all these data and to be able to discriminate between differences in gene expression, a gene showing a standard deviation in terms of p reentage of at least 90% and a difference of a factor 5 in expression as a result of Bax induction, was identified as a differentially express d candidate gene. (Table 1). Requantification of these candidates confirmed their selection.

When the expression patt rn of all 6144 genes is compared in the two experiments, it could be concluded that the expression profile of 142 genes (this is 2,3%) has been changed with at least of factor 5. An overview of these genes as well as the factors with which they are up- or down-regulated is shown in Table 1. The sequences of these genes and the amino acid sequences which they encode ar shown in Figure 1.

Example 3 . Quantification of Hybridisation Signals using the Pathways™ software

Quantification of the hybridisation signals was done using the Pathways TM Software (Research Genetics) and these signals were normalised against all data points. Comparison of these normalised data revealed differentially expressed candidate genes. Visual inspection of the hybridisation spots confirmed their selection. An overview of these genes as well as the factors with which they are up- or down-regulated is shown in Table 2.

Surprisingly, using this Software package for analysing the results in this example and when compared to the results of example 2, some additional genes were found which expression are up-or down-regulated upon *Bax* expression in *S. cerevisiae*.

The sequences of up- and down regulated genes and the corresponding amino acid sequences from Examples 2 and 3 are shown in Figure 1.

Example 4 Search for homologues in *Candida albicans*

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Sequence similarity searches against public and commercial sequenc databases were performed with the BLAST software package (Altschul *et al.*, 1990) version 2. Both the original nucleotide sequence and the six-frame conceptual translations were used as query sequences. The used public databases were the EMBL nucleotide sequence database (Stoesser *et al.*, 1998), the SWISS-PROT protein sequence database and its supplement TrEMBL (Bairoch and Apweiler, 1998), and the ALCES *Candida albicans* sequence database (Stanford University, University of Minesota). The commercial sequence database used was the PathoSeqTM microbial genomic database (Incyte Pharmaceuticals Inc., Palo Alto, CA, USA).

Sequ nce similarity search s were performed using th BLAST software packag version 2. The identity b tween 2 sequences was calculated as perc ntage identical residues, the similarity percentag between two sequences was calculated using BLOSUM62 as a scoring matrix.

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<u>Exampl 5</u>. Screening f r comp unds modulating expression of p lypeptides involved in induction of cell death of *C. albicans*

The method proposed is based on observations (Sandbaken *et al.*, 1990; Hinnebusch and Liebman 1991; Ribogene PCT WO 95/11969, 1995) suggesting that underexpression or overexpression of any component of a process (e.g. translation) could lead to altered sensitivity to an inhibitor of a relevant step in that process. Such an inhibitor should be more potent against a cell limited by a deficiency in the macromolecule catalyzing that step and/or less potent macromolecule, as compared to the wild type (WT) cell.

Mutant yeast strains, for example, have shown that some steps of translation are sensitive to the stoichiometry of macromolecules involved. (Sandbaken *et al.*, 1990). Such strains are more sensitive to compounds which specifically perturb translation (by acting on a component that participates in translation) but are equally sensitive to compounds with other mechanisms of action.

This method thus not only provides a means to identify whether a test compound perturbs a certain process but also an indication of the site at which it exerts its effect. The component which is present in altered form or amount in a cell whos growth is affected by a test compound is potentially the site of action of the test compound.

The assay to be set up involves measurement of growth or death rate of an isogenic strain which has been modified only in a certain specific allele, relative to a wild type (WT) Candida albicans strain, in the presence of R-compounds. Strains can be ones in which the expression of a specific protein is impaired upon induction of antisense or strains which carry disruptions in an essential gene. An in silico approach to find novel genes in Candida albicans will be performed. A number of essential genes identified in this way will be disrupted (in one allele) and the resulting strains can be used for comparative growth and/or death rate screening.

30 <u>Example 6</u>. Assay for High Throughput screening for drugs

 $35~\mu l$ minimal medium (S medium + 2% galactose + 2% maltose) is transferred in a transparent flat-bottomed 96 well plate (MW96) using an automated pipetting system (Multidrop, Labsystems). A 96-channel pipettor (Hydra, Robbins Scientific) transfers 2.5 μl of R-compound at $10^{-3}~M$ in DMSO from a stock plat into the assay plate.

The selected *Candida albicans* strains (mutant and parent (CAI-4) strain) are stored as glycerol stocks (15%) at -70°C. The strains are streaked out on selective plates (SD medium) and incubated for two days at 30°C. For the parent strain, CAI-4, the medium is always supplemented with 20 µg/ml uridine. A single colony is scooped up and resuspended in 1 ml minimal medium (S medium + 2% galactose + 2% maltose). Cells are incubated at 30°C for 8 hours while shaking at 250 rpm. A 10 ml culture is inoculated at 250.000 cells/ml. Cultures are incubated at 30°C for 24 hours while shaking at 250 rpm. Cells are counted in Coulter counter and the final culture (S medium + 2% galactose + 2% maltose) is inoculated at 20.000 to 50.000 cells/ml. Cultures are grown at 30°C while shaking at 250 rpm until a final OD₆₀₀ of 0.24 (+/-0.04) is reached.

200 µl of this yeast suspension is added to all wells of MW96 plates containing R-compounds in a 450 µl total volume. MW96 plates are incubated (static) at 30°C for 48 hours.

Optical densities are measured after 48 hours.

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Test growth is expressed as a percentage of positive control growth for both mutant (x) and wild type (y) strains. The ratio (x/y) of these derived variables is calculated.

Tabl 1.

Tabl 1.		
ORF	Qt	Sequence ID Number
YAR061W	7.80	SEQ ID NO 1
YAR073W	11.19	SEQ ID NO 3
YBL048W	5.07	SEQ ID NO 5
YBL051C	5.22	SEQ ID NO 7
YBL066C	6.04	SEQ ID NO 9
YBL078C	6.94	SEQ ID NO 11
YBR072W	26.56	SEQ ID NO 13
YBR073W	5.46	SEQ ID NO 15
YBR086C	7.14	SEQ ID NO 17
YBR093C	11.05	SEQ ID NO 19
YBR181C	0.15	SEQ ID NO 21
YCL007C	20.99	SEQ ID NO 23
YCL016C	23767.57	SEQ ID NO 25
YCR052W	10.51	SEQ ID NO 27
YCR064C	14.91	SEQ ID NO 29
YCR073WA	5.92	SEQ ID NO 31
YDL010W	5.31	SEQ ID NO 33
YDL036C	5.34	SEQ ID NO 35
YDL083C	0.16	SEQ ID NO 37
YDL125C	6.80	SEQ ID NO 39
YDL133CA	0.21	SEQ ID NO 41
YDL136W	0.20	SEQ ID NO 43
YDL167C	6.37	SEQ ID NO 45
YDL184C	0.21	SEQ ID NO 47
YDL191W	0.17	SEQ ID NO 49
YDR103W	6.26	SEQ ID NO 51
YDR238C	5.75	SEQ ID NO 53
YDR259C	9.68	SEQ ID NO 55
YDR294C	8.38	SEQ ID NO 57
YDR430C	5.66	SEQ ID NO 59
YDR438W	6.47	SEQ ID NO 61
YDR450W	0.16	SEQ ID NO 63
YDR471W	0.11	SEQ ID NO 65
YDR486C	5.27	SEQ ID NO 67
YDR499W	6.14	SEQ ID NO 69
YDR507C	6.34	SEQ ID NO 71
YDR515W	5.42	SEQ ID NO 73
YDR518W	6.15	SEQ ID NO 75
YDR519W	5.57	SEQ ID NO 77
YER102W	0.19	SEQ ID NO 79
YER153C	5.63	SEQ ID NO 83
YFL014W	41.08	SEQ ID NO 85
YFL015C	5.62	SEQ ID NO 87
YFR022W	9.44	SEQ ID NO 89
YGL011C	6.14	SEQ ID NO 91
YGL031C	0.11	SEQ ID NO 93
YGL032C YGL043W	0.14	SEQ ID NO 95
YGL102C	10.74	SEQ ID NO 97
YGL102C	0.15	SEQ ID NO 99
YGL130W	0.17 8.35	SEQ ID NO 101
. GE 10000	0.33	SEQ ID NO 103

YGL213C 6.02 SEQ ID NO 107 YGL260W 6.61 SEQ ID NO 109 YGL260W 6.61 SEQ ID NO 111 YGR118W 0.17 SEQ ID NO 115 YGR118W 0.17 SEQ ID NO 115 YGR142W 8.91 SEQ ID NO 117 YGR236C 12.72 SEQ ID NO 121 YGR284C 5.95 SEQ ID NO 123 YGR285C 5.84 SEQ ID NO 127 YHR010W 0.20 SEQ ID NO 127 YHR021C 0.16 SEQ ID NO 127 YHR021C 0.16 SEQ ID NO 127 YHR021C 0.16 SEQ ID NO 129 YHR011C 0.10 SEQ ID NO 131 YHR217C 7.6 SEQ ID NO 133 YIL112W 11.15 SEQ ID NO 133 YIL115C 7.67 SEQ ID NO 137 YIL148W 0.13 SEQ ID NO 139 YIL15W 0.13 SEQ ID NO 144 YJL034W 11.61 SEQ ID NO 145 YJL179W 0.19 SEQ ID NO 153 <t< th=""><th>YGL147C</th><th>0.08</th><th>SEQ ID NO 105</th></t<>	YGL147C	0.08	SEQ ID NO 105
YGL260W 6.61 SEQ ID NO 111 YGR085C 0.16 SEQ ID NO 113 YGR118W 0.17 SEQ ID NO 113 YGR142W 8.91 SEQ ID NO 117 YGR236C 12.72 SEQ ID NO 121 YGR284C 5.95 SEQ ID NO 123 YGR285C 5.84 SEQ ID NO 125 YHR010W 0.20 SEQ ID NO 127 YHR021C 0.16 SEQ ID NO 129 YHR141C 0.10 SEQ ID NO 133 YHL112W 11.15 SEQ ID NO 133 YIL115C 7.67 SEQ ID NO 135 YIL15DC 7.67 SEQ ID NO 137 YIL148W 0.13 SEQ ID NO 139 YIL15OC 6.83 SEQ ID NO 143 YIL15OC 6.83 SEQ ID NO 145 YJL034W 11.61 SEQ ID NO 145 YJL070C 5.29 SEQ ID NO 155 YJL180C 0.14 SEQ ID NO 155 YJL181W 0.21 SEQ ID NO 155 YJL188C 0.1 SEQ ID NO 161 <	YGL213C	6.02	SEQ ID NO 107
YGR085C 0.16 SEQ ID NO 113 YGR118W 0.17 SEQ ID NO 115 YGR142W 8.91 SEQ ID NO 117 YGR236C 12.72 SEQ ID NO 121 YGR284C 5.95 SEQ ID NO 123 YGR285C 5.84 SEQ ID NO 125 YHR010W 0.20 SEQ ID NO 129 YHR021C 0.16 SEQ ID NO 129 YHR021C 0.16 SEQ ID NO 131 YHR217C 7.6 SEQ ID NO 133 YIL112W 11.15 SEQ ID NO 133 YIL148W 0.13 SEQ ID NO 137 YIL148W 0.13 SEQ ID NO 139 YIL150C 6.83 SEQ ID NO 144 YJL034W 11.61 SEQ ID NO 145 YJL070C 5.29 SEQ ID NO 147 YJL179W 0.19 SEQ ID NO 155 YJL18W 0.21 SEQ ID NO 155 YJL18Y 0.21 SEQ ID NO 157 YJL18W 0.21 SEQ ID NO 163 YJL199W 0.08 SEQ ID NO 163	YGL235W	6.23	SEQ ID NO 109
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YGR142W 8.91 SEQ ID NO 117 YGR236C 12.72 SEQ ID NO 119 YGR277C 6.27 SEQ ID NO 121 YGR284C 5.95 SEQ ID NO 123 YGR285C 5.84 SEQ ID NO 125 YHR010W 0.20 SEQ ID NO 127 YHR021C 0.16 SEQ ID NO 129 YHR141C 0.10 SEQ ID NO 131 YHR217C 7.6 SEQ ID NO 133 YIL112W 11.15 SEQ ID NO 133 YIL115C 7.67 SEQ ID NO 137 YIL148W 0.13 SEQ ID NO 143 YIL15OC 6.83 SEQ ID NO 144 YJL034W 11.61 SEQ ID NO 145 YJL035C 14.48 SEQ ID NO 145 YJL179W 0.19 SEQ ID NO 155 YJL180C 0.14 SEQ ID NO 155 YJL181W 0.21 SEQ ID NO 155 YJL188C 0.1 SEQ ID NO 166 YJL199W 0.08 SEQ ID NO 166 YJL199W 0.13 SEQ ID NO 165 <	YGR118W	0.17	SEQ ID NO 115
YGR277C 6.27 SEQ ID NO 121 YGR284C 5.95 SEQ ID NO 123 YGR285C 5.84 SEQ ID NO 125 YHR010W 0.20 SEQ ID NO 127 YHR021C 0.16 SEQ ID NO 131 YHR141C 0.10 SEQ ID NO 133 YIL112W 11.15 SEQ ID NO 133 YIL115C 7.67 SEQ ID NO 137 YIL148W 0.13 SEQ ID NO 139 YIL150C 6.83 SEQ ID NO 143 YIL167W 6.66 SEQ ID NO 143 YJL034W 11.61 SEQ ID NO 144 YJL035C 14.48 SEQ ID NO 147 YJL070C 5.29 SEQ ID NO 147 YJL179W 0.19 SEQ ID NO 153 YJL180C 0.14 SEQ ID NO 155 YJL181W 0.21 SEQ ID NO 157 YJL188C 0.1 SEQ ID NO 161 YJL199W 0.08 SEQ ID NO 163 YJL198W 0.08 SEQ ID NO 165 YJL198W 0.2 SEQ ID NO 169 <t< td=""><td>YGR142W</td><td>8.91</td><td></td></t<>	YGR142W	8.91	
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YGR285C 5.84 SEQ ID NO 125 YHR010W 0.20 SEQ ID NO 127 YHR021C 0.16 SEQ ID NO 129 YHR141C 0.10 SEQ ID NO 131 YHR217C 7.6 SEQ ID NO 133 YIL112W 11.15 SEQ ID NO 135 YIL115C 7.67 SEQ ID NO 137 YIL148W 0.13 SEQ ID NO 139 YIL150C 6.83 SEQ ID NO 141 YIL167W 6.66 SEQ ID NO 143 YJL034W 11.61 SEQ ID NO 145 YJL035C 14.48 SEQ ID NO 147 YJL070C 5.29 SEQ ID NO 151 YJL179W 0.19 SEQ ID NO 151 YJL180C 0.14 SEQ ID NO 155 YJL181W 0.21 SEQ ID NO 157 YJL188C 0.1 SEQ ID NO 163 YJL199W 0.08 SEQ ID NO 163 YJL199W 0.09 SEQ ID NO 165 YJL197W 0.13 SEQ ID NO 167 YJL198W 0.2 SEQ ID NO 173 <tr< td=""><td>YGR277C</td><td>6.27</td><td>SEQ ID NO 121</td></tr<>	YGR277C	6.27	SEQ ID NO 121
YHR010W 0.20 SEQ ID NO 127 YHR021C 0.16 SEQ ID NO 129 YHR141C 0.10 SEQ ID NO 131 YHR217C 7.6 SEQ ID NO 133 YIL112W 11.15 SEQ ID NO 135 YIL115C 7.67 SEQ ID NO 137 YIL148W 0.13 SEQ ID NO 139 YIL150C 6.83 SEQ ID NO 141 YIL167W 6.66 SEQ ID NO 143 YJL034W 11.61 SEQ ID NO 145 YJL035C 14.48 SEQ ID NO 147 YJL070C 5.29 SEQ ID NO 151 YJL179W 0.19 SEQ ID NO 153 YJL180C 0.14 SEQ ID NO 155 YJL181W 0.21 SEQ ID NO 157 YJL188C 0.1 SEQ ID NO 161 YJL19W 0.13 SEQ ID NO 163 YJL19W 0.13 SEQ ID NO 165 YJL19W 0.13 SEQ ID NO 165 YJL19W 0.13 SEQ ID NO 165 YJL19W 0.13 SEQ ID NO 177	YGR284C	5.95	SEQ ID NO 123
YHR021C 0.16 SEQ ID NO 129 YHR141C 0.10 SEQ ID NO 131 YHR217C 7.6 SEQ ID NO 133 YIL112W 11.15 SEQ ID NO 135 YIL115C 7.67 SEQ ID NO 137 YIL15C 6.83 SEQ ID NO 143 YIL15OC 6.83 SEQ ID NO 143 YIL167W 6.66 SEQ ID NO 145 YJL034W 11.61 SEQ ID NO 145 YJL035C 14.48 SEQ ID NO 147 YJL070C 5.29 SEQ ID NO 149 YJL078C 5.16 SEQ ID NO 151 YJL179W 0.19 SEQ ID NO 153 YJL180C 0.14 SEQ ID NO 155 YJL187C 0.17 SEQ ID NO 155 YJL188C 0.1 SEQ ID NO 163 YJL190C 0.09 SEQ ID NO 165 YJL197W 0.13 SEQ ID NO 165 YJL198W 0.2 SEQ ID NO 165 YJL197W 0.13 SEQ ID NO 165 YJL197W 0.13 SEQ ID NO 167	YGR285C	5.84	SEQ ID NO 125
YHR141C 0.10 SEQ ID NO 131 YHR217C 7.6 SEQ ID NO 133 YIL112W 11.15 SEQ ID NO 135 YIL115C 7.67 SEQ ID NO 137 YIL148W 0.13 SEQ ID NO 149 YIL150C 6.83 SEQ ID NO 143 YIL167W 6.66 SEQ ID NO 143 YJL034W 11.61 SEQ ID NO 145 YJL035C 14.48 SEQ ID NO 147 YJL070C 5.29 SEQ ID NO 147 YJL179W 0.19 SEQ ID NO 151 YJL179W 0.19 SEQ ID NO 155 YJL181W 0.21 SEQ ID NO 157 YJL188C 0.1 SEQ ID NO 157 YJL188C 0.1 SEQ ID NO 161 YJL189W 0.08 SEQ ID NO 165 YJL197W 0.13 SEQ ID NO 165 YJL198W 0.2 SEQ ID NO 167 YJL198W 0.2 SEQ ID NO 177 YJR049C 0.17 SEQ ID NO 173 YLR040C 10.13 SEQ ID NO 177	YHR010W	0.20	SEQ ID NO 127
YHR217C 7.6 SEQ ID NO 133 YIL112W 11.15 SEQ ID NO 135 YIL115C 7.67 SEQ ID NO 137 YIL148W 0.13 SEQ ID NO 139 YIL15OC 6.83 SEQ ID NO 141 YIL167W 6.66 SEQ ID NO 143 YJL034W 11.61 SEQ ID NO 145 YJL035C 14.48 SEQ ID NO 147 YJL070C 5.29 SEQ ID NO 149 YJL078C 5.16 SEQ ID NO 151 YJL179W 0.19 SEQ ID NO 153 YJL180C 0.14 SEQ ID NO 157 YJL187C 0.17 SEQ ID NO 157 YJL188C 0.1 SEQ ID NO 161 YJL189W 0.08 SEQ ID NO 165 YJL199W 0.13 SEQ ID NO 167 YJL198W 0.2 SEQ ID NO 167 YJL198W 0.2 SEQ ID NO 173 YJR049C 0.17 SEQ ID NO 173 YLR040C 10.13 SEQ ID NO 177 YLR088W 6.09 SEQ ID NO 177 <tr< td=""><td>YHR021C</td><td>0.16</td><td>SEQ ID NO 129</td></tr<>	YHR021C	0.16	SEQ ID NO 129
YIL112W 11.15 SEQ ID NO 135 YIL115C 7.67 SEQ ID NO 137 YIL148W 0.13 SEQ ID NO 139 YIL15OC 6.83 SEQ ID NO 141 YIL167W 6.66 SEQ ID NO 143 YJL034W 11.61 SEQ ID NO 145 YJL070C 5.29 SEQ ID NO 147 YJL078C 5.16 SEQ ID NO 151 YJL179W 0.19 SEQ ID NO 153 YJL180C 0.14 SEQ ID NO 155 YJL181W 0.21 SEQ ID NO 157 YJL187C 0.17 SEQ ID NO 161 YJL188C 0.1 SEQ ID NO 163 YJL190C 0.09 SEQ ID NO 163 YJL197W 0.13 SEQ ID NO 165 YJL198W 0.2 SEQ ID NO 167 YJL198W 0.2 SEQ ID NO 167 YJR049C 0.17 SEQ ID NO 173 YLR040C 10.13 SEQ ID NO 175 YLR048W 8.55 SEQ ID NO 177 YLR048W 6.09 SEQ ID NO 183 <tr< td=""><td>YHR141C</td><td>0.10</td><td>SEQ ID NO 131</td></tr<>	YHR141C	0.10	SEQ ID NO 131
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		1	
YML063W 0.16 SEQ ID NO 211			
	IVML063W	0.16	SEQ ID NO 211



YML128C	5.1	SEQ ID NO 213
YML130C	5.41	SEQ ID NO 215
YMR022W	6.45	SEQ ID NO 217
YMR118C	5.13	SEQ ID NO 217
YMR143W	0.08	
YMR174C		SEQ ID NO 221
YMR191W	6.75	SEQ ID NO 223
YMR230W	9.56	SEQ ID NO 225
YNL054W	0.13	SEQ ID NO 227
	5.19	SEQ ID NO 229
YNL067W	0.12	SEQ ID NO 231
YNL075W	0.16	SEQ ID NO 233
YNL096C	0.14	SEQ ID NO 235
YNL162W	0.07	SEQ ID NO 237
YNL178W	0.11	SEQ ID NO 239
YNL182C	0.18	SEQ ID NO 241
YNL190W	0.07	SEQ ID NO 243
YNL208W	5.87	SEQ ID NO 245
YNL210W	0.02	SEQ ID NO 247
YOL031C	5.32	SEQ ID NO 249
YOL048C	14.34	SEQ ID NO 251
YOR010C	7.27	SEQ ID NO 253
YOR019W	5.19	SEQ ID NO 255
YOR027W	6.03	SEQ ID NO 257
YOR031W	5.35	SEQ ID NO 259
YOR096W	0.12	SEQ ID NO 261
YOR248W	0.18	SEQ ID NO 263
YOR293W	0.11	SEQ ID NO 265
YOR312C	0.12	SEQ ID NO 267
YOR369C	0.21	SEQ ID NO 269
YPL047W	5.09	SEQ ID NO 271
YPL090C	0.1	SEQ ID NO 273
YPL137C	10.41	SEQ ID NO 275
YPL159C	5.61	SEQ ID NO 277
YPL175W	5.95	SEQ ID NO 279
YPL180W	7.68	SEQ ID NO 281
YPL218W	6.26	SEQ ID NO 283
YPR102C	0.17	SEQ ID NO 285

Table 2.

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ORF	Qt	Sequence ID Number
YGR236C	7.25	SEQ ID NO 119
YDR442W	0.049	SEQ ID NO 459
YGR182C	0.602	SEQ ID NO 467
YGR106C	0.478	SEQ ID NO 465
YKR040C	2.23	SEQ ID NO 471
YJL188C	0.075	SEQ ID NO 161
YOR096W	0.067	SEQ ID NO 261
YOR293W	0.107	SEQ ID NO 265
YDR450W	0.056	SEQ ID NO 63
YML026C	0.051	SEQ ID NO 209
YHR021C	0.114	SEQ ID NO 129
YLR167W	0.033	SEQ ID NO 183
YGL147C	0.061	SEQ ID NO 105
YGR085C	0.107	SEQ ID NO 463
YOR312C	0.083	SEQ ID NO 267
YOL127W	0.101	SEQ ID NO 473
YHR010W	0.077	SEQ ID NO 127
YDR471W	0.046	SEQ ID NO 65
YDL191W	0.128	SEQ ID NO 49
YDL136W	0.125	SEQ ID NO 43
YLR325C	0.061	SEQ ID NO 199
YJL189W	0.07	SEQ ID NO 163
YIL148W	0.145	SEQ ID NO 139
YHR141C	0.069	SEQ ID NO 131
YBL003C	0.119	SEQ ID NO 457
YDR529C	0.352	SEQ ID NO 461
YGR183C	0.781	SEQ ID NO 469

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- Use of a nucleic acid molecule encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which nucleic acid sequence is selected from:
 - (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
 - (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300,

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- (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;
- (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261,



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263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481 or 483;

- (e) a nucleic acid sequence which is more than 70% identical, preferably mor 10 than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 15 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 20 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 25 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481 or 483; and
 - (f) a nucleic acid sequence encoding a functional fragment of any of th nucleic acid sequences as specified in a) to e),
- 30 (g) the complement of any of the nucleic acid sequences as specified in a) to f), for the preparation of a medicament for treating diseases associated with yeast or fungi.
- Use of a polypeptid which is involved in a pathway ventually leading
 to programmed c II death of y ast or fungi, said polypeptide being s lected from:

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- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a protein having an amino acid sequence which is more than 70% similar, 20 preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 25 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 30 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 35 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432,

- 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;
- (c) a protein having an amino acid sequence which is more than 70% identical. preferably more than 80% identical, more preferably more than 90% 5 identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 10 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, • 15 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 20 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484; and,
 - (d) a functional fragment of any of said proteins as defined in a) to c), for the preparation of a medicament for treating diseases associated with yeast or fungi.
 - 3. A pharmaceutical or fungicidal composition comprising a nucleic acid molecule as defined in claim 1 or a polypeptide as defined in claim 2 together with a pharmaceutically acceptable carrier diluent or excipient therefor.
- 4. A vaccine for immunizing a mammal against yeast or fungal infections comprising at least one nucleic acid molecule as defined in claim 1 or at least one polypeptide as defined in claim 2 in a pharmaceutically acceptable carrier.
- A genetically modified yeast or fungus in which modification results in
 the ov rexpression or underexpression of at least one of the nucleic acids as defined in
 claim 1 or the polypeptides as defined in claim 2, which ov rexpression or

underexpr ssion of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified y ast or fungus.

6. A method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast or fungi or in metabolic pathways in which said polypeptides are involved, which method comprises:

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- (a) contacting a compound to be tested with yeast or fungal cells having a mutation which results in overexpression or underexpression of at least one of the polypeptides as defined in claim 2, in addition to contacting wild type cells with said compound,
- (b) monitoring the growth, death rate or activity of said mutated cells compared to said wild type cells; wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,
- (c) alternatively monitoring the growth, death rate or activity of said mutated cells compared to mutated cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast of fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway.
- (d) alternatively monitoring changes in morphologic and/or functional properties of components in said mutated cells caused by the addition of th compound to be tested.
- 7. A method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast and fungi or in metabolic pathways in which said polypeptides are involved, which method comprises:
 - (a) contacting a compound to be tested with yeast or fungal cells transformed, transfected or infected with an expression vector comprising an antisens sequence of at least one of the nucleic acid sequences as defined in claim
 1, which expression results in underexpression of said polypeptide, in addition to contacting one or more wild type cells with said compound,
 - (b) monitoring the growth, death rat or activity of said transformed, transfected or infected cells compared to said wild type cells; wherein differential growth or activity of said transformed, transfected or infect d yeast or fungal cells is

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indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,

- (c) alternatively monitoring the growth, death rate or activity of said transformed, transfected or infected cells compared to transformed, transfected or infected cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast of fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,
- (d) alternatively monitoring changes in morphologic and/or functional properties of components in said transformed, transfected or infected cells caused by the addition of the compound to be tested.
- 8. A method of identifying compounds which bind to or modulate th properties of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi, which method comprises:
 - (a) contacting a compound to be tested with at least one of the polypeptides as defined in claim 2,
 - (b) detecting the complex formed between the compound to be tested and said polypeptide,
 - (c) alternatively, examining the diminution of complex formation between said polypeptide and a binding partner, caused by the addition of the compound being tested.
 - (d) alternatively, examining the alteration in the functional activity of the polypeptide, caused by the addition of the compound being tested.
- 9. A method of identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises:
 - (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid molecule as defined in claim 1 joined in frame with a reporter gene,
 - (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested.

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- 10. A method according to any of claims 6 to 9 wherein said yeast or fungus is chos n from Saccharomyces cerevisiae, Schizosaccharomyces pombe, Candida albicans, or Aspergillus fumigatus.
- 5 11. A compound identifiable according to the method of any of claims 6 to 9.
 - 12. A compound according to claim 11 for use as a medicament.
- 13. A method for preparing a pharmaceutical composition for treating
 10 diseases associated with yeast or fungi comprising admixing a compound according to claim 12 with a suitable pharmaceutically acceptable carrier.
 - 14. Use of a compound according to claim 11 or 12 for the preparation of a medicament for treating diseases associated with yeast and fungi.
 - 15. Use of a compound according to claim 11 or 12 or a genetically modified organism as defined in claim 5 for the preparation of a medicament for modifying the endogenic flora of humans and other mammals.
- 16. Use of a compound according to claim 12 where the yeast or fungus is chosen from Candida spp., Aspergillus spp., Microsporum spp., Trichophyton spp., Fusarium spp., Zygomycetes spp., Botritis, spp., Cladosporium spp., Malassezia spp., Epidermophyton floccosum, Blastomyces dermatitidis, Coccidioides immitis, Histoplasma capsulatum, Paracoccidioides brasiliensis, Cryptococcus neoformans, and Sporothrix schenckii.
 - 17. A nucleic acid sequence encoding a polypeptide which is involved in a pathway for programmed cell death of yeast or fungi selected from:
- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452,

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- 454, 476, 478, 480, 482 or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;
- (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;
- (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NOs 285, 287, 289, 291, 295, 297, 299, 301, 303, 305, 307, 309, 311, 315, 317, 319, 321, 323, 325, 327, 329, 331, 337, 341, 343, 345, 347, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 379, 381, 383, 385, 387, 389, 391, 393, 397, 401, 403, 405, 407, 409, 411, 415, 417, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 475, 477, 479, 481 or 483;
- (e) a nucleic acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NOs 285, 287, 289, 291, 295, 297, 299, 301, 303, 305, 307, 309, 311, 315, 317, 319, 321, 323, 325, 327, 329, 331, 337, 341, 343, 345, 347, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 379, 381, 383, 385, 387, 389, 391, 393, 397, 401, 403, 405, 407, 409, 411, 415, 417, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 475, 477, 479, 481 or 483; and,

- (f) a nucleic acid sequence encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e),
- (g) the complement of any of the nucleic acid sequences as specified in a) to e).
- 5 18. A nucleic acid according to claim 16 characterized in that it is derived from Candida albicans.
 - 19. A nucleic acid molecule capable of selectively hybridizing to a nucleic acid sequence as defined in claim 1 or the complement thereof.
 - 20. A nucleic acid sequence according to any of claim 17 to 19 which is mRNA
- 21. A nucleic acid sequence according to any of claims 17 to 19 which is 15 DNA.

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- 22. A nucleic acid sequence according to any of claims 17 to 19 which is cDNA.
- 23. An antisense molecule comprising a nucleic acid sequence capable of selectively hybridizing to the nucleic acid sequences according to any of claims 17 to 22.
- 24. An isolated protein which is involved in a pathway for programmed cell death of yeast or fungi selected from:
 - (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484, or ncoding a functional equivalent, derivative or bioprecursor of said protein;
 - (b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308,

- 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484:
- (c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484; and,
- (d) a functional fragment of any of said proteins as defined in a) to c)

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- 25. An expression vector comprising a nucleic acid sequence according to any of claims 17 to 23.
- 26. An expression vector according to claim 25 which comprises an inducible promoter.
 - 27. An expression vector according to claim 25 or 26 which comprises a sequence encoding a reporter molecule.
 - 28. A host cell transformed, transfected or infected with the vector of any of claims 25 to 27.
- 29. A nucleic acid molecule according to any of claims 17 to 23 for use as a 30 medicament.
 - 30. A polypeptide according to claim 24 for use as a medicament.
- 31. An antibody capable of specifically binding to a polypeptide according to 35 claim 24.

- 32. An antibody according to claim 31 for use as a medicament.
- 33. A pharmaceutical composition comprising an antibody according to claim 31 or 32.

34. Use of an antibody according to claim 31 or 32, or an antibody capable of binding to at least one of the polypeptides as defined in claim 2, for the preparation of a medicament for treating diseases associated with yeast and fungi.

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- 35. Use of an antibody according to claim 34 where the fungus is *Candida albicans*.
- 36. A nucleic acid probe which comprises a fragment of at least 15 contiguous nucleotides of a nucleic acid molecule as defined in claim 17 and which selectively hybridises with any of said nucleic acid molecules.
 - 37. A nucleic acid primer which comprises a fragment of at least 15 contiguous nucleotides of a nucleic acid molecule as defined in claim 17 and which selectively amplifies any of said nucleic acid molecules.

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- 38. A genetically modified mammalian cell or non-human organism in which modification results in the overexpression or underexpression of at least one of the nucleic acids as defined in claim 1 or a human homologue thereof or at least one of the polypeptides as defined in claim 2 or a human homologue thereof, which overexpression or underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified mammalian cell or in said genetically modified non-human organism.
- 39. A method for identifying compounds for stimulating or inhibiting apoptosis comprising the use of at least one of the nucleic acid sequences as defined in claim 1 or a human homologue thereof and/or at least one of the polypeptides as defined in claim 2 or a human homologue thereof and/or a genetically modified mammalian cell or non-human organism according to claim 38.
 - 40. A compound identifiabl according to the m thod of claim 39.

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- 41. A compound according to claim 40 for use as a medicament.
- 42. A method for preparing a pharmaceutical composition for treating proliferative disorders or for preventing apoptosis in certain diseases comprising admixing a compound according to claim 40 or 41 with a suitable pharmaceutically acceptable carrier.
- 43. Use of a compound according to claim 40 or 41 for the preparation of a medicament for treating proliferative disorders or for preventing apoptosis in certain
 disorders.
 - 44. Use of a nucleic acid molecule selected from any of the nucleic acid molecules as defined in claim 1 or a human homologue thereof for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

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45. Use of a polypeptide selected from any of the polypeptides as defined in claim 2 or a human homologue thereof for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

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46. A pharmaceutical composition for use as a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases comprising a nucleic acid molecule as defined in claim 1 or a human homologue thereof or a polypeptide as defined in claim 2 or a human homologue thereof together with a pharmaceutically acceptable carrier diluent or excipient therefor.

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47. A vaccine for immunizing mammals against proliferative disorders or for preventing apoptosis in certain diseases comprising least one nucleic acid molecule as defined in claim 1 or a human homologue thereof or at least one polypeptide as defined in claim 2 or a human analogue thereof in a pharmaceutically acceptable carrier.

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48. Use of an antibody according to claim 31 or 32 or an antibody capabl of binding to at least one of the polypeptides as defined in claim 2 or a human homologue thereof for the preparation of a medicament for tr ating proliferative disorders or for the previous of apoptosis in certain diseases.

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- 49. An expression vector comprising a human homologue of a nucleic acid sequence as defined in claim 1.
- 50. An expression vector according to claim 49 which comprises an inducible promoter.

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- 51. An expression vector according to claim 49 or 50 which comprises a sequence encoding a reporter molecule.
- 52. A host cell transformed, transfected or infected with the vector of any of claims 49 to 51.
 - 53. A nucleic acid molecule comprising a human homologue of at least on of the nucleic acid sequences as defined in claim 1.
- 15 54. An antisense molecule comprising a nucleic acid sequence capable of selectively hybridising to the nucleic acid molecule of claim 53.
 - 55. A polypeptide encoded by a nucleic acid molecule according to claim 53.

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FIG. 1:

YAR061W, 704 bp, CDS: 501-704 (SEQ ID NO 1) AAAATTTGGCACTTCAGAGCTTATCGTATCTTCTCCCGGAGTTCCTCAAGACTTATACTT CAGCCCGTTTAGGAATGCATAAAAGCAAATAGGATTCGTTACAACTGCTGCAGGACTCTT TAGGACTGCATCAAGGTAAGCCTCGCTGCACCTAAACGCAAAATGTGGTTGTAACCTTTT TAATTTTTTTCTTGAACTTGTTGAGTCGTAATAAATCGTTTCTGGGAAGTGGAAGGTAAT AATGTAATGGAATCGGCGTTACTCGCATGTGCAGATATCAGCGACAAAAAGTGTTGTAGG GACGTTTCGATACCAAAATTTCCTAAATACAGCGCAGGAACATCACTACGCTAAACAAAT CGTAGCGCATACATCTGATCGAAAAAAGACAGTTCCCAAAACAATGACATATGAAGAGAC CAGCATCAAAATTTTCATCATTAACAGCATGGCTAAAAGTTATTGTTTAATATACCCATA AAAATGGGATGAATGTCAACTTTTATAAATACTCATTACTGGATTCAACAACGTATTCCT ACCCGCAATATATGACTTCTGGATATGCCTCGAATTGGAATTAG

YAR061W, 67 aa (SEQ ID NO 2) MPYHYLFLALFTYLATSNVVSGSTQACLPVGPRKNGMNVNFYKYSLLDSTTYSYPQYMTS **GYASNWN**

YAR073W, 1712 bp, CDS: 501-1712 (SEQ ID NO 3) AGTGGCTCATGATCTGTAAATGATCGGTTGACCGCAGTATTATATAATAACATCCGTATA AGTACATATACTACCATGTCTGTTCTCTACATTGCTTTTTATTCAAGATTATTGGTTTTC CTAACCGCCGCGCGCAGGTACCCCGCGCATCTCTTCTTCTCGAAGAAAGCGGAAAAA ACAAAAAAAAAGTATAAATAGTGGAGTCTTTTCCCATTTAACATTTAGAAAAAATTCG AATGGAAATTTCTTGCCGAACATTTAACCGGAGACCCTTGGCGGCTTTTTCTCAGTTTCG TGGGCTAGTACATTTTACCTAGTATGCTGGGAACTTTTTTTCCGTATTCTATTCC TTGCCTTACTTTTCTTATCATTTTTTATATAACCAATTTCAAAAATACTTTTTAACTGTC ATAGACGCATTTTGTTTATTACAAATTAAAAGAATCAAATATAATATGTGCAATTAATAA CTCCACAAGTAGCGAAAGCAATGGCCGCCATTAGAGACTACAAGACCGCACTAGATCTTA CCAAGAGCCTACCAAGACCGGATGGTTTGTCAGTGCAGGAACTGATGGACTCCAAGATCA GAGGTGGGTTGGCTTATAACGATTTTTTAATCTTACCAGGTTTAGTCGATTTTGCGTCCT CTGAAGTTAGCCTACAGACCAAGCTAACCAGGAATATTACTTTAAACATTCCATTAGTAT CCTCTCCAATGGACACTGTGACGGAATCTGAAATGGCCACTTTTATGGCTCTGTTGGATG GTATCGGTTTCATTCACCATAACTGTACTCCAGAGGACCAAGCTGACATGGTCAGAAGAG TCAAGAACTATGAAAATGGGTTTATTAACAACCCTATAGTGATTTCTCCAACTACGACCG TTGGTGAAGCTAAGAGCATGAAGGAAAAGTATGGATTTGCAGGCTTCCCTGTCACGGCAG ATGGAAAGAGAAATGCAAAGTTGGTGGGTGCCATCACCTCTCGTGATATACAATTCGTTG AGGACAACTCTTTACTCGTTCAGGATGTCATGACCAAAAACCCTGTTACCGGCGCACAAG GTATCACATTATCAGAAGGTAACGAAATTCTAAAGAAAATCAAAAAGGGTAGGCTACTGG TTGTTGATGAAAAGGGTAACTTAGTTTCTATGCTTTCCCGAACTGATTTAATGAAAAATC AGAAGTACCCATTAGCGTCCAAATCTGCCAACACCAAGCAACTGTTATGGGGTGCTTCTA TTGGGACTATGGACGCTGATAAAGAAAGACTAAGATTATTGGTAAAAGCTGGCTTGGATG TCGTCATATTGGATTCCTCTCAAGGTAACTCTATTTTCCAATTGAACATGATCAAATGGA TTAAAGAAACTTTCCCAGATTTGGAAATCATTGCTGGTAACGTTGTCACCAAGGAACAAG CTGCCAATTTGATTGCTGCCGGTGCGGACGGTTTGAGAATTGGTATGGGAACTGGCTCTA TTTGTATTACCCAAAAAGTTATGGCTTGTGGTAGGCCACAAGGTACAGCCGTCTACAACG TGTGTGAATTTGCTAACCAATTCGGTGTTCCATGTATGGCTGATGGTGGTGTTCAAAAAC ATTGGTCATATTATTACCAAAGCTTTGGCTCTTGGTTCTTCTACTGTTATGATGGGTGGT ATGTTGGCCGGTACTACCGAATCACCAGGTGA

YAR073W, 403 aa (SEO ID NO 4) MAAIRDYKTALDLTKSLPRPDGLSVQELMDSKIRGGLAYNDFLILPGLVDFASSEVSLQT KLTRNITLNIPLVSSPMDTVTESEMATFMALLDGIGFIHHNCTPEDQADMVRRVKNYENG FINNPIVISPTTTVGEAKSMKEKYGFAGFPVTADGKRNAKLVGAITSRDIOFVEDNSLLV **QDVMTKNPVTGAQGITLSEGNEILKKIKKGRLLVVDEKGNLVSMLSRTDLMKNOKYPLAS** KSANTKQLLWGASIGTMDADKERLRLLVKAGLDVVILDSSOGNSIFOLNMIKWIKETFPD LEIIAGNVVTKEQAANLIAAGADGLRIGMGTGSICITQKVMACGRPOGTAVYNVCEFANO FGVPCMADGGVQKHWSYYYQSFGSWFFYCYDGWYVGRYYRITR

WO 01/02550 PCT/BE00/00077

YBL048W, 103 aa (SEQ ID NO 6)
MILFKNLVFLPSILIGYISIRVSLLVWVNWVLVWSSCFQVAFIFSLWYFILSIYTFFYSK
KIKQIISYEPSYFVFSYRAIDLCPERVLLYFFCIFNNVVFPML

YBL051C, 2507 bp, CDS: 501-2507 (SEQ ID NO 7) GGGAAATATCAATTCCCGTATTTCAATGTTAGTAATTTGCCTTCGTAAATTACGGAATCA CATAGCTTTCATTTGTTCCTTTGATATATTTCCCTACTACATACTCTTTTCAATAACTC TACAGGGTCTGACATTTTTAACTTTCAGGTTAATGATGGTGTTCTTACTATATTCTCGAG TCGTACAGAAGTTAGTTCAGATAAACTGCTTCGGTGCTGCCCACTTCTTATCATTACTTC AACTTTACCTTCCCTATACCTGTGTGTCCTTATTAATTCAAGTTAATCCGAGGTAATAGA TTAGGGTAACCTTCAATGATGTCACGAAACACGGATGCTGCAACTTTGCGATTTTTTCCT GGAAAAGAATAACAATTAAAGGCAGCCTTTCAGCTGAGATTACCAGCAGGTCTTTGGAGA GTGTTCAACAACAATAAGAAATGGAGACCAGTTCTTTTGAGAATGCTCCTCCTGCAGCCA TCAATGATGCTCAGGATAATAATATAAATACGGAGACTAATGACCAGGAAACAAATCAGC AATCTATCGAAACTAGAGATGCAATTGACAAAGAAAACGGTGTGCAAACGGAAACTGGTG AGAACTCTGCAAAAAATGCCGAACAAAACGTTTCTTCTACAAATTTGAATAATGCCCCCA CCAATGGTGCTTTGGACGATGATGTTATCCCAAATGCTATTGTTATTAAAAACATTCCGT ATGCCTTCAATTACCACTTTGATAACGGTATTTTCAGAGGACTAGCCTTTGCGAATTTCA CCACTCCTGAAGAAACTACTCAAGTGATAACTTCTTTGAATGGAAAGGAAATCAGCGGGA GGGAGAAGAGAGAAAAGAGGACAATTAGAAGAACAACACAGATCGTCATCTAATCTTT TATTCTCGACTCTAATGAACGGCATTAATGCTAATAGCATGATGAACAGTCCAATGAATA ATACCATTAACAATAACAGTTCTAATAACAACAATAGTGGTAACATCATTCTGAACCAAC CCCAGATGTCCACTGAGAGATTTTATGCGCCTTTACCATCAACTTCCACTTTGCCTCTCC CACCCCAACAACTGGACTTCAATGACCCTGACACTTTGGAAATTTATTCCCAATTATTGT TATTTAAGGATAGAGAAAAGTATTATTACGAGTTGGCTTATCCCATGGGTATATCCGCTT CCCACAAGAGAATTATCAATGTTTTGTGCTCGTACTTAGGGCTAGTAGAAGTATATGATC CAAGATTTATTATCAGAAGAAAGATTCTGGATCATGCTAATTTACAATCTCATTTGC AACAACAAGGTCAAATGACATCTGCTCATCCTTTGCAGCCAAACTCCACTGGCGGCTCCA TGAATAGGTCACAATCTTATACAAGTTTGTTACAGGCCCATGCAGCAGCTGCAGCGAATA GTATTAGCAATCAGGCCGTTAACAATTCTTCCAACAGCAATACTATTAACAGTAATAACG GTAACGGTAACAATGTCATCATTAATAACAATAGCGCCAGCTCAACACCAAAAATTTCTT CACAGGGACAATTCTCCATGCAACCAACACTAACCTCACCTAAAATGAACATACACCATA GTTCTCAATACAATTCCGCAGACCAACCGCAACAACCTCAACCACAAACACAGCAAAATG TTCAGTCAGCTGCGCAACAACAACAATCTTTTTTAAGACAACAAGCTACTTTAACACCAT CCTCAAGAATTCCATCCGGTTATTCTGCCAACCATTATCAAATCAATTCCGTTAATCCCT TACTGAGAAATTCTCAAATTTCACCTCCAAATTCACAAATCCCAATCAACAGCCAAACCC

TATCCCAAGCGCAACCACCAGCACAGTCCCAAACTCAACAACGGGTACCAGTGGCATACC AAAATGCTTCATTGTCTTCCCAGCAGTTGTACAACCTTAACGGCCCATCTTCAGCAAACT CACAGTCCCAACTGCTTCCACAGCACACAAATGGCTCAGTACATTCTAATTTCTCATATC AGTCTTATCACGATGAGTCCATGTTGTCCGCACACAATTTGAATAGTGCCGACTTGATCT ATAAATCTTTGAGTCACTCTGGACTAGATGATGGCTTGGAACAGGGCTTGAATCTTAAGCGGACTGGATTTACAAAACCAAAACAAGAAGAATCTATGGTAA

YBL051C, 668 aa (SEQ ID NO 8)
METSSFENAPPAAINDAQDNNINTETNDQETNQQSIETRDAIDKENGVQTETGENSAKNA
EQNVSSTNLNNAPTNGALDDDVIPNAIVIKNIPFAIKKEQLLDIIEEMDLPLPYAFNYHF
DNGIFRGLAFANFTTPEETTQVITSLNGKEISGRKLKVEYKKMLPQAERERIEREKREKR
GQLEEQHRSSSNLSLDSLSKMSGSGNNNTSNNQLFSTLMNGINANSMMNSPMNNTINNNS
SNNNNSGNIILNQPSLSAQHTSSSLYQTNVNNQAQMSTERFYAPLPSTSTLPLPPQQLDF
NDPDTLEIYSQLLLFKDREKYYYELAYPMGISASHKRIINVLCSYLGLVEVYDPRFIIIR
RKILDHANLQSHLQQQGQMTSAHPLQPNSTGGSMNRSQSYTSLLQAHAAAAANSISNQAV
NNSSNSNTINSNNGNGNNVIINNNSASSTPKISSQGQFSMQPTLTSPKMNIHHSSQYNSA
DQPQQPQPQTQQNVQSAAQQQQSFLRQQATLTPSSRIPSGYSANHYQINSVNPLLRNSQI
SPPNSQIPINSQTLSQAQPPAQSQTQQRVPVAYQNASLSSQQLYNLNGPSSANSQSQLLP
QHTNGSVHSNFSYQSYHDESMLSAHNLNSADLIYKSLSHSGLDDGLEQGLNRSLSGLDLQ
NQNKKNLW

YBL066C, 3674 bp, CDS: 501-3674 (SEQ ID NO 9) ATCCCAAGAAGAAGATTAGACTGATTTTTACCTACCCTTCCACCGTCGGAAGAAACACTT CGAAGGCTAAATTTGGTCAATTTAATGAAATTAAACCCTATTTAAGATTCACCAAGTCGA ACTTTTATCTATCTTTCATTCTTATTATATCTCATCTCGTACGAAGGGCCGCTCATTGGA TAATAAACTCTCTGCAGAAACCTTAATGTCAAAGGTCCCGTATACAGATTATATTGGCTC TGCGTATACGCATTCTCGTCATGGTGAAGGATAATCGAGATTCTGACCAAGACCAAGATT TTAGTTCTGCTCACATGAAAAGACAACCGGAGCAGCAACAGTTGCAACAGCACCAGTTCC CAAGTAAGAAACAACGAATATCTCACCATGATGACAGTCATCAAATCAACCATAGACCAG TTACCTCATGTACACATTGTAGACAGCACAAAATCAAATGCGATGCTAGTCAAAATTTCC GGCCTAAGAAGGGCTCACAGTTGCAACTACTGAGACAAGATGTGGATGAAATCAAATCTA AACTCGATACTCTTCTGGCCAATGACAGCGTTTTCGTTCATCTTTTACAACAGATTCCCA TGGGCAATAGCCTTTTGAATAAGCTCAATCTGCATCCAACTCCAACTCCGGGTACTATTA TCCCTAACCCAGATTCTTCTCCTTCCTCAGGTTCTCCAACTTCTTCCGCGGCTCAACGAG ATTCTAAGGTTTCAGTTCAAACTTATTTGTCCAGGGAACCCCAACTCTTACAAGCAAATC AGGGCAGCAATACGAATAAATTTAAAGCAAATAATGAAGCATCTTCTCACATGACGTTGC GCGCATCTTCTTTAGCGCAAGATTCGAAAGGCTTGGTTGCAACAGAGCCAAATAAGCTGC CCCCGCTGCTAAATGACTCAGCATTGCCTAATAATTCAAAAGAATCTTTACCTCCTGCTT TGCAAATGGCTTTTTATAAGAACAACTCTGCAGGTAACACTCCGAACGGCCCCTTCTCTC CAATTCAAAAAACATATTCCCCTCATACTACGTCGACCACCGTTACAACGACAACAAATC AACCACCATTTGCAGCAACAAGCCACGTAGCAACAATAACAATGCAGATAGGACGAAGA CGCCGGTAGTAGCCACCACCACGACTATGCCATTATTGCCTTCGCCGCATGCAAATGTAG ATGAGTTTGTACTGGGCGATATTAGTATTTCCATTGAAAAAGCGAATAGATTACACCATA TTTTCGTGACTAGGTATCTGCCGTATTTTCCTATTATGTATTCCAATAACGCCACCGAAT TATACTCCCAATCTCAGTTGCTTTTCTGGACCGTGATGTTGACGGCATGTCTGATC CTGAACCGACGATGTATTGCAAGCTAAGCTCTTTGATCAAGCAACTTGCCATAGAGACCT GCTGGATAAGAACACCTAGATCCACACATATTTCGCAAGCTTTGTTAATATTGTGCATTT GGCCTTTGCCTAACCAAAAAGTCCTAGATGATTGTTCTTACCGTTTTGTAGGATTAGCAA AGTCACTGTCTTATCAATTAGGTTTGCACAGAGGTGAATTCATTTCTGAATTCACAAGAA CTCAAACATCAATGCCAAATGCAGAAAAGTGGAGAACTAGGACTTGGCTGGGAATATTTT TATTAGAAAAAGCCTTATCCTGTGGTGACGAAGAATCAGAAGAAGATAACAATGACAGTA TTGACAATAACAACAATGATAAAAGGAACAAGAAGACGAGCCGCACGTTGAAAGTAAAT ACAAACTACCGGGCAGTTTTAGAAGATTGCTCAGCCTGGCGAATTTCCAAGCAAAATTGT CTCATATCATTGGTTCTTCCACTTCCAGTCCTGATGGTTTATTGGAACCAAAGTATCGTG

CTGAGACACTGTCCATCTTGGGAAAAGAGTTAGATTTATTAGCAAAAACTTTAAATTTCC CATTCCTACCGAAACACCTCCTACCGATCAAATTCCATATGTCACAGAGGCCTATCTAA TGCCTATTTATATTAGACAAGCTGCTACATTTTCTGCACTGATTCTCTTTAAATTGCAGT TGACTCCTTTACTTCCTGACAATATTTTGATTCAGCAAGGCAATCCGTGGTCACTATCC ATAGACTTTATAGAAATCAGTTAACTGCGTGGGCCACTAGTGTTGAGAATGATATTTCGA GAACTGCAAGTATGTTAGAAAAACTGAACTTCGTACTGATCATGCATCCAGAAGTTTTTG TGGAAGAAGACGGTATTATTTCTAGGATGAGATCACATTTAACAGGGTCTCTATTCTATG ATTTGGTTTGGTGTGTTCACGAGGCGAGAAGAAGGGAAATGGATCCCGAATATAACAAGC AAGCCTTAGAGAAAGCCGCTAAGAAAAGAAAATTTTCCTCAAATGGTATCTACAATGGCA CTTCGTCTACGGGTGGCATAACGGACAGAAAACTATATCCATTGCCACTATATAACCATA TCTCCAGAGATGACTTTGAAACTGTAACAAAAACAACACCAAGTGGAACCACTGTTACCA CTTTAGTTCCTACTAAGAATGCCTTAAAGCAGGCAGAAAAGCTAGCCAAGACAAATAACG GAGATTCTGACGGTTCTATAATGGAGATTAACGGGATACCTCTTTCCATGCTCGGGGAAA CAGGCAGCGTAAAATTTCAAAGTTTATTCGCTAATACCTCGAATAGTAACGATTATAATA ATAATAGGACGTTATTGGATGCGTCTAATGACATATCAATTCCCTCTAATTCAATTTATC CAGTGGCTTCTGTCCCCGCTTCGAATAACAATCCACAAAGTACTAAGGTAGACTATTATA GTAACGGACCTAGTGTAATTCCTGATCTCTCCATGAAAAGATCAGTAAGCACTCCCGTTA ATCATTTTCCTGCGTCCGTTCCAGGGTTAAGGAACCACCCCGTTGGCAACTTATCTAATA ATGTTACATTGGGAATAGACCACCCTATTCCAAGGGAGCACAGTAATTTACAAAATGTCA CCATGAATTATAATAATCAATTCAGCAACGCCAACGCGATTGGAAGATCACAAAGTAGTA TGTCCCATTCACGTACACCTTTGTTTCGGTCAATATATGACAGTTGGATTCCGCGTCCGA **CCCCGGTCCTCTAA**

YBL066C, 1057 aa (SEQ ID NO 10) MVKDNRDSDQDQDFSSAHMKRQPEQQQLQQHQFPSKKQRISHHDDSHQINHRPVTSCTHC RQHKIKCDASQNFPHPCSRCEKIGLHCEINPQFRPKKGSQLQLLRQDVDEIKSKLDTLLA NDSVFVHLLQQIPMGNSLLNKLNLHPTPTPGTIIPNPDSSPSSGSPTSSAAQRDSKVSVQ TYLSREPQLLQANQGSNTNKFKANNEASSHMTLRASSLAQDSKGLVATEPNKLPPLLNDS ALPNNSKESLPPALQMAFYKNNSAGNTPNGPFSPIQKTYSPHTTSTTVTTTTNQPPFAAT SHVATNNNADRTKTPVVATTTTMPLLPSPHANVDEFVLGDISISIEKANRLHHIFVTRYL PYFPIMYSNNATELYSQSQLLFWTVMLTACLSDPEPTMYCKLSSLIKQLAIETCWIRTPR STHISQALLILCIWPLPNQKVLDDCSYRFVGLAKSLSYQLGLHRGEFISEFTRTQTSMPN **AEKWRTRTWLGIFFAELCWASILGLPPTSQTDYLLEKALSCGDEESEEDNNDSIDNNNND** KRNKKDEPHVESKYKLPGSFRRLLSLANFQAKLSHIIGSSTSSPDGLLEPKYRAETLSIL GKELDLLAKTLNFQSDDTVNIYFLYVKLTVCCFAFLPETPPTDQIPYVTEAYLTATKIVT LLNNLLETHQLIELPIYIRQAATFSALILFKLQLTPLLPDKYFDSARQSVVTIHRLYRNQ LTAWATSVENDISRTASMLEKLNFVLIMHPEVFVEEDGIISRMRSHLTGSLFYDLVWCVH EARRREMDPEYNKQALEKAAKKRKFSSNGIYNGTSSTGGITDRKLYPLPLYNHISRDDFE TVTKTTPSGTTVTTLVPTKNALKQAEKLAKTNNGDSDGSIMEINGIPLSMLGETGSVKFQ SLFANTSNSNDYNNNRTLLDASNDISIPSNSIYPVASVPASNNNPQSTKVDYYSNGPSVI PDLSMKRSVSTPVNHFPASVPGLRNHPVGNLSNNVTLGIDHPIPREHSNLQNVTMNYNNQ FSNANAIGRSQSSMSHSRTPLFRSIYDSWIPRPTPVL

WO 01/02550 PCT/BE00/00077

CATTTGGCAGGTAG

YBL078C, 117 aa (SEQ ID NO 12) MKSTFKSEYPFEKRKAESERIADRFKNRIPVICEKAEKSDIPEIDKRKYLVPADLTVGQF VYVIRKRIMLPPEKAIFIFVNDTLPPTAALMSAIYQEHKDKDGFLYVTYSGENTFGR

YBR072W, 1145 bp, CDS: 501-1145 (SEQ ID NO 13) GCAGCAGCAACTCCGTGTGTACCCCTAACTCCGTGTGTACCCCTAAAGAACCTTGCCTGT ATGCGTCCAAAAATATAGGGTGCTCGTAACAGTAAGGTATTCGCACTTAGCGTGCTCGCA ACACAAAATTAAGTAATATGCGAGTTTTAGATGTCCTTGCGGATCTATGCACGTTCTTGA GTGGTATTTCATAACAACGGTTCTTTTTCACCCTTATTCCTAAACATATAAATAGGACCT CCATTAGTTAGAGATCTGTTTTTAATCCATTCACCTTTCATTCTACTCTCTTATACTAAT AAAACCACCGATAAAGATATATCAGATCTCTATTAAAACAGGTATCCAAAAAAGCAAACA AACAAACTAAACAAATTAACATGTCATTTAACAGTCCATTTTTTGATTTCTTTGACAACA TCAACAACGAAGTTGATGCCTTTAACAGATTGCTGGGTGAAGGCGGCTTAAGAGGCTACG CACCAAGACGTCAGTTAGCAAACACACCCGCAAAGGATTCTACTGGCAAGGAAGTTGCTA GACCAAATAACTATGCTGGCGCTCTTTATGATCCCAGAGATGAAACCTTAGATGATTGGT TCGACAATGACTTGTCCCTGTTCCCATCTGGTTTCGGTTTCCCTAGAAGTGTCGCAGTTC CAGTTGATATTTTGGACCATGACAACAACTACGAGTTGAAAGTCGTGGTTCCTGGTGTCA AAAGCAAGAAGGACATTGATATTGAGTACCATCAAAACAAGAACCAAATTTTGGTTTCTG GTGAAATTCCATCTACCTTGAATGAAGAGAGTAAAGACAAGGTCAAGGTCAAGGAGAGCA GCTCTGGTAAGTTCAAGAGAGTCATCACTTTGCCAGACTACCCAGGTGTGGATGCAGACA ACATTAAAGCAGACTACGCAAATGGTGTTTTGACATTAACAGTTCCAAAATTGAAGCCTC AGAAGGATGGTAAGAACCACGTCAAGAAGATTGAGGTTTCTTCTCAAGAATCGTGGGGTA ACTAA

YBR072W, 214 aa (SEQ ID NO 14)
MSFNSPFFDFFDNINNEVDAFNRLLGEGGLRGYAPRRQLANTPAKDSTGKEVARPNNYAG
ALYDPRDETLDDWFDNDLSLFPSGFGFPRSVAVPVDILDHDNNYELKVVVPGVKSKKDID
IEYHQNKNQILVSGEIPSTLNEESKDKVKVKESSSGKFKRVITLPDYPGVDADNIKADYA
NGVLTLTVPKLKPQKDGKNHVKKIEVSSQESWGN

YBR073W, 3377 bp, CDS: 501-3377 (SEQ ID NO 15) AGAAGGATGGTAAGAACCACGTCAAGAAGATTGAGGTTTCTTCTCAAGAATCGTGGGGTA TGGCTTGAAACATATGTCATCACATCTGAGCGATTTTACCTCTTAGAATTAGTTTAGATA TATATGAGTTGATGAATAAATAGTTATAAAAACTTGCTTTGGCTTCGATATATGACCGTT ATTTTTGACTAAGTTTTAACGAAGGAATCTAACCTCGTTCTTGTAATTACCAAAATCTTC AACAACGCGCTGTTGGAGGTATCTCTATGGATGTGGCTTGAAATATGGATGTCTTGCCTA CTTCTACTTCTGGGAAAGGCATTTTTACTCGATCGCGTTAATATATGCATCAAGAAAATA TCCTACAGGAGGTAAAAAACAGCTCGGTATATCAAACGGTATTTGATTCCGGTACTACTC AAATGCAGATACCGAAATATGAGAACAAGCCATTCAAGCCTCCAAGAAGGGTTGGATCAA ATAAGTACACAACTCAAACCAACCGCCACTGCAGTCACAACAGCCCCTATATCTAAAG CCAAAGTTACTGTCAACTTGAAAAGAAGCATTTCGGCGGGACCTACTTTAAATCTTGCCA AGAAGCCGAATAATCTGTCCTCAAATGAAAACACTAGATATTTTACTATCATGTACAGGA AGCCTACTACCAAAAAGCACAAGACTTGGAGTGGTGATGGCTACGCTACCTTAAAAGCCA GTAGCGATAAGTTATGCTTTTATAACGAAGCAGGGAAATTTCTTGGGTCAAGTATGCTAC CAAGTGATTCAGATTCTCTCTCGAAACTCTTTTCAAAGCAGGCTCCAATGAAGTACAAT TGGATTACGAATTGAAGGAAAATGCAGAAATACGTAGCGCCAAAGAAGCCTTATCACAAA ACATGGGAAATCCCAGCCCACCGACCACAAGCACAACAGAAACAGTGCCTTCTACGAAGA ATGACGGTGGCAAATACCAAATGCCTCTGTCTCAGCTGTTTTCACTAAACACTGTGAAAA GATTCAAATCAGTAACAAAGCAAACAAATGAACACATGACCACAGTACCTAAAACCAGTC AAAATTCCAAAGCCAAAAAATATTATCCAGTATTTGATGTCAACAAAATCGATAATCCTA TAGTAATGAACAAAAATGCAGCCGCTGAAGTTGACGTAATTGTTGATCCATTACTGGGCA AATTCTTGCGCCCTCATCAGAGGGAAGGGGTGAAGTTCATGTATGATTGCTTAATGGGCT TGGCAAGACCAACTATTGAAAATCCGGATATCGATTGTACTACTAAAAGTTTAGTGTTAG

AAAATGACTCAGATATTAGTGGATGCCTTTTTGGCTGATGATATGGGTTTAGGTAAAACAC TAATGAGTATAACTTTGATTTGGACATTAATTAGGCAAACTCCTTTTGCATCAAAAGTTT CATGTTCGCAATCAGGCATACCATTAACTGGACTTTGTAAGAAGATTTTAGTCGTTTGTC CCGTTACTTTAATAGGAAATTGGAAAAGAGAATTTGGAAAAATGGTTAAATTTGTCAAGAA TAGGTGTTTTGACATTAAGCTCAAGGAATTCTCCTGATATGGATAAAATGGCTGTCAGAA ATTTTTTAAAAGTGCAACGAACTTATCAAGTCTTGATTATTGGCTACGAAAAACTCTTGA GCCATCGACTAAAAAACGGGGCTTCTAAAATTTTAAATACGCTGAAGAGTTTAGACATAA GAAGGAAGCTTTTGCTTACGGGAACTCCTATACAAAATGATCTTAATGAGTTTTTCACTA TTATAGATTTCATAAACCCAGGAATCCTTGGAAGCTTCGCTTCTTTCAAAAGAAGATTCA TTATCCCTATAACTAGAGCCAGAGACACTGCAAACAGATACAACGAAGAATTGTTGGAAA CAAATGCGATTTTAGAAAAGTACCTTCCTCCAAAGACGGATATAATTTTATTCTGTAAAC CATACAGCCAACAGATATTGGCATTCAAAGATATTTTGCAGGGCGCACGTTTAGATTTTTG GACAATTGACGTTCAGTTCTTCGCTAGGACTAATAACATTACTGAAAAAAGGTTTGTAACT CTCCTGGATTGGTTGGCTCAGATCCCTATTACAAATCACATATAAAGGATACCCAATCTC AGGACAGCTATAGTCGTTCTTTGAACTCTGGTAAGTTAAAGGTATTAATGACATTACTAG AAGGTATTAGGAAGGGTACCAAGGAGAAGGTCGTCGTAGTGTCTAACTACACTCAAACAT TGGATATAATTGAAAATTTGATGAATATGGCTGGGATGTCACATTGCAGACTCGACGGTT CCATACCTGCTAAACAAAGGGACTCTATCGTCACATCTTTCAATCGGAATCCAGCCATAT GACTTATTTATTTGATAATGATTGGAATCCTTCAGTAGATTTGCAAGCGATGTCACGAA TTCATAGAGATGGTCAAAAAAAGCCGTGCTTCATATATAGACTTGTCACAACTGGGTGTA TCGATGAGAAAATATTGCAAAGGCAATTAATGAAGAACAGTTTGAGCCAAAAATTTCTAG GTGACTCGGAGATGAGAAATAAAGAATCTTCTAATGATGATCTTTTCAATAAAGAGGACT TGAAGGACCTGTTTTCTGTCCATACAGATACCAAGAGTAACACACATGACTTAATTTGTT CTTGCGATGGTTTAGGTGAGGAAATTGAATATCCTGAAACAAATCAACAGCAGAACACCG TAGAGCTGAGAAAGCGTAGCACTACGACATGGACAAGTGCGCTGGATTTACAAAAGAAAA TGAATGAAGCAGCCACCAACGATGATGCCAAAAAGTCACAATACATTAGGCAATGTCTCG TTCATTATAAGCATATCGATCCAGCAAGACAAGATGAATTATTTGATGAGGTTATCACAG ATTCGTTCACCGAATTGAAAGATAGTATTACCTTTGCGTTTGTAAAGCCCCGGCGAGATAT **GTCTCAGAGAACAATGA**

YBR073W, 958 aa (SEQ ID NO 16) MAVISVKPRRREKILQEVKNSSVYQTVFDSGTTQMQIPKYENKPFKPPRRVGSNKYTQLK PTATAVTTAPISKAKVTVNLKRSISAGPTLNLAKKPNNLSSNENTRYFTIMYRKPTTKKH KTWSGDGYATLKASSDKLCFYNEAGKFLGSSMLPSDSDSLFETLFKAGSNEVQLDYELKE NAEIRSAKEALSQNMGNPSPPTTSTTETVPSTKNDGGKYQMPLSQLFSLNTVKRFKSVTK OTNEHMTTVPKTSQNSKAKKYYPVFDVNKIDNPIVMNKNAAAEVDVIVDPLLGKFLRPHQ REGVKFMYDCLMGLARPTIENPDIDCTTKSLVLENDSDISGCLLADDMGLGKTLMSITLI WTLIRQTPFASKVSCSQSGIPLTGLCKKILVVCPVTLIGNWKREFGKWLNLSRIGVLTLS SRNSPDMDKMAVRNFLKVQRTYQVLIIGYEKLLSVSEELEKNKHLIDMLVCDEGHRLKNG **ASKILNTLKSLDIRRKLLLTGTPIQNDLNEFFTIIDFINPGILGSFASFKRRFIIPITRA** RDTANRYNEELLEKGEERSKEMIEITKRFILRRTNAILEKYLPPKTDIILFCKPYSQQIL **AFKDILQGARLDFGQLTFSSSLGLITLLKKVCNSPGLVGSDPYYKSHIKDTQSQDSYSRS** LNSGKLKVLMTLLEGIRKGTKEKVVVVSNYTQTLDIIENLMNMAGMSHCRLDGSIPAKQR DSIVTSFNRNPAIFGFLLSAKSGGVGLNLVGRSRLILFDNDWNPSVDLQAMSRIHRDGQK KPCFIYRLVTTGCIDEKILQRQLMKNSLSQKFLGDSEMRNKESSNDDLFNKEDLKDLFSV HTDTKSNTHDLICSCDGLGEEIEYPETNQQQNTVELRKRSTTTWTSALDLQKKMNEAATN DDAKKSQYIRQCLVHYKHIDPARQDELFDEVITDSFTELKDSITFAFVKPGEICLREQ

CACAAGCGGTTGAGCATACTATGTCGCAGACAATTACATCTCTAGATCCGAATTGTGTTA TTGTATTCAATAAAACTTCGAGTGCAAACGAGAAGAGTTTGAATGTCGAATTCAAACGTT TGAATATACATTCTATTATCGAACCTGGCCATGATCTGCAAACAAGCTATGCGTTTATTA GAATCCATCAGGATAATGCGAAACCGCTTTTTTCATTTTGCAGAATCTGGACTTCATTG **AATCCATCATACCATATCATGATACTGAATTGTCCGATGATTTGCATAAACTGATTTCTA** TCAGCAAATCAAAAATACTGGAGGCTCCAAAACAGTATGAGTTGTACAACCTATCGAATT TGACCAATAATCCCAAACAATCCTTATATTTTGCATTCTTACAGAACTATATAAAATGGT TGATTCCCTTCTCCTTTTTTGGATTATCAATTAGATTTTTATCTAATTTTACGTATGAAT TCAATTCCACATACTCGCTGTTCGCCATCCTATGGACATTGTCATTTACAGCCTTTTGGC TTTATAAATATGAACCATTTTGGTCTGATAGACTGAGTAAATACTCATCATTTTCTACCA TTGAGTTTCTTCAAGATAAACAGAAAGCCCAAAAAAAAGCTAGTTCGGTTATCATGTTGA AGAAATGTTGTTTTATTCCTGTGGCTTTGTTGTTTGGCGCAATATTACTATCATTCCAGC TATATTGTTTTGCGTTGGAAATTTTCTACAAGCAAATTTATAACGGCCCAATGATTTCCA TCTTGTCTTTTTTGCCTACTATACTTATTTGCACGTTTACTCCGGTTTTAACTGTGATTT ACAACAATATTTCGTAGAACCAATGACAAAGTGGGAAAATCATAGCAGTGTTGTGAATG CAAAGAAATCTAAAGAAGCTAAGAACTTTGTTATTATTTTTCTATCCAGTTACGTTCCCC TATTAATTACACTATTTCTTTATCTGCCAATGGGGCATTTGTTGACCGCAGAAATAAGAA TTCAATTTAGCATGGAAAACTTTGTTCCAAGCCTTGTTAGCATTGCTCAGCAGAAAATTA ATGGACCAAATCCTAACTTTGTCAAAGCTGAGAGTGAAATCGGTAAAGCTCAACTCAGCT CATCAGATATGAAAATTTGGTCAAAGGTTAAGTCGTACCAAACAGACCCCTGGGGAGCAA CATTTGATTTGGACGCCAACTTCAAAAAGCTTCTTCTACAATTCGGGTATCTTGTTATGT TTTCTACAATTTGGCCACTAGCTCCATTTATCTGTTTGATAGTCAATTTGATTGTTTACC AAGTCGATTTGAGGAAAGCTGTGCTTTATAGTAAACCTGAGTATTTTCCATTTCCAATCT ACGATAAGCCATCCTCTGTGTCTAATACCCAAAAACTGACGGTTGGTCTATGGAACTCTG TCTTAGTTATGTTCTCCATCTTAGGTTGTGTTATCACTGCTACTTTGACCTATATGTACC ACCTAGCAAATCCAATAAACCACTCGTGGATAAATATTGTACTATATGCTGTTTTTATTG AGCATGTTAGTGTTGCTATTTTCTTTCTTTTCTCTAGTATTTTGAAATCTTCCCATGATG ACGTTGCAAATGGCATTGTGCCAAAGCATGTAGTTAACGTGCAAAACCCACCAAAACAAG AAGTCTTTGAAAAAATTCCCTCCCTGAATTTAATTCGAATAACGAAAAAGAACTAGTTC CTTCTGCCAATGGATATGAGGCACATGCTGCCACTCATGCCAACAATGATCCGTCTTCTT TATCCTCAGCCTCCTCGCCTTCATTATCTTCTTCTTCTTCTAGCAGCAAAACCGGTGTAG TCAAAGCTGTTGATAACGATACAGCCGGATCTGCTGGTAAAAAGCCATTGGCCACAGAAA GTACTGAAAAAAGAAATTCTTTGGTGAAGGTGCCTACCGTTGGCTCATATGGTGTTGCGG GCGCCACTTTACCAGAAACAATTCCAACATCTAAAAATTACTACTTAAGGTTTGATGAGG ACGGTAAATCCATTAGGGATGCGAAATCCAGTGCAGAATCTTCCAACGCCACCAATAACA ACACCTTAGGCACGGAAAGTAAGCTTTTGCCAGATGGTGACGCCGTTGATGCACTAAGTA GAAAAATTGATCAAATACCCAAAATTGCTGTTACTGGTGGCGAAAATAACGAAAATACCC AGGCCAAAGACGATGCTGCCACTAAGACTCCACTCATTAAAGATGCAAATATTAAGCCTG AAAAGACTGAAGTAAGCACGAAAAATGGCCCATCAAGATCTATTTCCACGAAGGAAACTA AGGATTCTGCGAGACCATCTAATAACAATACTACTACTACTACTACAGATGCTACTC AGCCCACCATCATCACCACCACCGCCATCGTGATGCTGGAGTGAAGAATGTCACGA ACAATTCTAAGACAACCGAATCCTCTTCCTCTTCATCGGCGGCAAAGGAAAAACCAAAAC ATAAAAAGGGGCTATTGCATAAGCTGAAAAAGAAGCTTTAA

YBR086C, 946 aa (SEQ ID NO 18)
MSQTITSLDPNCVIVFNKTSSANEKSLNVEFKRLNIHSIIEPGHDLQTSYAFIRIHQDNA
KPLFSFLQNLDFIESIIPYHDTELSDDLHKLISISKSKILEAPKQYELYNLSNLTNNPKQ
SLYFAFLQNYIKWLIPFSFFGLSIRFLSNFTYEFNSTYSLFAILWTLSFTAFWLYKYEPF
WSDRLSKYSSFSTIEFLQDKQKAQKKASSVIMLKKCCFIPVALLFGAILLSFQLYCFALE
IFYKQIYNGPMISILSFLPTILICTFTPVLTVIYNKYFVEPMTKWENHSSVVNAKKSKEA
KNFVIIFLSSYVPLLITLFLYLPMGHLLTAEIRTKVFNAFSILARLPTHDSDFIIDTKRY
EDQFFYFIVINQLIQFSMENFVPSLVSIAQQKINGPNPNFVKAESEIGKAQLSSSDMKIW
SKVKSYQTDPWGATFDLDANFKKLLLQFGYLVMFSTIWPLAPFICLIVNLIVYQVDLRKA
VLYSKPEYFPFPIYDKPSSVSNTQKLTVGLWNSVLVMFSILGCVITATLTYMYQSCNIPG
VGAHTSIHTNKAWYLANPINHSWINIVLYAVFIEHVSVAIFFLFSSILKSSHDDVANGIV

PKHVVNVQNPPKQEVFEKIPSPEFNSNNEKELVQRKGSANEKLHQELGEKQPASSANGYE AHAATHANNDPSSLSSASSPSLSSSSSSSKTGVVKAVDNDTAGSAGKKPLATESTEKRNS LVKVPTVGSYGVAGATLPETIPTSKNYYLRFDEDGKSIRDAKSSAESSNATNNNTLGTES KLLPDGDAVDALSRKIDQIPKIAVTGGENNENTQAKDDAATKTPLIKDANIKPVVNAAVN DNQSKVSVATEQTKKTEVSTKNGPSRSISTKETKDSARPSNNNTTTTTTTDATQPHHHHH HHRHRDAGVKNVTNNSKTTESSSSSSAAKEKPKHKKGLLHKLKKKL

YBR093C, 1904 bp, CDS: 501-1904 (SEQ ID NO 19) ACGTATTTGGAAGTCATCTTATGTGCGCTGCTTTAATGTTTTCTCATGTAAGCGGACGTC GTCTATAAACTTCAAACGAAGGTAAAAGGTTCATAGCGCTTTTTCTTTGTCTGCACAAAG TAAAAGTGATTAAAAGAGTTAATTGAATAGGCAATCTCTAAATGAATCGATACAACCTTG GCACTCACACGTGGGACTAGCACAGACTAAATTTATGATTCTGGTCCCTGTTTTCGAAGA GATCGCACATGCCAAATTATCAAATTGGTCACCTTACTTGGCAAGGCATATACCCATTTG GGATAAGGGTAAACATCTTTGAATTGTCGAAATGAAACGTATATAAGCGCTGATGTTTTG CTAAGTCGAGGTTAGTATGGCTTCATCTCTCATGAGAATAAGAACAACAACAATAGAGC AAGCAAATTCGAGATTACCAATGTTTAAATCTGTTGTTTATTCAATTTTAGCCGCTTCTT TGGCCAATGCAGGTACCATTCCCTTAGGCAAACTAGCCGATGTCGACAAGATTGGTACCC AAAAAGATATCTTCCCATTTTTGGGTGGTGCCGGACCATACTACTCTTTCCCTGGCGACT GACATGGTGAAAGATACCCTACTGTCAGTCTGGCTAAGACTATCAAGAGTACATGGTATA AGTTGAGCAATTACACTCGTCAATTCAACGGCTCATTGTCATTCTTGAACGATGATTACG AGTTTTTCATCCGTGATGACGATGATTTGGAAATGGAAACCACTTTTGCCAACTCGGACG ATGTTTTGAACCCATACACTGGTGAAATGAACGCCAAGAGACATGCTCGTGACTTCTTGG CTCAATACGGTTACATGGTCGAAAACCAAACCAGTTTCGCCGTTTTTACCTCTAATTCTA AGAGATGTCATGACACTGCTCAATATTTCATTGATGGTTTAGGTGACCAATTCAACATCA CCTTGCAGACTGTCAGTGAAGCTGAATCCGCTGGTGCCAACACTTTGAGTGCTTGTAACT CATGTCCTGCTTGGGACTACGATGCCAATGATGACATTGTAAATGAATACGACACCAT ACTTGGATGACATTGCCAAGAGATTGAACAAGGAAAACAAGGGTTTGAACTTGACCTCAA CTGACGCTAGTACTTTATTCTCGTGGTGTGCATTTGAAGTGAACGCTAAAGGTTACAGTG ATGTCTGTGATATTTTCACCAAGGATGAATTAGTCCATTACTCCTACTACCAAGACTTGC ACACTTATTACCATGAGGGTCCAGGTTACGACATTATCAAGTCTGTCGGTTCCAACTTGT TCAATGCCTCAGTCAAATTATTAAAGCAAAGTGAGATTCAAGACCAAAAGGTTTGGTTGA GTTTTACCCACGATACCGATATCCTAAACTTTTTGACCACCGCTGGTATAATTGACGACA AAAACAACTTAACTGCCGAATACGTTCCATTCATGGGCAACACTTTCCACAGATCCTGGT ACGTTCCTCAAGGTGCTCGTGTCTACACCGAAAAATTCCAATGTTCTAACGACACCTACG TCAGATACGTCATTAACGATGCTGTTGTTCCAATTGAAACCTGTTCCACTGGTCCAGGGT TCTCTTGTGAAATCAATGACTTCTACGACTATGCTGAAAAGAGAGTAGCCGGTACTGACT TCCTAAAGGTCTGTAACGTCAGCAGCGTCAGTAACTCTACTGAATTGACCTTCTACTGGG ACTGGAACACTACTCATTACAACGCCAGTCTATTGAGACAATAG

YBR093C, 467 aa (SEQ ID NO 20)
MFKSVVYSILAASLANAGTIPLGKLADVDKIGTQKDIFPFLGGAGPYYSFPGDYGISRDL
PEGCEMKQLQMVGRHGERYPTVSLAKTIKSTWYKLSNYTRQFNGSLSFLNDDYEFFIRDD
DDLEMETTFANSDDVLNPYTGEMNAKRHARDFLAQYGYMVENQTSFAVFTSNSKRCHDTA
QYFIDGLGDQFNITLQTVSEAESAGANTLSACNSCPAWDYDANDDIVNEYDTTYLDDIAK
RLNKENKGLNLTSTDASTLFSWCAFEVNAKGYSDVCDIFTKDELVHYSYYQDLHTYYHEG
PGYDIIKSVGSNLFNASVKLLKQSEIQDQKVWLSFTHDTDILNFLTTAGIIDDKNNLTAE
YVPFMGNTFHRSWYVPQGARVYTEKFQCSNDTYVRYVINDAVVPIETCSTGPGFSCEIND
FYDYAEKRVAGTDFLKVCNVSSVSNSTELTFYWDWNTTHYNASLLRO

TAATTTGAATAGTGTGCCCTTCAAAACATTTGGAAGTCATTAATTGAAACTATCCAGTGT GAATAGACGACTGAGCCATCATGAAGGTATGTAATATCACCCAAATCCTTAGAATTCTAA TGAATCAGCACGCGCTAACCGGCTGTTTCTGACTGTTTTGATAAACGTATACCCACAAATT AGTGCACTATAATAAAAATTCTCAAGAACAACGTTGTTTAAACGAGATAATTCCCTCTAA TATACACGTACCGACACTTAGGAAAATATCTCGCTAAGTTCAAATTAAGGAATGAAAAAG GAATTTACGAAAAGGGTTTAGAAATATCAATGAAAATAAGAAAAACCTGTAACGGAAGAA AGGACAGCAGGATTCGTTGGAATTTGTCGATATTGGCTTCGGACAACTTTACTAACAAA TGGTATTATTATAACAGTTGAACATTTCTTACCCAGTCAACGGGTCTCAAAAGACCTTC GAAATTGATGATGAACACCGTATTCGTGTTTTCTTCGACAAGAGAATCGGTCAAGAAGTC GATGGTGAAGCCGTTGGTGATGAATTCAAGGGCTACGTCTTCAAGATCTCTGGTGGTAAC GACAAACAAGGTTTCCCAATGAAGCAAGGTGTTTTGTTGCCAACTAGAATCAAGTTGTTG GTCAGAGGTGCCATTGTTGGTCCAGATTTGGCTGTCTTGGCTTTTGGTCATTGTCAAGAAG GGTGAACAAGAATTGGAAGGTCTAACTGACACTACTGTTCCAAAGAGATTGGGTCCAAAG AGAGCTAACAACATCAGAAAGTTCTTCGGTTTGTCCAAGGAAGATGACGTTCGTGATTTC GTCATCAGAAGAGAAGTCACCAAGGGTGAAAAGACTTACACCAAGGCTCCAAAGATCCAA AGATTGGTTACTCCTCAAAGATTGCAAAGAAGAGACACCAAAGAGCTTTGAAGGTCAGA AACGCTCAAGCTCAAAGAGAAGCTGCTGCCGAATACGCTCAATTGTTGGCTAAGAGATTG TAA

YBR181C, 236 aa (SEQ ID NO 22)
MKLNISYPVNGSQKTFEIDDEHRIRVFFDKRIGQEVDGEAVGDEFKGYVFKISGGNDKQG
FPMKQGVLLPTRIKLLLTKNVSCYRPRRDGERKRKSVRGAIVGPDLAVLALVIVKKGEQE
LEGLTDTTVPKRLGPKRANNIRKFFGLSKEDDVRDFVIRREVTKGEKTYTKAPKIQRLVT
PQRLQRKRHQRALKVRNAQAQREAAAEYAQLLAKRLSERKAEKAEIRKRRASSLKA

YCL007C, 893 bp, CDS: 501-893 (SEQ ID NO 23) ATTACTTTAAATTGTTTGTCTATTCCAACATAATCATTAGCAGCACATGTCGAGCAACAG ATAAACACAGCAGCGCACGGTGAACCACATAAGTGTATGTGCACACGCGTGTTTTGTGC AGTGTATTACCAACTTGCGCATGCAAGGATATCACACTCCTGTTTCTGCCTCATGTCTTT TAAAACGCTTCCACGGGACATGGGTTCTAATTATGGAGAAGATCAAGCTTTGAAATGGCC CGTTTACACATTTTGATACAACCGTAGACGCCGTCTCGTTTCAAAGACCGTGTGGTTGTC TATCAGTATATACTCATTGTGTTTTTCAAAAAATCTCTGGGTTGTTTAGATGCCACTATA TTTCTATTCGTATTTATTTTTATGTATACTTATTTTGCTTATTTTTCTTATACTCAGGAA ACGTCACTTGGCTTGATATACTCGACGCTTTATTCTGCAAATTCAGGTCTCAAATCTGAA ${\tt CGGCGTGGAGCCACCAAGGGATGGAGCTGGCAAAGGAACGTAATGGCCCACATCAAAAAC}$ ACAAACTCTTGTTAGTAAAAAAGAAAGGGAAACTAGTAATATGGAGACACATCGTAAAAA AAATGTTGCACATACGCTTGGTTGTTCTTTGGAGCCATTATCCAGAACAGCACGGACATG GCACTAACCACTATGAATACACCAACAACAGTATAGCTAAATTGGACGCGCAGAGAGTTA GTAGAAGAAGAAGAAAAGGGAAGCGGAGAGAGAGATTATGACACATACAAACTAC TCATTACTCTTTGTTCTTTATTATTCGTTGGACCTTTGTTTCTTAAAGTATAG

YCL007C, 130 aa (SEQ ID NO 24)
MELAKERNGPHQKHHGQCQNHCTSPNTVRQNKTNKLLLVKKKGKLVIWRHIVKKMLHIRL
VVLWSHYPEQHGHGTNHYEYTNNSIAKLDAQRVSRRRKKREAERRDYDTYKLLITLCSL
LFVGPLFLKV
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AATCAGAATTTGAGACCAGAGAGACACATGGCGAATTGAACTTGAATTCAGTACCAATAT
ACAACGGAGAACTGGATTTCTCCGACAAAATCATGAAGAGGTCATCTACAAAGGTTATCG
GGACCCTGGAAGAACTACTTGAGAACTCACCATGTTCTGCGCTAGAAGGTATATCAAAAT
GGCATAAGATTGGTGGATCTGTGAAAGACGGTGTTGTTGTGTATTCTTTCACAAGACTTCC
TTTTCAAAGCACTGCATGTACTACTGATGAGCGCAATGGCAGAATCACTCGATCTACAGC
ATCTGAATGTTGAGGATACACATCACGCTGTGGGGAAGGACATTGAGGACGAGTTCAATC
CATACACAAGAGAAATCATTGAAACAGTGCTGAATAAATTTGCTGTTCAAGAGCAAGAGG
CTGAAAACAATACGTGGCGCTTTGAGAATAACCGTTTATAGCTCAGTGGTACGGGATTCAAG
CGCTAAGGAAATATGTTTCTGGAATAAGCATGCCAATTGATGAGTTCCTCATCAAGTGGA
AGTCCCTTTTCCCCACCTTTCTTCCCATGTGACATTGACATTGACATGCTGCGAGGCTATC
ATTTCAAGCCTACCGATAAGACTGTCCAGTATATAGCGAAAAGCACACTACCAATGGACC
CCAAAGAACGGTTTAAAGTCCTGTTTAGGCTACAGTCACAGTGGGACTTTCATCAAGTCA
AGCCTCTAATTGAAGAACTAAATTCAAGAGGTATGAAAATAGACAGTTTCATCATGAAGT
ATGCCCGCCGTAAAAGACTGGGCAAAAAGACCGTTGTCACGAGCAGGTAG

YCL016C, 309 aa (SEQ ID NO 26)
MREFVPEQPITFDETLLFGLSKPYMDVVGFAKTESEFETRETHGELNLNSVPIYNGELDF
SDKIMKRSSTKVIGTLEELLENSPCSALEGISKWHKIGGSVKDGVLCILSQDFLFKALHV
LLMSAMAESLDLQHLNVEDTHHAVGKDIEDEFNPYTREIIETVLNKFAVQEQEAENNTWR
LRIPFIAQWYGIQALRKYVSGISMPIDEFLIKWKSLFPPFFPCDIDIDMLRGYHFKPTDK
TVQYIAKSTLPMDPKERFKVLFRLQSQWDLEDIKPLIEELNSRGMKIDSFIMKYARRKRL
GKKTVVTSR

YCR052W, 1952 bp, CDS: 501-1952 (SEQ ID NO 27) GTCATCGACAGCAAATTGCTGGAAGAGTTCAAGGACAACGTGAGATACACCTTGGAAAAAT GACCCTGAGGAAGGAGCCGATGAGGCCACTCTGCAACGCAGGAGGCAGTTGGAACAGATC ATTACGGGAGACAACGCTGAGGAGGAGTTGGAAAGGTACATCCGTGCTATGGTCAGAGAG CAGATGCTGGGCCAGGGCTCCATGGCGGGTTCCGGGGACGAACCAGATTCCAAGAGAAGA AAATAACGACCCAGCACAAAGGCTCTTACAGCTTGCTAAAAGAAATTGAACGCGACGCTA CATGAACTACTTCTTTCTCTTACATAGTCTTTTCCCTTATGTATCTTTTCTGTACATTAA TAGACGTTCTTACAAGGTAAAATTTCACCGCGTTTTTAAATAGAATGAAAAAAACGTTGT AGAGTGAAAGAAAAGCAACAAATATACAGTTCACAAGGCAGCTTCGTATAGTAATACAGC ACGAAAAACAGCTCATAGAAATGGTAACACAGACCAATCCGGTCCCTGTTACATATCCAA CGGATGCTTATATCCCCACGTATCTGCCCGATGATAAGGTCTCCAATCTGGCAGATTTGA **AAAAATTGATAGAAATGGATTCCAGACTAGATTTGTATCTGACAAGAAGGAGGCTGGATA** CGTCCATCAATTTACCTACAAACACCAAGACCAAGGACCATCCCCCCAATAAAGAGATGC TGAGGATTTACGTCTACAACACTACGGAAAGCAGCCCTCGCAGCGATTCTGGCACCCCAG CGGACTCAGGCAAGACTACATGGACACTGAGAATAGAAGGTAAGCTTCTGCACGAGTCCG CAAACGGAAAGCACCCATTTAGTGAGTTTTTGGAAGGTGTCGCGGTCGACTTTAAAAGAC **ATCTGCAACAACCCGAATACAATGATCAAGATAGCACCATGGGCGATAACGACAACGGCG** AGGATGAGGACAGTGCAGAGGCAGAATCCAGGGAGGAAATTGTAGACGCACTGGAATGGA ACTACGATGAAAACAACGTTGTGGAGTTTGATGGTATCGACATCAAGAGGCAAGGCAAGG ATAATTTGCGATGCAGTATAACCATCCAGTTGAGGGGTGTCGACGGTGGAAAAGTACAGT ACTCGCCCAACTTAGCTACCTTGATAGGTATGCAAACGGGCTCCGTTAATGACGCGGTTT AAGATGGTTCCAACGATGCCGAAGACAGCAGTAACGAGAATAACAATAAAAACGGTGCTG GTGACGATGATGCCGTCGAGGGAAGTACTCCAAAGGATAAGCCCGAATTGGGTGAAGTGA AGCTAGATTCACTCTTACAAAAGGTATTGGATACAAACGCCGCGCACCTCCCCTTGATGA ATGTTGTGCAAACCGTGAACAACTGGTATCACCCCTACCGCCCATCATCCTAGATTATA CAATTGATCTTTCCAAAGATACCACCTATGGTGCTACCACCTTGGATGTAGATGTCGC ACATTCTCCACCAGCCTCAACCCCAGCCAAATTTACAAAAAGAGGAAGAAACAGATGCTG AAGACACAGCAAAACTACGTGAAATCACAAAGCTTGCCTTGCAGTTGAACTCTAGTGCTC AAAAATACCAGTTTTTCCACGAACTGTCTTTGCATCCAAGAGAAACGCTGACTCACTACT TATGGTCTTCCAAGCAAAACGAGCTTGTGCTGCAGGGCGACCAATACTTCAATGAAGATG CTGCAAGAACGAGTGACATATACAGTAACAACAACAATGACAGGTCACTAATGGGCAATA TCTCACTACTGTACTCCCAAGGAAGACTATAA

YCR052W, 483 aa (SEQ ID NO 28) MVTQTNPVPVTYPTDAYIPTYLPDDKVSNLADLKKLIEMDSRLDLYLTRRRLDTSINLPT NTKTKDHPPNKEMLRIYVYNTTESSPRSDSGTPADSGKTTWTLRIEGKLLHESANGKHPF SEFLEGVAVDFKRLKPLGMGKKRKRDSSLSLPLNLQQPEYNDQDSTMGDNDNGEDEDSAE AESREEIVDALEWNYDENNVVEFDGIDIKRQGKDNLRCSITIQLRGVDGGKVQYSPNLAT LIGMQTGSVNDAVYSIYKYILINNLFVTEQTEAQDGSNDAEDSSNENNNKNGAGDDDGVE GSTPKDKPELGEVKLDSLLQKVLDTNAAHLPLMNVVQTVNKLVSPLPPIILDYTIDLSKD TTYGATTLDVDVSHILHQPQPQPNLQKEEETDAEDTAKLREITKLALQLNSSAQKYQFFH ELSLHPRETLTHYLWSSKQNELVLQGDQYFNEDAARTSDIYSNNNNDRSLMGNISLLYSQ GRL

YCR064C, 911 bp, CDS: 501-911 (SEQ ID NO 29) GCGTCGCGTTCTCGCGTCTGTTTTGTTTTTTCGCGTTCCAATGACCAAAATGGGAAAGTG TGGCCAGAACAATACTGCAACGTGCATATAGTCGTTAGTCTGTGCTTGCACATCCACGGC AGCCGCAGTGGACGCACTGATGGAAGGACACCTGTGTGCCCTTTTTGCGTGCTTCTTCCT CTAACTGTGCACGAGGCACCCTGCAGATGCAAGTGCTACCGTTGTTAGTTTCGTTCTTTT GAATGCAGCGCAGACAGCACAGTTTTTCATACCCGGTTTTGCGCCATTTGGCAATTAGCA ATTTATCAGCATACTTTTCCTTTATCAACCAATCGTAAAGGTCTTTTGGAGATGGCCTTTC TCTTGTAGTACAGAGTATATATGTATCTAGAGCGCTGGTGGTGGAGTTGCATTATCTCCC AGAGCTGCTCATTGGACTTTGCTGCGAGCTTAGACGACTTGTCCTTTTTGGGCATCTCTGA GTTGGATTTCGAAATCTGTGAGGGTTGGCTTGATTTTTTCGAACCCGTCAGGTGCAGGCT TGGATCTTCTGGTCTTTATGCGCGGCATGTCGTTTTGTGAGGTGAGCTTTGCTAGTCTTG AGTATTTCACTTTCCGTTGTGAACGACAAATGTACTATGCGTTCAAGAGCCAACGCAGTA TCATCGTCAAAGTTCCTACCACACGCGTGTGATTGATCTTGTACTGGTTGTAAATGTGC TAAGTCTGTGA

YCR064C, 136 aa (SEQ ID NO 30) MYLERWWWSCIISQSCSLDFAASLDDLSFWASLSWISKSVRVGLIFSNPSGAGLDLLVFM RGMSFCEVSFASLDGCRGVYIDDESLRKFFFFFQYFTFRCERQMYYAFKSQRSIIVKVPT TTRVIDLVLVVNVLSL

YCR073W-A, 1448 bp, CDS: 501-1448 (SEQ ID NO 31) GTTTATGGCTGGAATGACTTGATAATCTCTTCACGAGCTTACTTGAGATGGTATGAGGAG CCAGAACTCTCCCGCCTTCAGCCGCTTTTTGTTGCTGTGTATTCAGTATATCCATCATCA TTTTCACCTACAAGGAACTACCTTTTATAGCCACCCTAAGTAAAACAACATTAGCTTAGC ATCCTCAATTCTTATCGTATGTTGTTGCTGCTATTTTTATCCTATTGTTCCTGGCATCGC TTTTTTACATAAGGTACCAAGGCAAGAGAAAAGACCCGCGAAATTTTCAATTCGAGACAT AGGGTTAATACGAAATATGTTAAGGTCTAGTTTCCAAAAAATGAAGAAAATGTGATTAGA CATCCTGGGGAAATTAGGTTTAAATAGGGCGGCGCTACAGGGGTTTTCCTAACAAATTT CAATGATAATAGTGGCATCATCATCGTCATATCCAGTGTAGGTATGGACTAGAACAGAAA GCAATTTGCAGCAAGACAATATGACTACGACGGTACCCAAGATATTCGCGTTTCACGAGT TTTCAGACGTGCAGAGGCCGTAGCTGACCATGTAGTCCACGCGCAAGACGGTGCATTGG CTCCAAAGAACGAGAGGAAACACTCTGTTCCCAACATCAGCATGAATGCACTGGATATGA CGAGAGAGGCCTCTTGCAAAAGCACAGCATCTGCCGCGGAAGGGAAAAGTGGTAGCAGTG GTAGTGGCAGTGGTAGCAGTAAGCCCAAAAAGGAGAAACGGTTCAAGATTGCTCTCTCCG GTGGGTCATTGATCGAAGTGCTACACGAAGGTCTGCTAAAACGAGACGATGTACGGTGGG GAGACTGGGACATTTACTTTGCAGACGAGAGACTTGTACCCTTCAGCTCGAATGAAAGCA ATTATGGATGCGCCAAAAGGAAGATTTTGGACCTGATAGACACGGCGAAGTATGGAACTC CGAAGGTGTACCACATTGACGAGTCATTGATTGACGACCCGCAAGAATGCGTTGATAACT ATGAAAAGGTGCTAATCCGCGGGTTTGCCGGTAGAGATTCCGTCAAACTTCCGATGTTCG ACTTGTTCCTGCTTGGTTGTGCCCCCGATGGTCATATCGCATCACTCTTCCCTAACTTCC AGGACAATCTACGTGAGAAACTTGCATGGGTGGTGCCCGTGGAGAACGCTCCTAGTGGGC . CCTCGACCAGAATTTCGCTGACTATACCTGTAATCTGCCATTCTCACAGGGTTACTTTCG TTGTCGAAGGTGCAACCAAGGCGCCCATCATCAAGACCATTATGGAAAGGCCTGAAAAGG GCCTACCTAGCAGTATTGTCAACGAAGGTGCTGCTGGTCGTGTATCATGGTTTGTTGACG ACGATGCTCTTACGGACGTCCTCGTCACCAAAAAAAAGTATAAATTCCACCAAGGTTTGT **CTATTTAA**

YCR073W-A, 315 aa (SEQ ID NO 32)

MTTTVPKIFAFHEFSDVAEAVADHVVHAQDGALAPKNERKHSVPNISMNALDMTREASCK STASAAEGKSGSSGSGSGSKPKKEKRFKIALSGGSLIEVLHEGLLKRDDVRWGDWDIYF ADERLVPFSSNESNYGCAKRKILDLIDTAKYGTPKVYHIDESLIDDPQECVDNYEKVLIR GFAGRDSVKLPMFDLFLLGCAPDGHIASLFPNFQDNLREKLAWVVPVENAPSGPSTRISL TIPVICHSHRVTFVVEGATKAPIIKTIMERPEKGLPSSIVNEGAAGRVSWFVDDDALTDV LVTKKKYKFHQGLSI

YDL010W, 1196 bp, CDS: 501-1196 (SEQ ID NO 33) TAGTAATTAGTTCTTATGATGGATTTAATGGCGTAGTTCATCCGCGTTTAATTTAACTA GAGGATAATCTACTTGCAGCATGAATGAAAATAGTAAGCCAGTAAGGATGCACTGACAGA CTCAGCTACCGATTAGTGTTGTTGACTTTTCCGCAAGATCCTTTTCTCCCTCTTTTGGACC TAGTCATCCCTCCACACAAGATTCGCTCTTAAGTAGTGGCGCAGGCTGTTCGCTTTTAAG CATAGTGCTTAATGTCGAAGGCTTTATAGATCCCAAATACTACGCCTTGAGAAATTGAAT GCACTAGCAGTTAGTTAACTTTCTGGAACGCGCATGACGCGTCCCGGGGCGCCTGAGGCG GAACTTTTAAGCAAATTATCGTAAGATAGAAAAGACGAAACCTTAGCAACCTAGCGGTTT **AATATAGAAACAATTTTATTATGATACCTTCCAATAAGAGAAATGCTAGAATTTTAAGCA** TTACAACGCTATTATTGTTGTTAGTGTTTTTCGTAGCGCAAAATGCGAACTTCTTGACGG TAGAGATAAAAGAGGAAACTTCTAAAGCATTTAGTACTAATATGGACAATATGGCTGGAG GATCTTCCAGGGAATATGCTGCTATGCCGACTTCTACCACGAATAAGGGGAGCTCTGAAG TAGACGAAGAAATTAATGAAATAAAACAGAAGGTGGGACTCCAACAGCCCCATAGCATCGG TTGATGATAGTTTGTCGGCCATTAAAAACGATAAAGGGTCGCGAATAACCAAAGCTTTTA ATGTTCAAAAAGAATACTCCCTCATACTAGACTTGTCTCCGATTATAATATTTAGTAAAA GCACCTGTTCATATAGCAAGGGCATGAAGGAACTGCTTGAAAATGAGTATCAGTTTATCC CAAACTACTATATTATAGAACTTGACAAACATGGACATGGGGAAGAGCTGCAAGAATATA TCAAGTTGGTGACCGGTAGAGGAACTGTTCCAAACCTTTTGGTTAATGGAGTATCAAGAG GAGGTAATGAAGAAATCAAGAAACTGCACACTCAAGGGAAACTTTTAGAATCATTACAAG TCTGGAGTGATGGTAAATTCTCGGTTGAGCAACGTGAAAAACCTTCCAATAATTGA

YDL010W, 231 aa (SEQ ID NO 34) MIPSNKRNARILSITTLLLLLVFFVAQNANFLTVEIKEETSKAFSTNMDNMAGGSSREYA AMPTSTTNKGSSEVDEEINEIKQKVGLQQPIASVDDSLSAIKNDKGSRITKAFNVQKEYS LILDLSPIIIFSKSTCSYSKGMKELLENEYQFIPNYYIIELDKHGHGEELQEYIKLVTGR GTVPNLLVNGVSRGGNEEIKKLHTQGKLLESLQVWSDGKFSVEQREKPSNN

YDL036C, 1889 bp, CDS: 501-1889 (SEQ ID NO 35) TCAAATCCAGCTTCTTTTCAAGCAATATTGTCACAAACGATGATGAGAATAGCATTGAAG AGGATAAGAATTTACGCTATTCAGATGCTAGTGCATCTGAAAATTATCTGGTCAAGCCCA CAATACCAGGTACGACTCCTGATCCAATAATTGAGGCGCAGAACGATAATGATAGTAGTG ATAGTAGCGGCATAGATTTGATAGCCTTCTTAAGAAATGGACCATTATAAAGTTTTTGTA TCGCGATGTTTGAAAATGGAAAGTAAGGAACGTAATACAAATTGACAAGTAGCCGACATG AATGACGCTCACTTCTCTTATATATGTTAGGTAGTATATGCATTATAGAATTTATTCATT AACAAAAGACCGAGTTAAGAAAAAGTTCATAAAAAACTTTTGAAAATGGATGAGTGCTCG TATAATGGAATAGGAAACTTATGCAAAGAAATAATAGGTTAAGAAATTTGTTTACAGTGC CAGTAATAATGGCTCGACAACTCAAAAGGAATGCATTATCTGCAGGTCTTGCTTTTGCAG ATAAATCTACTTTTCAATCACGAACGATAGGCAGCAAAAAAGAGAAAACATAGACAACTAG ATCCAGAGTATGAAATTGTCATCGATGGCCCTCTAAGGAAAATCAAGCCCTACCATTTTA CGTACAGGACCTTTTGCAAAGAGCGTTGGAGAGATAAAAAATTGGTTGATGTCTTTATAT CTGAATTTCGAGATCGTGAATCTGAATATTATAAAAGAACAATCGAAAACGGGGACGTTC ATATAAACGATGAAACTGCGGACTTATCTACTGTAATTCGCAATGGTGACCTGATTACGC ATCAGGTACATAGACATGAACCTCCAGTCACTTCCAGGCCTATCAAAGTTATTTTTGAAG ATGATAACATAATGGTTATTGATAAACCGAGCGGTATACCTGTTCACCCAACTGGCCGAT **ATCGGTTCAATACAATTACGAAAATGCTTCAAAATAATCTCGGATTTGTTGTGAACCCAT** GTAATAGGTTAGATAGGCTTACAAGTGGATTAATGTTTTTGGCAAAAACTCCGAAGGGAG CCGATAATATCGGCGATCAACTAAAAGCTCGAGAAGTCACTAAGGAATACGTGGCCAAGG TAGTTGGAGAATTTCCAGAAACGGAAGTAATTGTTGAAAAACCTCTAAAAACTGATCGAGC CAAGGCTTGCTCTTAATGCAGTTTGTCAAATGGACGAGAAAGGAGCCAAACATGCAAAAA CTGTTTTTAACAGAATCAGCTACGACGGTAAAACGAGTATTGTAAAGTGCAAACCGCTTA
CCGGGCGATCACATCAAATTAGAGTACATTTACAGTACTTAGGCCACCCAATTGCTAACG
ATCCTATTTATTCCAATGATGAAGTATGGGGTAACAATCTCGGAAAAGGCGGCCAGGCTG
ACTTCGATATAGTTATTACTAAGCTAGACGAAAATAGGGAAAAAACCTGCTAAAAGTT
GGTTCCATAGTAATGGCGGGTACGGTGAGGTATTAAGGCAAGAAAAATGTTCTATTTGTG
AATCTGATTTGTATACTGATCCTGGCCCCAATGATCTTGATCTGTGGTTACATGCCTATC
TATACGAATCAACTGAGACTGAAGAAGAACCGAAAAAAAGTGGTGCTACAAAACAG
AGTATCCAGAATGGCCTCTGAGAAGAAGAAAAA

YDL036C, 462 aa (SEQ ID NO 36)
MQRNNRLRNLFTVPVIMARQLKRNALSAGLAFAGNATSNEFDEHLQNEVEREREIQKKKK
IKRTQSKKSPDLINKSTFQSRTIGSKKEKHRQLDPEYEIVIDGPLRKIKPYHFTYRTFCK
ERWRDKKLVDVFISEFRDRESEYYKRTIENGDVHINDETADLSTVIRNGDLITHQVHRHE
PPVTSRPIKVIFEDDNIMVIDKPSGIPVHPTGRYRFNTITKMLQNNLGFVVNPCNRLDRL
TSGLMFLAKTPKGADNIGDQLKAREVTKEYVAKVVGEFPETEVIVEKPLKLIEPRLALNA
VCQMDEKGAKHAKTVFNRISYDGKTSIVKCKPLTGRSHQIRVHLQYLGHPIANDPIYSND
EVWGNNLGKGGQADFDIVITKLDEIGKRKPAKSWFHSNGGYGEVLRQEKCSICESDLYTD
PGPNDLDLWLHAYLYESTETEEGTEKKKWCYKTEYPEWALRR

YDL083C, 1364 bp, exon1: 501-909, intron1: 910-1341, exon2: 1342-1364 (SEQ ID NO 37) TATTCCGACTAGAAAAAATTAAATTTTCTAACTACAAAAAATTGCCTGCATATATGTAA GGATGTAACAGGAAATGTATGGGTCACATATTAATAGCTTGTTTTACTCCATAAAAGAGT CTGATATTCAGAAAAAACACCCATACATGTTGAAAAATAATGCATTGTGAAAAAAAGTGG TTGAAAAATGTATGCGATCTAGGAAAAACTGAATTTTCCTTAGGTTGTCGCTCCTCCTCT AGAAGGATGCTGTGGCCTTTGACCTGGGCGGAAATTCTCTCTGTTTCCCTCTAGCTGAGG GAAACAGAACTGGTAGCAGTTCGTTCCGGCCAGGCCGCGTGAGCCTATACCACCGAATAT TATCCTAGCGCAGAGAGTAACACTGGCAAAGTCAAAAGTAAATGCCATGTAAAATGTATA GCAAGAGAATAAGCAACAAGATGTCTGCCGTCCCAAGTGTCCAAGTATGTTAAATAATTT AAACGATGTCACGAATTTGTGAGGGATATTGAAACCATGCAGTGAGATAATTTCAATTTA AGAACCATATCACCTGAATAAGACGGGTGGGGCAAGCACTAGATGCGAATCATAGTTTTA GAACAACGGATCACCATTTCACACGTTAAAGACCGAGTAGAAATAACCAATAAATTGTGT GGGAAAATATTATACTTAATTTCTCTGTGGAGTAAAGTAATGAGCGTCTTTTGCGGTCTT ATTTATTCATTCGCTCCCTTGCAATGAATTTTGAACAGAATGCTCCAAAGAGGAAGTGC CAGGGTACCTCACTTGTTTCACCCCTTTTACACAGTTCATAATATTTTTTGAGGATTTTTGAA TTTCTGTTTTACTAACATGTGACACGAAATGTTTTTCATTTTTGGTTTTATAACAGACTT TTGGTAAGAAGAAATCAGCTACCGCTGTTGCCCACGTCAAGGCCGGTAAGGGTTTGATTA AGGTCAACGGTTCTCCAATCACTTTGGTTGAACCAGAAATCCTAAGATTCAAGGTCTACG **AACCATTATTGTTGGTTTGGTTTGGACAAGTTCTCCAACATCGATATCAGAGTTAGAGTCA** CTGGTGGTGGTCATGTTTCTCAAGTCTACGCCATCAGACAAGCTATTGCTAAGGGTTTAG TCGCTTACCACCAAAAGTACGTTGACGAACAATCCAAGAACGAATTGAAGAAGGCCTTCA CCTCTTACGACAGAACTTTGTTGATCGCTGATTCTAGAAGACCAGAACCAAAGAAATTCG GTGGTAAGGGTGCTCGTTCTAGATTCCAAAAATCTTACCGTTAA

YDL083C, 143 aa (SEQ ID NO 38) MSAVPSVQTFGKKKSATAVAHVKAGKGLIKVNGSPITLVEPEILRFKVYEPLLLVGLDKF SNIDIRVRVTGGGHVSQVYAIRQAIAKGLVAYHQKYVDEQSKNELKKAFTSYDRTLLIAD SRRPEPKKFGGKGARSRFQKSYR

YDL125C, 1088 bp, exon1: 501-597, intron1: 598-708, exon2: 709-1088 (SEQ ID NO 39)

TTCAAAATACGAGTAAAGGAGATCCTAGGTGTGGATTAGTAAGGGGAGTGTGGCAACTTC
CTTTTTCCGGTTAATTCTCCGCGCTTTCGTTAGACTATTTTGCAAGGACCCAAATAGGAG
ACGCATGGAGGCTTCTACAAAACAGCGTGCCGTTTTGATGGCATGAGCAGGGGGCGCAAA
GGAAACACCGGTAAATCGCGCAAGACCTTGTTGGCCACGTAGCCTCAAAGGTTGAATTGA
CACTTGTCTACAGAACTTGAAAAGTACAAAAGGAGGTCACATAAAACAGTAAGCTTGAGA
AGCTTTAAGATATGGTGCGAATCGTTACAGAATATTCCTTGCAGAAATAATGGCGGGTCC
GTTCTCTTCTGAAGAAGTTACCGCCCTACTGAAGCATTGCTGTACGATCGTGTAATGTGA
TGTGTGTTCGACTGGAAAGCGGAGAACATTATGAAGTAAAAGGACAATCAGCACGCCTTC

YDL125C, 158 aa (SEQ ID NO 40) MEPLISAPYLTTTKMSAPATLDAACIFCKIIKSEIPSFKLIETKYSYAFLDIQPTAEGHA LIIPKYHGAKLHDIPDEFLTDAMPIAKRLAKAMKLDTYNVLQNNGKIAHQEVDHVHFHLI PKRDEKSGLIVGWPAQETDFDKLGKLHKELLAKLEGSD

YDL133C-A, 25 aa (SEQ ID NO 42) MRAKWRKKRTRRLKRKRRKVRARSK

1268 bp, exon1: 501-503, intron1: 504-908, YDL136W, 909-1268 (SEQ ID NO 43) CATGCGGACCTTGTGTTTTGTTTCTAGATTGTTTATTTTTTATGATTGTTGAAGATAT **AAACCACTGTATAGTTGTATAAGATAGGATAATGATGGTGCACTGAAAATAAACTTACTA** GCTCTTTAATATTGCAACGGCTTGTAACGGGCGCCATGATGACATTCAGAATTATACCAC TACTATATGAAAAAATGAAAAGAGGCCCTGCTTTGAACCCGTACATTTTATTCTATAATA ŤTGCATCTGTGGTTTGCCTGACGGCAGCGAGTCCAACAAAGTCTGGCATATGCTACGA TTTTACTGAAGATGAGGGTAAATAGAGGCCTGCAATCGTCATCATATGAGAAATGGATAT ATTGAAAATCTACTCACATCTCTTTTTTGGGGGTTTGGTAGTACAGTGAGAACACGATAA AGAACCAAATAGGACTAAAAATGGTATGTAGAGATGAATATACATGAAACGGACGTGATA CTGAAGAAATTTACAGCTACAGTATTACTGCAAACCTTGCAGGCAAATATCAGAGAGAT CTCACCAGCTACAACTTGGTAACAGAAATTTATAAGTTTATGGCACTTGTTAAAATTGTT TGGAAGTTTTCGAAATTATAATATTGGTCTTCAGAAACCTGGAACCACATGTGAACTATT TTTTTTGGATAATGCATTGCACAGAGCGTATTAGTGTATACGAGAATCTAAAAATTTGAA ATCAATAGGCCGGCGTTAAAGCTTACGAACTAAGAACCAAATCCAAGGAACAATTAGCTT CTCAATTGGTTGACTTGAAAAAGGAGTTGGCTGAATTGAAGGTCCAAAAGTTGTCCAGAC CATCTTTGCCAAAGATCAAGACCGTCAGAAAGAGTATCGCCTGTGTCTTGACCGTCATCA ACTTGAGAGCCAAGAAGACCAGAGCTTTGAGAAGAGCTTTGACCAAATTCGAAGCTTCCC **AGGCTTAA**

YDL136W, 120 aa (SEQ ID NO 44) MAGVKAYELRTKSKEQLASQLVDLKKELAELKVQKLSRPSLPKIKTVRKSIACVLTVINE QQREAVRQLYKGKKYQPKDLRAKKTRALRRALTKFEASQVTEKQRKKQIAFPQRKYAIKA

YDL167C, 2660 bp, CDS: 501-2660 (SEQ ID NO 45) TGGGTGTCGTCAAACAGGATGCCGTGGAATCATACGAACCGCACATTGTGGTAGAGCTAC AAAGCGATACGAAAGAAGATATGGTATCTAACGTATCCCGTATTGTTGCTTGGGAAAAGA TGTGGTTAGAACACATCCAGATGGAGTCACAAATGAATATCAAGGGCCTCGTAGCGATG ACGAAGACGATGAAGACAGTGAGTAGGCGTTCCATAACTTTGTGTATCTACATATATACA TATATAATTGTAAATTAGTAACAGTAGTAATAGTGGCGTATTATAAAGGGTTTTCTTT AAGTAATGTCATGTACTTGTTTAATGTGACTTTGGTAATATATTTTCATTCTCCGATGCC GATGCCCAGTGGAAAAGTTTAAAGTGAAAAATTTTTCAACACATACAAGTTTAATAAGTT GGTTTTGATGCAAATAGCATTACTAAAGAAGAGCGCTAGGATAATTGTGCATTGCTATTG TGATTTTTGATACAGAAATTATGCACTATGTGGTACTAGAGCTGCAAGTTGCGCATTTGC CAGATACCCCCAAGGATCAATGTCGCATTGCGAATATAGCATTTCAAATTGTGAATGCTG AAACATTAGTATGCCATTATGGGACCAATTCTTTACCGAGCATTGAAGTAAACGGGACGA CAAAGAGTTTGGAGAGTGCAATGGTGCAATTGGACAAGGATATTCATGACGTTATTGGTA ACGACGACTTTGTTCTTGTTTCCCTGTATTCAACATGGCATATCCGTGTTACCTTACCAC GTCAAGCGAGAGATGATGGGTTTATTCTTACTTCTTATTTACAACATCCGAAAGTATTTG ACTTATGGAAGGAATTCGATAGATGGTGTCAACCATCCGGAGATTTTGGGACAAAAGA AAGCAATCTCCAACAACAATTGTAATACTAAAAGTATTAGTATTAATGCAGCCAAAAATA CGAAGGATTTGGACGAAATAGTTAGAATATTGGAAGTTTCAATCCCAACTGAAGAGGCAG GCTCTGTTCCAGAGATATACTCTCTTTTAAAAAGGACAACGGATATATTAATACAATTGC ACAAAAAGTGTACTTCCCCTGAAGATATGGAATCTGTCTTAACAAAACCATATGACTCAC ACACCGATATTAGAGCGTTTTTGCAAGAGAAATCTAAGATTTTGTACATGAACAATTTAC CGCCCGACACACTCAAAGTGAGTTGGAATCATGGTTTACCCAATATGGTGTTAGACCAG TTGGGTTTTGGACTGTCAAAAACATCGTAGAAGATACGTCTAACGTTAATAATAACTGGA GTCTAAATAACAGTCCCTATGTGGAAGATCAAGATAGTATCTCAGGATTTGTTGTCTTCC AAACACATGAAGCAACTGAAGTACTAGCGTTGAATGGGAGATCAATCCTATCTAATC TGGCAAACACTAAGCAACCAAGGGTGGTGGAACATGTCCTTGAGCTTCAACCTTCTTCCA CAAGACCAGGTGACTGGAATTGCCCATCTTGTGGTTTTTCAAACTTTCAAAGACGTACTG ACAATAATGTTAACAGTAGTAGAAATAATTTAAACAATCGCGTGAACTCGGGATCTTCAA GCAATATTAGTAACACTGCAGCGAATCACCCCTATGGTGCCCCTGAGTTCAACATGATTG CTAACAACACGCCAGCAGCTTTAACATACAATAGAGCTCATTTTCCTGCAATTACGCCAT TGTCGCGACAAAATTCATTGAACATGGCACCATCGAACAGTGGGTCGCCGATAATTATAG CGGATCATTTTTCGGGAAATAATAATATAGCCCCAAATTATCGTTATAATAATAATAATA ACAATAACAACAATAATATTAACAATATGACCAATAATAGATATAACAATTAACAACA TCAACGGTAATGGGAATGGTAATGGGAACAACAGTAATAACAATAACAATCATAATAACA ATCATAATAACAATCATCATAATGGTAGTATCAATAGTAATAGTAATACCAATAATAATA ATAATAATAACAATGGTAACAATAGTAATAATTGTAATTCCAATATCGGTATGGGAGGAT GTGGCTCCAACATGCCATTTAGAGCAGGAGATTGGAAGTGTTCCACGTGCACGTATCATA ACTTTGCTAAAAACGTAGTGTGCTTACGCTGTGGTGGTCCAAAATCAATAAGCGGCGATG CAAGTGAAACCAATCATTACATAGATTCATCAACATTTGGACCAGCGTCGCGTACTCCCA GTAATAACAATATTTCTGTTAATACTAATGGTGGTAGCAATGCTGGTCGCACCGATGGGA ACGATAACAAAGGTCGTGATATTAGTTTGATGGAATTTATGTCACCACCGTTATCGATGG CAACAAAGTCAATGAAGGAGGGAGATGGGAATGGTAGCTCGTTTAACGAGTTCAAAAGTG ACAAAGCTAACGTTAATTTTTCCAATGTTGGTGATAATAGCGCTTTCGGTAATGGTTTTA **ATAGTTCAATACGTTGGTAG**

ISLMEFMSPPLSMATKSMKEGDGNGSSFNEFKSDKANVNFSNVGDNSAFGNGFNSSIRW

YDL184C, 25 aa (SEQ ID NO 48) MRAKWRKKRTRRLKRKRRKVRARSK

YDL191W, exon1: 501-503, intron1: 504-994, exon2: 1354 bp, 995-1354 (SEQ ID NO 49) TATTGACGTTTCGCTCTCAGGTCCACCGTGTTCTCAAAAGATACTTTTAAAACCTAAAAC ACACGAAATCATATTATGATAATTCAGAATGATAGTGTGGTACTGTGTCAATTGACTGTT CAAGACTGAAGAGGATCTTTGATTTGTTGTTACTCAACAAATAATCTTCACGAAAACTTT CTCAATCTGGGGACTGTATTAATCTCAGACCCATACATATCTACACCCATAACTTTTTAC GCGCAGCCTCTCCGGGTGAACCCCACGACAACTTACCTGGCACTCCATGCACTAACGGGC GGGTTTGGGCAGGATTCCAGCATCAATTTTGCAAAATTCACACCTGAGTAATTCATATAT GTAATATATGTTAAGCATACGCTGTCGATTAGCACTATTATTGACCGTAGAATAGGTAC AGTGAGACAGTATATTCGAAATGGTATGTTTGAGATGAACAAAATAATAAAGACTGACAA TTTGGAACGTAATTCATCCGTTGGCTATGTCTATTCAATACAGTTAGAATACGAAAGCTG ATACATCTTTAAATTCAGAGGTTTTGCTGAATTTTAATAGGGAAGTTTACGTTATGATTG TTGGCCGTAGATCGCCTAGCGTTTGACCAAATTTAATTCTCCTAATTTTTTTATTGTAAA GATGCCTGTGCTTGTTAGTTCATTATAAGTGCTAATAAAATACTAACGTTAATAAAAATT TGGAATATTATTTCATTTTTTATCCTATTAATAGGCCGGTGTTAAAGCTTACGAACTAAG AACCAAATCCAAGGAACAATTGGCTTCTCAATTGGTTGACTTGAAAAAGGAGTTGGCTGA ATTGAAGGTCCAAAAGTTGTCCAGACCATCTTTGCCAAAGATCAAGACCGTCAGAAAGAG TATCGCCTGTGTCTTGACCGTCATCAACGAACAACAAGAGAAGCTGTTAGACAATTATA CAAGGGTAAGAAGTACCAACCAAAGGACTTGAGAGCCAAGAAGACCAGAGCTTTGAGAAG AGCTTTGACCAAATTCGAAGCTTCCCAAGTTACCGAAAAGCAAAGAAGAAGCAAATCGC TTTCCCACAAAGAAAGTACGCTATTAAGGCTTAA

YDL191W, 120 aa (SEQ ID NO 50) MAGVKAYELRTKSKEQLASQLVDLKKELAELKVQKLSRPSLPKIKTVRKSIACVLTVINE QQREAVRQLYKGKKYQPKDLRAKKTRALRRALTKFEASQVTEKQRKKQIAFPQRKYAIKA

CCTCCTCTACATTTTCGTTCTCACCCAAATCTAGGGTCACTTCTTCAAACTCTTCTGGCA ATGAAGACGGTAACCTAATGAATACACCTTCTACGGTTTCCACTGATTATTTGCCACAAC ACCCTCACAGAACATCGTCTTTGCCAAGACCTAATTCCAATCTCTTTCACGCAAGTAATA GTAACCTATCCCGAGCAAATGAGCCCCCAAGGGCCGAAAATTTATCAGATAATATACCAC CCAAGGTCGCTCCATTTGGCTATCCAATACAAAGAACCTCTATTAAAAAATCCTTTTTGA ATGCTTCTTGTACGTTATGTGACGAGCCTATTTCTAACAGAAGAAAGGGAGAGAAAATTA TAGAGCTTGCATGTGGCCACTTAAGTCACCAAGAATGTCTTATTATCTCTTTTTGGCACCA CTTCAAAGGCAGACGTTCGTGCGCTATTTCCTTTTTTGTACCAAATGTAAAAAAGATACTA ACAAAGCCGTTCAATGCATTCCAGAAAATGATGAACTAAAGGATATTCTAATTTCTGATT TTTTGATTCATAAGATTCCTGATTCTGAGTTATCAATCACACCTCAGTCCCGCTTTCCTC CTTATTCACCACTCTTGCCTCCTTTTGGGTTATCCTATACACCTGTTGAAAGACAAACGA TATATTCTCAAGCTCCAAGTCTAAACCCAAATCTCATATTGGCTGCACCCCCCAAGGAAA GAAACCAAATTCCACAAAAAAAATCAAACTATACATTTTTACATTCACCCCTGGGGCACA GAAGAATTCCGTCCGGAGCAAACTCTATCTTAGCAGACACCTCTGTAGCGTTGTCAGCTA ATGATTCTATTTCTGCTGTTTCCAATTCGGTAAGAGCAAAGGATGACGAAACCAAAACAA CGTTGCCGCTGTTAAGGTCATATTTTATTCAAATTCTTTTGAACAATTTCCAGGAAGAAT TGCAGGATTGGAGAATAGACGGGGACTATGGATTACTAAGGTTGGTAGACAAATTGATGA TTTCCAAAGATGGTCAGAGATATATACAATGCTGGTGTTTCTTATTTGAAGACGCATTTG TAATAGCAGAAGTGGATAACGATGTTGATGTTTTGGAAATTAGACTAAAGAATTTAGAAG TATTTACACCTATTGCCAACTTGAGAATGACTACACTCGAAGCTTCAGTACTCAAATGCA CCTTAAATAAACAACATTGCGCCGATTTATCAGATCTTTACATTGTTCAGAATATAAATT CTGACGAAAGCACAACTGTACAGAAATGGATATCAGGTATATTGAATCAGGATTTTGTAT TCAATGAGGACAATATCACTTCGACCCTGCCTATTCTTCCCATTATAAAGAACTTTTCAA AAGTTGTTGAAGTTGGAAATGTGCACGATAATGATACTGTAATCATAAGGAGGGGATTCA CCTTAAATTCAGGAGAATGTTCTAGGCAGAGTACTGTCGACAGTATACAATCTGTTCTAA CCACGATAAGCTCAATTCTTTCCCTTAAACGAGAAAAACCTGATAATTTGGCAATAATCT TACAGATCGATTTTACGAAATTGAAGGAAGAAGACAGTTTAATTGTTGTTTATAACAGTC TAAAAGCTTTAACCATTAAATTTGCGCGTTTGCAGTTTTGTTTCGTTGATCGAAATAATT ATGTTCTGGACTATGGATCGGTATTACACAAGATAGATTCACTAGATTCCATCTCAAATC TCAAATCAAAGAGTTCCTCGACACAATTTTCACCTATTTGGTTGAAAAATACTCTATATC CCGAAAATATTCATGAACATTTGGGTATTGTTGCTGTATCAAATAGTAATATGGAAGCAA AAAAATCCATACTATTTCAAGATTACAGATGCTTTACAAGTTTTGGAAGAAGAAGGCCCA ATGAATTGAAGATTAAGGTGGGCTATTTGAACGTTGACTACAGTGATAAAATTGATGAAC TAGTCGAGGCCAGCTCCTGGACTTTTGTTTTAGAAACTCTTTGCTACAGTTTCGGTCTAA GTTTTGATGAACATGATGACGATGACGAAGAGGATAATGATGATTCGACCGATAATGAAC TTGATAATAGTTCAGGATCACTGTCGGATGCTGAATCTACAACTACTATTCATATTGATT CTCCATTTGATAATGAAAATGCTACCGCAAATATGGTGAATGACAGAAACCTTCTCACTG TGATTCCTAATATTAGATTTTCACTTCATTCTGAGGAGGAAGGTACTAATGAAAATGAAA ATGAAAATGATATGCCAGTATTATTACTTAGTGATATGGATAAAGGAATCGATGGCATAA CCAGACGCAGTTCATTCTCGAGTCTTATAGAGAGCGGTAATAACAACTGTCCCCTCCATA **TGGATTATATATAG**

YDR103W, 917 aa (SEQ ID NO 52) MMETPTDNIVSPFHNFGSSTQYSGTLSRTPNQIIELEKPSTLSPLSRGKKWTEKLARFQR SSAKKKRFSPSPISSSTFSFSPKSRVTSSNSSGNEDGNLMNTPSTVSTDYLPQHPHRTSS LPRPNSNLFHASNSNLSRANEPPRAENLSDNIPPKVAPFGYPIQRTSIKKSFLNASCTLC DEPISNRRKGEKIIELACGHLSHQECLIISFGTTSKADVRALFPFCTKCKKDTNKAVQCI PENDELKDILISDFLIHKIPDSELSITPQSRFPPYSPLLPPFGLSYTPVEROTIYSOAPS LNPNLILAAPPKERNQIPQKKSNYTFLHSPLGHRRIPSGANSILADTSVALSANDSISAV SNSVRAKDDETKTTLPLLRSYFIQILLNNFOEELODWRIDGDYGLLRLVDKLMISKDGOR YIQCWCFLFEDAFVIAEVDNDVDVLEIRLKNLEVFTPIANLRMTTLEASVLKCTLNKQHC ADLSDLYIVQNINSDESTTVQKWISGILNQDFVFNEDNITSTLPILPIIKNFSKDVGNGR HETSTFLGLINPNKVVEVGNVHDNDTVIIRRGFTLNSGECSRQSTVDSIQSVLTTISSIL SLKREKPDNLAIILQIDFTKLKEEDSLIVVYNSLKALTIKFARLQFCFVDRNNYVLDYGS VLHKIDSLDSISNLKSKSSSTQFSPIWLKNTLYPENIHEHLGIVÄVSNSNMEAKKSILFO DYRCFTSFGRRRPNELKIKVGYLNVDYSDKIDELVEASSWTFVLETLCYSFGLSFDEHDD DDEEDNDDSTDNELDNSSGSLSDAESTTTIHIDSPFDNENATANMVNDRNLLTEGEHSNI **ENLETVASSVQPALIPNIRFSLHSEEEGTNENENENDMPVLLLSDMDKGIDGITRRSSFS**

SLIESGNNNCPLHMDYI

YDR238C, 3422 bp, CDS: 501-3422 (SEQ ID NO 53) CCGTGTCAAGATCTAACACGGTAGTCAGCTACTACACAAGGTCTCAGAACAGAATGAGAA GTGGAACACTGGATAATGATTACGTGAACAGACAAAAGCTTCCTACACATATCTCTCTTC AAGATTATCGTGATGCTAATGCTAGAAGTAATATATCGCGTCAGGACTCTGTCTCCACAA CGAACTCTGATGTGGTAGACCTCAGCTATTCTCTGGGGCATGGCTTGCGTGTGGCAAACC CTGATTCAGACCCAGAATGATATCCTTCTCTGTAGTTTTTGTAGATGTCATATATGTACGT CCGTGTACTCGCTACACGTAGAAAGAAATCAGAAAACAACAGCTCGACAAGTGAAATTTG ACGTTCATTAAGACTCAGTTAAGATTGCCTTGAGAATAAACAAAAGTAATCACAGTTAAC TCGATCCTTCTCCGAGTATGGAGACTTACTCGAGTACCGATTTTCAGAAAGCTCTTGAAA AGGGATCTGATGAACAAAAAATTGACACGATGAAATCAATTTTAGTTACAATGCTGGAAG GAAATCCAATGCCTGAATTGTTGATGCACATAATAAGATTTGTCATGCCTTCTAAAAATA AGGAATTAAAAAAGCTTTTGTACTTCTACTGGGAAATTGTTCCCAAACTAGCTGAAGATG GAAAATTGAGACATGAAATGATTCTTGTCTGTAATGCCATTCAACACGATTTGCAACATC CTAATGAATATTAGAGGTAACACATTAAGGTTTTTAACGAAATTGAGAGAGGCCGAAC TCTTAGAACAGATGGTTCCCTCTGTCTTAGCGTGCTTGGAATACCGTCATGCATATGTTC GTAAGTATGCAATCCTAGCAGTTTTCTCCATTTTCAAGGTCAGCGAACATTTACTTCCCG ATGCTAAAGAAATCATCAATTCGTTCATAGTAGCTGAAACTGATCCAATATGTAAAAGAA ATGCATTTATTGGGTTAGCTGAATTAGATCGTGAAAATGCCTTACACTATTTAGAGAACA ATATTGCTGATATAGAAAACCTAGACCCTTTATTACAAGCTGTCTTTGTTCAATTTATCA GACAAGATGCAAACAGGACCCCTGCTTTGAAAGCCCAATATATCGAATTATTGATGGAAC TGCTTTCGACCACGACTTCCGATGAAGTCATCTTCGAGACCGCATTAGCCCTAACTGTGT AGGTTTCTGATAATAACATTAAGTTAATTGTTCTAGACCGTATTCAAGACATCAATGCTA ATAACGTAGGTGCTTTGGAAGAGTTAACCCTGGATATTTTGAGAGTCTTGAATGCAGAAG ATTTAGACGTTCGTTCAAAGGCGCTTGATATTTCAATGGACTTGGCCACATCCAGAAATG CTGAAGATGTTGTTCAGCTTTTGAAGAAAGAGCTGCAAACAACCGTAAATAACCCAGATC AAGACAAGGCAATGCAGTACAGACAATTGTTAATAAAAACTATTCGTACCGTGGCTGTAA ACTTTGTAGAAATGGCAGCAAGTGTTGTTTCGCTATTATTAGATTTCATCGGTGATTTAA ACTCGGTTGCCGCCAGTGGTATCATTGCCTTTATCAAAGAAGTGATCGAAAAATACCCAC AACTTAGAGCCAATATCCTTGAAAACATGGTTCAAACGCTAGACAAAGTGAGATCTGCTA AAGCTTACCGCGGTGCATTATGGATTATGGGTGAGTATGCTGAAGGAGAAAGTGAGATAC AACATTGTTGGAAGCACATTCGTAACAGCGTAGGTGAAGTTCCTATCCTTCAATCAGAAA TCAAAAAGTTAACACAAAACCAAGAACACCCGAAGAAAATGAGGTTGACGCTACCGCCA AGCCAACTGGTCCAGTTATTCTACCAGACGGTACGTATGCCACTGAAAGCGCTTTCGATG TGAAGACTTCTCAAAAGTCAGTTACCGATGAAGAACGTGATTCTAGACCTCCAATTCGCC GGTTTGTTTTAAGTGGTGATTTCTACACAGCTGCCATTCTGGCCAACACCATCATTAAAC TTGTTTTAAAATTCGAAAACGTTTCCAAGAACAAAACTGTCATCAATGCTCTAAAGGCGG AAGCTTTACTAATTTTAGTTAGTATTGTAAGAGTGGGTCAAAGCTCTTTGGTGGAGAAAA TTAATCCTGAGGAAAAGAAGGAAGAAGTTAAACTTCTGGAGGTTGCATTCCTGGACACCA CCAAATCCTCATTCAAGAGACAAATTGAAATTGCAAAGAAGAACAAGCATAAGAGAGCAT CTGGTGTGGATTCTACTAATGTGCAAAAAGATAGTATTGAAGAAGATTTACAACTGGCAA TGAAAGGAGATGCAATCCACGCTACTAGCAGCTCTAGTATTTCGAAGCTGAAGAAGATAG TGATTCCTCATGGCTTCCACAAATTCACTGTTACTGTCAAAGTTTCCTCTGCTGACACAG GTGTCATTTTCGGTAATATTATTTATGATGGTGCGCATGGTGAAGATGCTCGTTATGTTA TTTTAAACGACGTTCATGTTGACATTATGGATTATATCAAACCAGCCACTGCTGACGATG AACATTTCCGTACCATGTGGAATGCATTTGAGTGGGAGAACAAAATATCGGTCAAATCAC AACTACCAACATTGCATGCTTATTTGAGAGAACTGGTCAAGGGAACTAATATGGGTATTC TAACACCATCAGAGTCGTTGGGAGAAGATGATTGTAGGTTCTTAAGTTGTAATCTGTATG CGAAGTCGTCCTTTGGTGAAGATGCCCTAGCCAACTTGTGTATCGAAAAGGATTCCAAAA CCAATGATGTCATAGGTTATGTTCGTATCCGATCAAAGGGACAAGGTTTGGCTCTGTCCC WO 01/02550 PCT/BE00/00077

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YDR238C, 973 aa (SEO ID NO 54) MTSLSSOPAYTLVFDPSPSMETYSSTDFOKALEKGSDEOKIDTMKSILVTMLEGNPMPEL LMHIIRFVMPSKNKELKKLLYFYWEIVPKLAEDGKLRHEMILVCNAIOHDLOHPNEYIRG NTLRFLTKLREAELLEOMVPSVLACLEYRHAYVRKYAILAVFSIFKVSEHLLPDAKEIIN SFIVAETDPICKRNAFIGLAELDRENALHYLENNIADIENLDPLLQAVFVQFIRQDANRT PALKAQYIELLMELLSTTTSDEVIFETALALTVLSANPNVLVPAVNKLIDLAVKVSDNNI KLIVLDRIQDINANNVGALEELTLDILRVLNAEDLDVRSKALDISMDLATSRNAEDVVQL LKKELQTTVNNPDQDKAMQYRQLLIKTIRTVAVNFVEMAASVVSLLLDFIGDLNSVAASG IIAFIKEVIEKYPQLRANILENMVQTLDKVRSAKAYRGALWIMGEYAEGESEIOHCWKHI RNSVGEVPILQSEIKKLTQNQEHTEENEVDATAKPTGPVILPDGTYATESAFDVKTSOKS VTDEERDSRPPIRRFVLSGDFYTAAILANTIIKLVLKFENVSKNKTVINALKAEALLILV SIVRVGQSSLVEKKIDEDSLERVMTSISILLDEVNPEEKKEEVKLLEVAFLDTTKSSFKR QIEIAKKNKHKRALKDSCKNIEPIDTPISFRQFAGVDSTNVQKDSIEEDLQLAMKGDAIH ATSSSSISKLKKIVPLCGFSDPVYAEACITNNQFDVVLDVLLVNQTKETLKNLHVQFATL GDLKIIDTPQKTNVIPHGFHKFTVTVKVSSADTGVIFGNIIYDGAHGEDARYVILNDVHV DIMDYIKPATADDEHFRTMWNAFEWENKISVKSQLPTLHAYLRELVKGTNMGILTPSESL GEDDCRFLSCNLYAKSSFGEDALANLCIEKDSKTNDVIGYVRIRSKGQGLALSLGDRVAL **IAKKTNKLALTHV**

YDR259C, 1652 bp, CDS: 501-1652 (SEQ ID NO 55) AAACTTTGTTCAAGATTATGCTTTCTTTGTAATTTTAAACATAGTCTTGCACTTATTTTT ACTGCATGTGGATAAAAGTTTTTCGAATCGTTTGCAGGCAAATGTAAACTATTACTTTTT AATGATTTCTGATACTCTTTGATTCCATTCTGTCATACTTTTTTCTGCATTTGAAACGCT TAGTATCGAGAGTAGACTATCTTTGGAAAGCAATGCGAGTTGAGAGATTGTGGAGTGTAC TACAGAACCAATATTAAACACAATCTTTCCTCAAACTGTAACACCGAGTTTTTTTCCCCA CCAATCGTGAATCCGATAGCATATACTTTTGTCTAGAAATTTCAATAAACAACAGAATAA CGAAGAGTGCTAAGGGACAAATGCAAAACCCTCCGTTGATTCGTCCCGATATGTATAATC AGGGAAGCAGCTCAATGGCTACTTATAATGCCTCTGAGAAGAATCTAAATGAGCATCCTT CTCCGCAAATTGCACAGCCCAGCACGTCCCAAAAGTTACCTTATAGAATAAATCCTACAA CCACTAATGGGGACACCGACATATCTGTTAACAGCAATCCTATCCAGCCTCCTTTGCCAA ACTTGATGCATCTATCTGGTCCGTCTGACTATAGATCGATGCATCAAAGTCCTATACATC CATCTTATATCATCCCTCCGCATTCAAATGAAAGAAACAATCAGCTTCTTACAACAGAC CTCAAAATGCTCATGTTAGTATTCAACCTTCCGTGGTATTCCCCCCCTAAAAGTTATTCCA TATCTTATGCACCTTATCAAATAAATCCCCCTTTACCAAATGGACTTCCGAACCAGAGCA TATCTTTGAATAAGGAGTATATTGCAGAGGAGCAACTATCAACCCTCCCATCTCGCAATA CCAGTGTTACTACTGCACCTCCTTCTTTCAAAACAGTGCTGATACCGCTAAAAATTCAG CTGATAATAATGATAATGATAATGTAACCAAACCTGTTCCTGATAAAGACACCCAAC TCATAAGTAGTTCAGGCAAAACTTTAAGAAATACTAGAAGAGCTGCTCAAAATAGAACCG CTCAAAAGGCATTTAGACAAAGGAAAGAAAAATACATCAAGAATCTCGAACAAAAATCAA AGATATTTGACGATTTACTAGCAGAAAATAATAACTTCAAATCATTAAACGATTCATTAA GAAATGACAACAACATTTTAATAGCTCAGCATGAAGCTATAAGGAATGCAATTACTATGT TAAGAAGTGAGTATGATGTCTTATGTAACGAAAACAACATGTTGAAGAATGAGAATAGTA TAATAAAAATGAACACAACATGTCAAGAAATGAAAATGAAAACCTAAAACTTGAGAATA TAGTAGGGAGACACTCGGATAGTGCCACGTAA

YDR259C, 383 aa (SEQ ID NO 56)
MQNPPLIRPDMYNQGSSSMATYNASEKNLNEHPSPQIAQPSTSQKLPYRINPTTTNGDTD
ISVNSNPIQPPLPNLMHLSGPSDYRSMHQSPIHPSYIIPPHSNERKQSASYNRPQNAHVS
IQPSVVFPPKSYSISYAPYQINPPLPNGLPNQSISLNKEYIAEEQLSTLPSRNTSVTTAP
PSFQNSADTAKNSADNNDNNDNVTKPVPDKDTQLISSSGKTLRNTRRAAQNRTAQKAFRQ
RKEKYIKNLEQKSKIFDDLLAENNNFKSLNDSLRNDNNILIAQHEAIRNAITMLRSEYDV
LCNENNMLKNENSIIKNEHNMSRNENENLKLENKRFHAEYIRMIEDIENTKRKEQEQRDE
IEQLKKKIRSLEEIVGRHSDSAT

YDR294C, 2270 bp, CDS: 501-2270 (SEQ ID NO 57) CCGACAGTACGACTTAAAAAACAAAAACAACGTCCAGGTGGAAAAAGCTGCCGCAAATGG TACACGGTTTAGATCAACAAGATCCAATACCCCTAATTACACATGAATGTGACGTTTCCT AAAAGAAGTAGCCTGTATAATATAGAGAGATTTTATATACTTTCTTAATGAATTAGACTG TTTCTACAAGTATTTGACACTGGAAAAAAAGAGAAAGTACATAGAGATTGGCCAAATATT TAAATCTACACAGTTGCCTATCGTTTATCGCCTTATTCTTCAGAAACATTTCATCAACTA CCAACCGTTATAACTATTCCAGATCCTCTTTACCGAGCAAGTAGGCTAGCTTCTGTAAAG GGATTTTTCCATCTAATACAATGAGTGGAGTATCAAATAAAACAGTATCAATTAATGGTT GGTATGGCATGCCAATTCATTTACTAAGGGAAGAAGGCGACTTTGCCCAGTTTATGATTC TAACCATCAACGAATTAAAAATAGCCATACATGGTTACCTCAGAAATACCCCATGGTACA ATCTGTTGAAAGTTTATGGGCCGGTGAGGTTAGCAGTGAGAACATACGAGCATAGTTCCA GAAGATTGTTTCGTTGGTTATTGGACTCACCATTTTTGAGGGGGTACCGTAGAAAAGGAAG TCACAAAGGTCAAACAATCGATCGAAGACGAACTAATTAGATCGGACTCTCAGTTAATGA ATTTCCCACAGTTGCCATCCAATGGGATACCTCAGGATGATGTTATTGAAGAGCTAAATA ACCACGGTGGTGATGATTTGATCCACTTACAAACAATCGCATACGAAAAATATTGCGTTG CCAATCAATTACATCCCGATGTCTTTCCTGCCGTACGTAAAATGGAATCCGAAGTGGTTT CTATGGTTTTAAGAATGTTTAATGCCCCTTCTGATACAGGTTGTGGTACCACAACTTCAG GTGGTACAGAATCCTTGCTTTTAGCATGTCTGAGCGCTAAAATGTATGCCCTTCATCATC GTGGAATCACCGAACCAGAAATAATTGCTCCCGTAACTGCACATGCTGGGTTTGACAAAG CTGCTTATTACTTTGGCATGAAGCTACGCCACGTGGAGCTAGATCCAACGACATATCAAG TGGACCTGGGAAAAGTGAAAAAATTCATCAATAAGAACACAATTTTACTGGTCGGTTCCG CTCCAAACTTTCCTCATGGTATTGCCGATGATATTGAAGGATTGGGTAAAATAGCACAAA AATATAAACTTCCTTTACACGTCGACAGTTGTCTAGGTTCCTTTATTGTTTCATTTATGG AAAAGGCTGGTTACAAAAATCTGCCATTACTTGACTTTAGAGTCCCGGGAGTCACCTCAA TATCATGTGACACTCATAAATATGGATTTGCACCAAAAGGCTCGTCAGTTATAATGTATA GAAACAGCGACTTACGAATGCATCAGTATTACGTAAATCCTGCTTGGACTGGCGGGTTAT ATGGCTCTCCTACATTAGCAGGGTCCAGGCCTGGTGCTATTGTCGTAGGTTGTTGGGCCA CTATGGTCAACATGGGTGAAAATGGGTACATTGAGTCGTGCCAAGAAATAGTCGGTGCAG CAATGAAGTTTAAAAAATACATCCAGGAAAACATTCCAGACCTGAATATAATGGGCAACC CTAGATATTCAGTCATTTCATTTTCTTCAAAGACCTTGAACATACACGAACTATCTGACA GGTTGTCCAAGAAAGGCTGGCATTTCAATGCCCTACAAAAGCCGGTTGCACTACACATGG CCTTCACGAGATTGAGCGCTCATGTTGTGGATGAGATCTGCGACATTTTACGTACTACCG TGCAAGAGTTGAAGAGCGAATCAAATTCTAAACCATCCCCAGACGGAACTAGCGCTCTAT TAGACGCATTATACAAGTTGGGTCCAGGAGAGGATACCGCCACCAAGTAG

YDR294C, 589 aa (SEQ ID NO 58)
MSGVSNKTVSINGWYGMPIHLLREEGDFAQFMILTINELKIAIHGYLRNTPWYNMLKDYL
FVIFCYKLISNFFYLLKVYGPVRLAVRTYEHSSRRLFRWLLDSPFLRGTVEKEVTKVKQS
IEDELIRSDSQLMNFPQLPSNGIPQDDVIEELNKLNDLIPHTQWKEGKVSGAVYHGGDDL
IHLQTIAYEKYCVANQLHPDVFPAVRKMESEVVSMVLRMFNAPSDTGCGTTTSGGTESLL
LACLSAKMYALHHRGITEPEIIAPVTAHAGFDKAAYYFGMKLRHVELDPTTYQVDLGKVK
KFINKNTILLVGSAPNFPHGIADDIEGLGKIAQKYKLPLHVDSCLGSFIVSFMEKAGYKN
LPLLDFRVPGVTSISCDTHKYGFAPKGSSVIMYRNSDLRMHQYYVNPAWTGGLYGSPTLA
GSRPGAIVVGCWATMVNMGENGYIESCQEIVGAAMKFKKYIQENIPDLNIMGNPRYSVIS
FSSKTLNIHELSDRLSKKGWHFNALQKPVALHMAFTRLSAHVVDEICDILRTTVQELKSE
SNSKPSPDGTSALYGVAGSVKTAGVADKLIVGFLDALYKLGPGEDTATK

YDR430C, 3470 bp, CDS: 501-3470 (SEQ ID NO 59)
ACGTCATTTTGTTCTTGTGGAGCTGGTGGTTCTTGTGGAGCAGAT
TCCTGTGGAACTTGTGGTTCTTGTGGAGCATCTGGAGCCTGTGGTGGTTCTTGGTGCTGT
TCTTCGACTGGGGCATCGACAACAGATTCTGGTAGTTGCTCTACGTGAGTTTCTTGAGCT
TCAGACATTATCCTTATGGTTTTTAGCGTAATTGCTTAATTTTGATTCCTTCAAAAGTATA
TATATTTAGAAGAGAGAGAAATTATTTTTCTCATGTCCTTTTTAAATCCCTTTTGGGTGGCG
AAAAAAAAGAATGTAAAAAATTTTGCCCTTCGTTTACAGTGATAAATATACGGAGGGGCT
CTATGATAAAGGTAGTAAAATCATTGAATTGTTGAACAAGCATTGACAGATATGATAA

CAAGCAATTGTAATCAATAAGCCACCAATTAGAAGGCTACTCAAAAGAATAAAGTTACTA TAAAATATACTGCGGTATATATGTTGCGGTTTCAGCGATTTGCGTCCTCGTATGCCCAAG CACAGGCCGTTAGAAAATATCCAGTTGGAGGTATATTCCATGGTTATGAAGTGAGAAGAA TTCTACCGGTTCCGGAGCTGAGACTCACTGCGGTAGATTTGGTGCACTCCCAGACAGGAG CCGAGCATTTGCATATTGATAGAGACGACAAGAATAATGTGTTCAGCATTGCTTTTAAAA CCAACCCTCCAGATTCCACTGGGGTCCCTCATATTCTAGAGCATACAACGTTGTGTGGGT TCATGAACGCTATGACAGGTCCAGATTATACATTTTTTCCCTTTTCCACTACGAACCCTC AAGATTTCGCTAATTTAAGAGGTGTTTATTTAGACTCCACCTTGAATCCGCTACTTAAAC AAGAAGATTTTGATCAGGAGGGTTGGAGGTTGGAGCATAAAAACATCACAGACCCGGAGA GTAACATTGTTTTCAAAGGTGTTGTCTATAACGAAATGAAAGGTCAAATATCAAATGCCA ATTACTATTTCTGGAGTAAATTTCAACAGTCTATTTATCCTTCCCTGAATAACTCCGGCG GAGATCCTATGAAAATTACAGACTTGAGATACGGCGATCTCTTGGATTTCCATCACAAAA ATTACCATCCCTCCAATGCAAAAACTTTCACGTACGGTAACTTGCCATTGGTGGATACGT TAAAGCAATTAAATGAGCAGTTCAGTGGTTACGGGAAGAGAGCTCGAAAGGATAAGTTGT TAATGCCTATTGATTTAAAAAAAGACATAGATGTCAAGTTACTGGGTCAAATAGATACTA TGCTTCCACCGGAGAAGCAGACAAAAGCCTCAATGACGTGGATTTGTGGAGCGCCACAGG CTGTAATGTATCAAAAATTAATAGAATCAGGAATTGGTTTGGAGTTCTCCGTAAATTCAG TTGAAATATTTAAAGACACTGTAAATAATATTTTTCAAAACCTGTTGGAAACAGAACATC CTTTTGACCGCAAGCGTATCGATGCCATAATTGAACAATTGGAATTATCTAAGAAGGATC TCGATCCTTTTGAGAGCTTGTTGTTTGAGGACGTTTTGCAAAGATTTAGAGGTGACTTAG AAACGAAAGGTGATACTTTATTCCAAGATTTAATCCGTAAATATATCGTTCATAAACCTT GTTTCACGTTTTCCATTCAGGGATCTGAAGAGTTCTCTAAATCTTTGGATGATGAAGAAC AAACAAGACTGAGAGAAAAAATTACTGCCTTGGATGAACAAGACAAGAAAAAACATCTTTA AACGTGGTATACTGTTACAGGAGAAACAAAATGAAAAAGAAGATTTATCCTGTTTACCTA CCTTACAAATAAAAGACATCCCAAGAGCTGGTGATAAATATTCAATCGAACAGAAGAATA ATACAATGTCTAGGATTACTGATACCAATGGTATCACATATGTCAGAGGTAAACGTTTAC TAAATGACATAATACCCTTTGAACTCTTCCCATACTTACCTTTATTTGCTGAATCGTTAA CTAACCTAGGGACAACAACAGAATCCTTCAGTGAAATAGAAGATCAGATAAAATTACATA CGGGTGGTATATCAACACATGTAGAGGTTACATCTGACCCTAACACCACAGAGCCTCGCC GGTCTAAGATCTTACTAGAAACTGATTTCCATAAAAACAGCGATAAATTGAAAGTTCTTA TCCGCTTATTAGCATCTTCAAACACATCTTCTGTAGCAGATGCCGGTCATGCATTTGCAA GGGGCTATTCTGCCGCACATTATAGATCAAGTGGAGCTATAAATGAGACCCTCAATGGTA TTGAGCAACTACAATTTATAAATAGATTGCACAGCTTGTTAGACAATGAAGAAACTTTCC AAAGAGAAGTTGTCGACAAGCTAACTGAATTGCAAAAGTACATTGTTGATACCAATAACA TGAATTTTTTTATCACCTCAGACTCTGATGTTCAAGCGAAAACAGTAGAAAGCCAAATTT CAAAATTCATGGAGAGATTACCTCATGGCAGCTGCTTGCCCAATGGACCAAAGACTTCAG ATTATCCTCTTATTGGATCCAAATGTAAACATACTTTGATAAAATTTCCTTTTCCAGGTCC ATTACACATCCCAAGCTTTATTGGGTGTGCCGTATACACATAAGGATGGCTCTGCACTTC AAGTTATGTCAAATATGCTAACATTCAAACATTTGCACAGAGAAGTCAGAGAAAAGGGTG GTGCTTATGGTGGTGCTTCTTATAGCGCCTTAGCGGGTATTTTCAGTTTCTATTCCT ATAGGGATCCTCAGCCTTTGAAGAGTTTAGAAACCTTCAAGAATAGCGGGCGTTATATAC TGAACGATGCCAAGTGGGGCGTCACAGACCTTGATGAAGCTAAATTGACAATATTTCAAC AAGTAGACGCACCTAAAAGTCCCAAAGGAGAAGGCGTGACGTATTTCATGAGCGGTGTTA CAGACGATATGAAACAAGCAAGAAGGGAACAACTCTTAGACGTATCTCTCCTGGACGTTC ATAGAGTCGCCGAAAAATATCTACTAAACAAAGAAGGGGTGAGTACGGTCATTGGACCTG GAATCGAGGGAAGACTGTTTCACCAAATTGGGAGGTGAAGGAACTGTAG

YDR430C, 989 aa (SEQ ID NO 60)
MLRFQRFASSYAQAQAVRKYPVGGIFHGYEVRRILPVPELRLTAVDLVHSQTGAEHLHID
RDDKNNVFSIAFKTNPPDSTGVPHILEHTTLCGSVKYPVRDPFFKMLNKSLANFMNAMTG
PDYTFFPFSTTNPQDFANLRGVYLDSTLNPLLKQEDFDQEGWRLEHKNITDPESNIVFKG
VVYNEMKGQISNANYYFWSKFQQSIYPSLNNSGGDPMKITDLRYGDLLDFHHKNYHPSNA
KTFTYGNLPLVDTLKQLNEQFSGYGKRARKDKLLMPIDLKKDIDVKLLGQIDTMLPPEKQ
TKASMTWICGAPQDTYDTFLLKVLGNLLMDGHSSVMYQKLIESGIGLEFSVNSGVEPTTA
VNLLTVGIQGVSDIEIFKDTVNNIFQNLLETEHPFDRKRIDAIIEQLELSKKDQKADFGL

QLLYSILPGWTNKIDPFESLLFEDVLQRFRGDLETKGDTLFQDLIRKYIVHKPCFTFSIQ GSEEFSKSLDDEEQTRLREKITALDEQDKKNIFKRGILLQEKQNEKEDLSCLPTLQIKDI PRAGDKYSIEQKNNTMSRITDTNGITYVRGKRLLNDIIPFELFPYLPLFAESLTNLGTTT ESFSEIEDQIKLHTGGISTHVEVTSDPNTTEPRLIFGFDGWSLNSKTDHIFEFWSKILLE TDFHKNSDKLKVLIRLLASSNTSSVADAGHAFARGYSAAHYRSSGAINETLNGIEQLQFI NRLHSLLDNEETFQREVVDKLTELQKYIVDTNNMNFFITSDSDVQAKTVESQISKFMERL PHGSCLPNGPKTSDYPLIGSKCKHTLIKFPFQVHYTSQALLGVPYTHKDGSALQVMSNML TFKHLHREVREKGGAYGGGASYSALAGIFSFYSYRDPQPLKSLETFKNSGRYILNDAKWG VTDLDEAKLTIFQQVDAPKSPKGEGVTYFMSGVTDDMKQARREQLLDVSLLDVHRVAEKY LLNKEGVSTVIGPGIEGKTVSPNWEVKEL

YDR438W, 1613 bp, CDS: 501-1613 (SEO ID NO 61) CTTTTCTCAGCACCTGTCCAGAGACATAACATCACAATCACATCGCCCCAGTAAATGCA TACGCAAGATAAGATACAAACTGGCTACGGGAACACTACGCCAACGTGATTGGCAATTGT GCTCTAATAGTTACTCTATTATTGCTGTTAATTGACAATGTTTAGTCACGTGCAACACAA TTCAAGTCACGTGGAAAGGCCTTCACATGGTGATCCATCTTCTACATCTTCATCGGTCCT GCATAAAGTCATAATATGGGGCTACTGGAATGTATGCACTTAACAGTACTATTATATGGT GAGGCTGTAATGCTTACCGTTTTGTGGCTATTCTCGTATTCTGTAGGCCCCCCCATACAC ATTTTTCGGTAACTGCGGCATATAGATGAAAGTTGAAATGAATATTCAAAAGAATATATA TAATAATGCAGGAGATCAAGGAAGAATTAGATATGTATAAGAGTGATGGTAGAGGCAAAA **AATAAAAAGTAAGCAGGAGAATGAATCGTGTTTGGTATAGACGTAGATCATATGATAGGGG** TCCTGCTTCTGGCCGTAGTGGTGTTTTTGGGTTTGGCGCTTCGTGTTTGACTAATGAAT AGGAACGGACAGAACATTACCTATTCACACACAAGAATCTTTTTCAGAGTTCCTAC CTTTACTATCTTCAACTCCTTCTACTTCTTCAAATTTGTCTTCGATAGCGGACACGAAAG TGAAGGATACAATGAGGTTGAGTCTGCTATTTTGCGTCTTGTGGTTCGTGGCAAATTTGG CGGCTAACGCTGCTTTGTCGTATACCACAGTGGCTTCGTCAACAATTCTTTCATCGACAT CCTCATTTTTTACCTTATTTCTTGCCACTAGTCTAGGAATAGAAACTTTTTCGACAAAA AACTGCTGGGGTTATTTGTGTCTTTGTTTGGAATTATCTTAATTGTGATGCAATCCTCGA GGTCATTGGGTTACAGTGTCTATACAACCCTTTTGAAATACGAAATATCATCCAAAGGTC TCAGACTAGACATTCAGATGTTTCTTGGTTATGTTGGTATCTTCACGTTTCTGTTGTTTT GGCCAATTTTAATAATCCTGGATATAACACATATGGAAACTTTTGAACTACCAAGTAACT TCCACATTTCTTTTCTTGTCATGTTAAATTGTATCATTATCTTTGTTAGTGACTATTTTT GGTGTAAAGCCCTCATTTTGACATCACCCTTGGTGGTTACCGTTGCCTTAACTTTTACTA TCCCGTTAGCCATGTTCGCTGATTTTGTATGGCGAGAGGCATTTTTTACGCCTTGGTATA TCATTGGTGTTATTTTCATTTTTGTTTCATTCTTTCTAGTTAACCATCGGGGAGAATCTG CTGTTGAAAAGGACTGTGCTGCGGTTGAAAAAGGACCTATCTTGGATGCCTAA

YDR438W, 370 aa (SEQ ID NO 62)
MNRVGIDVDHMIGVLLLAVVVVFWVGASCLTNELLETNAYNKPFFLTYLNISSFALYLTP
DLWRIIQSRRKSLQERTERTLPIHTQESFSEFLPLLSSTPSTSSNLSSIADTKVKDTMRL
SLLFCVLWFVANLAANAALSYTTVASSTILSSTSSFFTLFLATSLGIETFSTKKLLGLFV
SLFGIILIVMQSSKQQDSVSASSFLVGNTLALLGSLGYSVYTTLLKYEISSKGLRLDIQM
FLGYVGIFTFLLFWPILIILDITHMETFELPSNFHISFLVMLNCIIIFVSDYFWCKALIL
TSPLVVTVALTFTIPLAMFADFVWREAFFTPWYIIGVIFIFVSFFLVNHRGESAVEKDCA
AVEKGPILDA



YDR450W, 146 aa (SEQ ID NO 64)
MSLVVQEQGSFQHILRLLNTNVDGNIKIVYALTTIKGVGRRYSNLVCKKADVDLHKRAGE
LTQEELERIVQIMQNPTHYKIPAWFLNRQNDITDGKDYHTLANNVESKLRDDLERLKKIR
AHRGIRHFWGLRVRGQHTKTTGRRRA

YDR486C, 1289 bp, CDS: 501-1289 (SEO ID NO 65) ACTGCATACACAATAACTGTAGATGTAGCCCAAGGCACTACCACAGGTATTTCTGCTCAC GACAGGTCGATGACTTGTAGGGCTCTTGCAGACTCTTCCTCTACGCCAAAATCATTTTTA AAACCAGGCACATCTGTCCCTTGAGAGCCGCTGATGGCGGTGTTTTGCAGAGAAGAGGC CACACTGAGGCCGGTGTCGATTTGTGTAAACTAAGTGGACTAAGTCCCGTCGCTGTTATT GGCGAATTGGTTAACGATGACGAACAAGGAACTATGATGAGATTAAATGACTGCCAAGCG TTTGGTAAGAAACATGGCATTCCTTTGATCTCCATCGAAGAATTGGCCCAATATTTGAAG AAATAATCTGGTGAACATTTTCTCCATTCATTCTATCACAACAGACTCACACATATATAC ATGTATATTTGTAACTTTGTATATATCTTTTGTTTTTTGACCTTTTTCTTCCTCTATG TTTTTCAGCCATACAAAAATATGGGATTTTTAGCAAGAGAAAAAGTACATCTAAAAAAG TAGTAATAGGAGGAAGCCAAGATTGGTTGAAACACAGTTATAAACTCTTCAAGGCAATTA TGAACAGGATTTTCGGATATGGGAACAAAAAGAGCCATGATCAGCTCTTACAAGAGTCGA ATCAGTCCATGAATCAGGCCCAACAATCACTATCGAACAGAATATCCCAGTTAGATACTC AAATCGCCCAGTTAAACTTCCAGCTGCAAAATATTCAAAAGAATTTGCAAAGATCAAACA AAAATATGAAGGATTCTTTAGATTCTCAATCCTGGTCCATGACGCAAGCCCAGTTAACAA ATGATAACTTACAGAACACAATGATCACTATAAACGCACTAAAGCAAACAACAATGCCA TGAAGGCTCAATACGGCAAGATAAATATCGACAAACTACAGGACATGCAGGATGAGATGC TGGATTTAATAGAACAAGGGGATGAGCTGCAAGAAGTCTTGGCAATGAATAATAACAGTG GCGAGCTCGACGACATTAGTGATGCAGAGCTGGATGCAGAGCTGGATGCTCTGGCACAAG TAGGTGCGAATGCGCCACCGGCTTTTATTGATGAAGAGCCAAACTTAGATACTGAAGACA AAAATAAAGCTTTAGAAAGCGCTCAGTGA

YDR486C, 262 aa (SEQ ID NO 66)
MGFLAREKVHLKKVVIGGSQDWLKHSYKLFKAIMNRIFGYGNKKSHDQLLQESNQSMNQA
QQSLSNRISQLDTQIAQLNFQLQNIQKNLQRSNNKQPSLRKQALKILNKRKQLENMKDSL
DSQSWSMTQAQLTNDNLQNTMITINALKQTNNAMKAQYGKINIDKLQDMQDEMLDLIEQG
DELQEVLAMNNNSGELDDISDAELDAELDALAQEDFTLPTSENSLGNDMPSYLLGANAPP
AFIDEEPNLDTEDKNKALESAQ

YDR471W, 136 aa (SEQ ID NO 68) MAKFLKAGKVAVVVRGRYAGKKVVIVKPHDEGSKSHPFGHALVAGIERYPSKVTKKHGAK KVAKRTKIKPFIKVVNYNHLLPTRYTLDVEAFKSVVSTETFEQPSQREEAKKVVKKAFEE RHQAGKNQWFFSKLRF

YDR499W, 2744 bp, CDS: 501-2744 (SEQ ID NO 69) TAACAATAGAAAAAATACACACACATTAGATTGGAATTAGAGCTTAAGTGGTACAAACT AGGGCTAATAAAGAGGTAACGGTCGGTTCTCTACTAAGGTTCGTATTGTGTGGCACCGAT AGCAAAGCAGTAAAAAGTCTCTGAATAAGGATAGTAACCTGTAGTAACTCCAAAATTTAT CTTACAAAGAGCTATTAGTATCTTGGTTCTTCTATTTTCTTCGATTATTGGTGATTTTTC CCGCCTCTAGCCAAATCCGAGCGTTCCATCGATTTTTTGGGGAAAACAGCACATGCAATA AAATAAAAAGCAAACAAATACGCGATAGTGCACGAAACGTCAACACAATCATCAAACTCT ATGATGATATTCTTTTGGAATTAGGCACCAGGCCTCCAAGGTTTACTCAAATACCGCCAT CATCAGCAGCATTACAAACACAAATTCCCACTACTTTGGAGGTTACAACGACCACATTAA ACAATAAACAGAGTAAAAATGATAACCAACTGGTTAACCAACTGAATAAAGCTCAAGGTG AAGCAAGCATGCTTCGTGATAAAATAAACTTTTTGAACATTGAAAGGGAAAAGGAAAAGA ATATTCAAGCCGTCAAAGTTAATGAATTGCAAGTCAAGCATCTTCAAGAGTTGGCTAAAT TAAAACAAGAATTACAGAAACTGGAAGATGAGAAGAAGTTCTTACAGATGGAAGCGAGAG GAAAATCGAAAAGGGAAGTTATTACGAATGTAAAACCACCGTCAACAACATTATCAACAA ACACAAACACTATAACGCCAGATTCGTCCTCAGTTGCAATCGAAGCAAAACCTCAATCAC ACCCAAATAGGATTATTCCCGATGAAACGAGTTTATTTCTAGAGTCAATATTACTTCATC AAATAATAGGCGCTGACCTGAGCACAATAGAATATTAAATAGATTGAAGCTTGACTACA TCACAGAGTTTAAATTTAAGAATTTCGTCATTGCTAAAGGAGCCCCCATAGGGAAGTCCA TAGTTTCTCTACTTTTGCGATGTAAAAAGACGTTGACCCTCGACAGGTTCATAGATACTT TGCTAGAGGATATAGCTGTTTTGATCAAGGAAATATCAGTTCATCCAAATGAATCGAAAT TAGCTGTCCCATTTCTCGTTGCATTGATGTATCAGATTGTACAATTTCGTCCTAGTGCCA CTCATAATTTAGCACTGAAGGATTGTTTTCTTTTTTATTTGCGATTTAATAAGAATCTATC ATCATGTATTGAAAGTACCGATACATGAATCAAATATGAATTTGCATGTAGAACCTCAGA TTTTCCAATATGAACTGATAGACTATTTGATAATTTCGTATTCCTTTGATCTCCTAGAAG GTATATTAAGGGTACTGCAGTCGCATCCTAAGCAAACTTATATGGAATTTTTTGATGAAA ATATTCTAAAATCATTTGAATTTGTCTACAAACTAGCACTAACCATTTCATACAAGCCAA TGGTAAATGTAATATTTAGTGCAGTCGAGGTCGTTAATATTATCACTAGTATAATATTAA ATATGGACAATTCCTCAGATCTGAAATCCTTGATAAGCGGTAGTTGGTGGAGAGATTGTA TTACAAGATTATACGCTCTTTTGGAAAAGGAAATTAAGAGTGGCGACGTATATAATGAAA ATGTGGATACTACAACTCTTCATATGTCGAAGTACCATGACTTTTTTGGGTTAATCCGAA ATATAGGTGATAATGAATTGGGAGGATTGATATCAAAGCTGATTTATACTGACCGATTGC CCCCTATAATAGGTTACAAGATGGAAAAATGGCTTTTGAAGTTAAAAGATGAAGTTTTAA ATATTTTTGAAAATTTATTAATGATCTATGGAGACGATGCGACCATAGTAAATGGAGAAA TGCTCATCCACTCCTAAATTCTTATCCAGGGAGCAAGCGTTAATGATAGAAAGGTACG

TGGACAAGACTCCCCGAACTTGGACCTCAGATGCCATCTTATTGAACATACTTTAACCA
TAATATATAGGCTATGGAAAGACCATTTCAAACAATTGCGTGAAGAACAAATCAAGCAGG
TAGAAAGCCAATTGATTATGTCACTATGGAGGTTTCTCGTATGCCAAACCGAAACTGTGA
CAGCAAACGAAAGAGAAATGAGAGATCATCGACACCTTGTAGATAGTTTGCATGATCTGA
CGATAAAGGATCAAGCCTCTTATTACGAAGATGCCTTTGAGGATTTACCAGAATATATCG
AAGAAGAATTGAAGATGCAATTGAATAAAAGAACGGGGAGAATAATGCAAGTAACG
ATGAGAAATTTCAAGAAAATGGCAAGAACTATTCTTGAGTCAAAATCATTCGATCTAACCA
CACTAGAGGAGGCCGATTCATTATATATCTCAATGGGACTGTAA

YDR499W, 747 aa (SEQ ID NO 70)
MRRETVGEFSSDDDDDILLELGTRPPRFTQIPPSSAALQTQIPTTLEVTTTTLNNKQSKN
DNQLVNQLNKAQGEASMLRDKINFLNIEREKEKNIQAVKVNELQVKHLQELAKLKQELQK
LEDEKKFLQMEARGKSKREVITNVKPPSTTLSTNTNTITPDSSSVAIEAKPQSPQSKKRK
ISDNLLKKNMVPLNPNRIIPDETSLFLESILLHQIIGADLSTIEILNRLKLDYITEFKFK
NFVIAKGAPIGKSIVSLLLRCKKTLTLDRFIDTLLEDIAVLIKEISVHPNESKLAVPFLV
ALMYQIVQFRPSATHNLALKDCFLFICDLIRIYHHVLKVPIHESNMNLHVEPQIFQYELI
DYLIISYSFDLLEGILRVLQSHPKQTYMEFFDENILKSFEFVYKLALTISYKPMVNVIFS
AVEVVNIITSIILNMDNSSDLKSLISGSWWRDCITRLYALLEKEIKSGDVYNENVDTTTL
HMSKYHDFFGLIRNIGDNELGGLISKLIYTDRLQSVPRVISKEDIGMDSDKFTAPIIGYK
MEKWLLKLKDEVLNIFENLLMIYGDDATIVNGEMLIHSSKFLSREQALMIERYVGQDSPN
LDLRCHLIEHTLTIIYRLWKDHFKQLREEQIKQVESQLIMSLWRFLVCQTETVTANEREM
RDHRHLVDSLHDLTIKDQASYYEDAFEDLPEYIEEELKMQLNKRTGRIMQVKYDEKFQEM
ARTILESKSFDLTTLEEADSLYISMGL

YDR507C, 3929 bp, CDS: 501-3929 (SEQ ID NO 71) CTCTTTAAATATTCTATGTACTTTGTGCAAACATCATTGTCATCACATAAATGCATTCCT ACTATTACTAACTTGAACTTCACTTCACTGGAAGAACTGGGTTATTCAAGGTAAAGAAAT CATTTGTTTTGCGCCAAGTTTCGTCTGACAAGAATTTTTTTATTATTATTTCCCACTTTTC ATCGAAGGAAACGCGTCAAATCCATTCGTTACTACGCGCAATCTGCGTTATTTCCTTTTT CGGCATACCATCGCGAAATATCAACGGCCACACCATAGATTCCTTTTGATGTTAAATTAA AAGCGACTGAATGAAGTGCACACATTTTTTATTTCTTCTTGATTTTCTTTTCTATTTTGT TTTGCTTTCTCTCTGTCGACAACGTCTCAACTGTACTCACCATTAGTATTCTCGAAGGC ATACAATAATAACATTCAAAATGGCAATCAATGGTAACAGTATTCCTGCCATAAAGGATA ATACCATCGGTCCATGGAAACTAGGTGAAACTCTCGGTCTAGGGAGCACTGGTAAAGTCC AGCTTGCTCGTAATGGATCCACAGGACAAGAGGCGGCAGTTAAGGTAATATCAAAAGCAG TATTCAATACCGGTAATGTCAGCGGTACTTCGATTGTTGGCTCCACCACCCCAGATGCTC TACCATATGGTATAGAACGCGAAATAATCATTATGAAGTTGTTAAACCACCCAAATGTGT TACGTTTATATGATGTCTGGGAAACAAATACAGATTTATACCTTGTTTTAGAATACGCGG AGAAAGGTGAGTTGTTCAACTTATTGGTTGAGAGGGTCCTCTGCCAGAGCATGAAGCTA TCAGGTTTTTTAGACAAATTATTATTGGTGTGTCGTACTGTCATGCGTTGGGTATTGTCC ATCGTGATCTAAAACCGGAAAATCTATTATTAGATCATAAATATAACATCAAGATTGCAG ATTTTGGTATGGCTGCTTTGGAAACTGAAGGAAAGCTACTGGAGACGTCGTGCGGATCAC CACATTATGCTGCACCAGAAATTGTATCTGGTATACCGTATCAAGGTTTCGCAAGTGATG TGTGGTCATGCGGTGTGATCCTATTCGCCCTTCTTACTGGTCGGTTACCCTTTGACGAGG AAGATGGAAATATAAGAACACTATTACTTAAAGTTCAAAAAGGTGAGTTCGAAATGCCTT CTGATGATGAAATTTCGCGTGAAGCTCAGGATTTGATTAGAAAAATCTTAACCGTTGATC CTGAAAGAAGAATCAAGACCAGAGATATACTCAAACATCCGCTATTACAAAAATATCCAA GTATAAGAGATTCTAAAAGTATTAGAGGCTTACCAAGAGAAGACACATATCTCACGCCAT TATCAGAAAGTAATTCTTCTATTGACGCTACGATTTTGCAAAATTTAGTAATATTATGGC ATGGAAGAGATCCTGAAGGAATTAAGGAAAAACTAAGAGAACCTGGCGCTAATGCAGAAA AGACATTATATGCACTACTGTATAGATTTAAGTGTGACACTCAAAAAGAGCTTATTAAGC AACAGCAAGTTAAGAAGAGGCAGTCAATTAGTAGCGTTTCTGTTTCCCCATCTAAAAAAG TATCGACAACTCCACAACGCAGAAGAAATAGAGAATCTTTAATTAGTGTAACATCTTCTC GTAAAAAGCCAATATCCTTCAACAAATTCACTGCCTCCAGTGCCTCCTCCAGCAATCTAA CTACACCCGGTTCTTCAAAACGCCTTTCAAAAAACTTCTCTTCAAAGAAGAAATTATCTA CAATCGTTAACCAATCTTCTCCAACACCAGCATCACGTAATAAAAGAGCTTCGGTTATAA ATGTGGAAAAGAATCAAAAAAAGAGCCTCTATCTTTTCTACTACCAAGAAGAACAAAAGAT CTTCTAGATCTATCAAGAGAATGTCATTGATACCAAGCATGAAACGTGAATCGGTGACAA CAAAATTAATGTCAACATATGCGAAATTGGCAGAGGATGACGATTGGGAATACATTGAGA

CAAAATTCTTGGGTTCATCATTTAATATCGATAAAGAGTTGAAATTGTCTAAAATGGAAT ATCCAAGTATAATTGCACCACAAAGATTGTCAGAGGAGCGAGTGGTGTCAGATTCTAATG ATGGATATGAATCTTTGATCCTCCCGAAGGATGGGAATGGCGTATCTCAATTAAAGGATA GTACCGCAACAACTGCTCCCGTCTCTGATGGTAGGTTGAGGAAGATCTCTGAAATTAGAG TACCACAATTTACTAGAAAATCAAGGCATTTTAGTGAGTCCAATAAAAGGCTATCTGTCC TGTCGATGTACTACCAAGGAGTCGTTTACCAACTTGGTTGATATTTTGAAAAACGGTA ACCTTGATGTCAATAACCAACAAGAAGCCAAAGAATTCCAACACCAAGAAGTGCGGATGATT CAGAATTTCTTTTGAAACTGTCAACGAAGAAGCTGAATATACAGGAAATAGTTCGAACG ATGAGAGATTGTACGATGTCGGTGATTCCACTATCAAAGACAAATCCGCGTTAAAGCTGA CGATCCTTCCTCCGCTTAATGGTGACAATGAATTGCGTAAACAGAATAGCCAAGAGGGTG ACCAGGCACATCCAAAGATTAAATCGATGATACCAGAATCAGGCTCTTCTTCACATACTG AGGATCAAGAAAAAGAGAGAAAGTAGTAGATGATATGGAGCCACCATTGAACAAATCTG TGCAAAAAATTAGGGAAAAAAATGCTGGCTCGCAGGCAAAGGATCATTCAAAAGATCACT TAAAAGAGCATAAGCAGGATAAAAATACAGCAATTGGAAATGGTTCCTTCTTTAGAAAAT TCTCAAAATCTTCGGACAAAACAATGGAATTGTATGCCAAGATTTCTGCAAAACAATTGT TTAATGGTTTAGAGAAGCTGTTGCGTGGTTGGACTCAGTATGGTTTAAAAAATATAAAAT CGCACCCAACAATCTGACCTTAACGGGTAAACTATCGAGTGATAATATATTCTCACTAC GTTCAACACTCTTTGAGGTTAATATTTATCCGAGAGGTAAGATGAGCGTTGTGCAGTTCA AGAAAGTTTCTGGTTCATTCAAAGCTGTCAAAAAGTTGGTCAATGAAGTTGAGAACGTCC TGAATAAGGAAGGCGTTCTACAAAAATAG

YDR507C, 1142 aa (SEO ID NO 72) MAINGNSIPAIKDNTIGPWKLGETLGLGSTGKVQLARNGSTGQEAAVKVISKAVFNTGNV SGTSIVGSTTPDALPYGIEREIIIMKLLNHPNVLRLYDVWETNTDLYLVLEYAEKGELFN LLVERGPLPEHEAIRFFRQIIIGVSYCHALGIVHRDLKPENLLLDHKYNIKIADFGMAAL ETEGKLLETSCGSPHYAAPEIVSGIPYQGFASDVWSCGVILFALLTGRLPFDEEDGNIRT LLLKVQKGEFEMPSDDEISREAQDLIRKILTVDPERRIKTRDILKHPLLQKYPSIRDSKS IRGLPREDTYLTPLSESNSSIDATILQNLVILWHGRDPEGIKEKLREPGANAEKTLYALL YRFKCDTQKELIKQQQVKKRQSISSVSVSPSKKVSTTPQRRRNRESLISVTSSRKKPISF NKFTASSASSSNLTTPGSSKRLSKNFSSKKKLSTIVNQSSPTPASRNKRASVINVEKNQK RASIFSTTKKNKRSSRSIKRMSLIPSMKRESVTTKLMSTYAKLAEDDDWEYIEKETKRTS SNFATLIDEIFEYEKYEQIRKEKEELERKVREAKAREELERRRRKQEEKERARKLLEKED LKRKQEELKKQIEIDISDLEQELSKHKEEKLDGNIRSISAPMENEEKNINHLEVDIDNIL RRRNFSLQTRPVSRLDPGIMFSSPTEEVSPVEPKRTENERLTTEKKILETIRRSKFLGSS FNIDKELKLSKMEYPSIIAPQRLSEERVVSDSNDGYESLILPKDGNGVSQLKDSTATTAP VSDGRLRKISEIRVPQFTRKSRHFSESNKRLSVLSMYSTKESFTNLVDILKNGNLDVNNO QSQRIPTPRSADDSEFLFETVNEEAEYTGNSSNDERLYDVGDSTIKDKSALKLNFADRFN GSNEAKQTDNLHLPILPPLNGDNELRKQNSQEGDQAHPKIKSMIPESGSSSHTEKEEENE EKEEKKPEQHKQEEDQEKREKVVDDMEPPLNKSVQKIREKNAGSQAKDHSKDHLKEHKQD KNTAIGNGSFFRKFSKSSDKTMELYAKISAKQLFNGLEKLLRGWTQYGLKNIKSHPNNLT LTGKLSSDNIFSLRSTLFEVNIYPRGKMSVVQFKKVSGSFKAVKKLVNEVENVLNKEGVL OK

YDR515W, 1844 bp, CDS: 501-1844 (SEQ ID NO 73) GAGTTGAATCTATGCGTAACCATTTTGACTACCGCTTCGTATGCTTTCTTGCACTTTGTG GAGCTACTCATACAATAGCTTATAATCTGTGTAGTCAAACTATATACTAGGCAAATTACT AGTAAATGCAGTATTCATATGTCCTCAAACCGTTTTTTTGCAGTATGTTATTGATCCATCG AATCAAAATTTTTCACCGCCCAAGAGAAAAAAAGATCTTACTATTTTTGTGCTTATGAAAAAA

CCACATCGCCATGGAAATCATCTTCGCCAGATAGCAATACAGTAATTCCTGTAGAGGAAC TAAGAGATATATCAAAGACTGCAAAGCCAAGTAAAAATGGTTCGGGGTCAATTAAATTAA CAAGCAATACCAAATGGACTCCAATTACGCCGTCTGTTATAATCTCAGGTTCCAAGGACA CAAATTCAAAGTCAGGAAAGAACTCTAAAAATTCTAAGACTAATAAAAAATGAAAAAGC GTGGCAAATATAACGATATCAATAAAAAGGACTTTAACGGTCAAACCAACAGTACAT CGGAAATAAGTAACGTTTCCAATCTTGAATCCAAACCTTTAGATGCTAACGCTAAAGTAA ACAATTCAACCAACGGTAGACAATCAAGAAATTATCAAAACAGGAATGGCAAAACAAGAT ACAACAATAGTAGACACAGTCAGGCGGCTAATAATGCCATCTCCTTCCCAAATAATT ATCAGGCTAGACCTGAATATATTCCCAATGCCAGCCACTGGTTGAACAACAATTCAAGAA ATAGCTATAAACAACTGTCATACTTCCGTCAACAGCAGTATTATAATAACATCAACTATC AACAACAATTGCAAACACCATATTATTACTCAATGGAACCTATTTTTAAATCTATCGAAA GTATCAAAAACCAAATTGAATTCTATTTTAGTGAAGAGAACTTGAAAACAGATGAATTTT TAAGATCTAAATTCAAAAAAGCCAATGACGGATTTATCCCCATGAGTTTGATAGGGAAAT TTTACCGTATGGTTAATTTATCTCTTGGTGGAGACCCAAATTTAATTTTGGCATCTATGA GAGAAGTTTTACAACATAAAGAAACAAACCATTTGGAAATTGCCCTTGGAAGCATAGAAG GTGCTCAGAAGAACATGGCAGATGATTTCAATCCATTGGAAAACTATTTTATTAGGCGCG AAAATTGGGCTGAATACGCTATGGAAAGTAATTTTGATGAAAATGATGACGAAACTGAAA AATACAACATTGAGAAACTATTGGGACCGAACGATTTAGACAATTATTCTTATATGGGCT ATCCAAACTTCTTTCCCAGTAATGAAAATGGGAAAAAGAGTCAGAGCTATGACCAAGGTG AAATTAGCAGGCAGTTTGAACAAAACTTACAAATAAATGATTAA

YDR515W, 447 aa (SEQ ID NO 74)
MSSQNLNDNPKNTSSAAEDKKKQTSSLKLAPIPTTSPWKSSSPDSNTVIPVEELRDISKT
AKPSKNGSGSIKLTSNTKWTPITPSVIISGSKDTNSKSGKNSKNSKTNKKMKKRGKYNND
INKKDFNGQTNSTSEISNVSNLESKPLDANAKVNIHSSSGATANGNIKRITNNNNSTNGR
QSRNYQNRNGKTRYNNNSRHSQAANNAISFPNNYQARPEYIPNASHWLNNNSRNSYKQLS
YFRQQQYYNNINYQQQLQTPYYYSMEPIFKSIESIKNQIEFYFSEENLKTDEFLRSKFKK
ANDGFIPMSLIGKFYRMVNLSLGGDPNLILASMREVLQHKETNHLEIALGSIEGAQKNMA
DDFNPLENYFIRRENWAEYAMESNFDENDDETEKYNIEKLLGPNDLDNYSYMGYPNFFPS
NENGKKSQSYDQGEISRQFEQNLQIND

YDR518W, 2054 bp, CDS: 501-2054 (SEQ ID NO 75) GCAGCAGGGCAAGATGACAACCCTGTTCCTGTTCCTGTTCCAGTAGAATCTGAGACGGC TTTTGTGCCATCAGCATTCACAGCACCACCGGTGCCAACAAAGAAGAAATCAAAAAATAA AAAGGGTACCCAGCCATTGGCAATGGATGACTATTTTAATGAAGGCAGAGATAAGTCATC TACCGCTGCGAAGTCAGCAGAATCTGACATCCTCGCCCCACCACCACAAAAACAGTCATC CTCTGATTAACTTTCCTGGTTAGTCTTTTGGTTTTGTTTCATAGCAAAATTAAATATATA TATATAAGCTTGCTTTCCCTTCAAAACACGTAAACGATAGTTGGCAATGTACGAAAAGTA CCGAGACTTTTTTCAAAGGCACGCGTGTCCTTTTTTGTTAAGACAATAGATATTTTAGC ATTCAGAAAGTTTCAATTTCCAAGACTTGACGTTTCAATTATATGGCAATCTCCCAACAA GCACCCGCTCATATAATACCATGCAAGTGACCACAAGATTTATATCTGCGATAGTCTCGT TTTGCCTGTTTGCTTCTTTCACGTTGGCTGAAAACAGCGCAAGAGCTACGCCGGGATCAG TCGTCGAGTTTTTTGCTCCATGGTGTTTGCATTCTCAGATCTTACGCCCTCACTTAGAAG ACAGTATGGTTTGCCTGCAACAAACTATAAATACCTACCCAACCTTGAAAATCTTTAAAA ATGGTCGTATTTTGATGGTCAAGTCTATCGCGGTGTCAAGATCACCGATGAAATCACTC AACCATACTTGGAAAATGCAACTTTACCAGTAGTAATAAACAGAGGCTTGACAGGCTTGA ATGAAACGTATCAAGAAGTCGCACTGGACCTTGCTGAGGATTACGTCTTTTTATCCCTTC TAGATTCAGAAGATAAGTCATTATCAATCCACTTGCCAAACACTACAGAACCAATTCTGT TTGATGGAAATGTAGACTCTTTGGTCGGAAATTCCGTTGCTCTAACTCAGTGGTTAAAAG

YDR518W, 517 aa (SEQ ID NO 76)
MQVTTRFISAIVSFCLFASFTLAENSARATPGSDLLVLTEKKFKSFIESHPLVLVEFFAP
WCLHSQILRPHLEEAASILKEHNVPVVQIDCEANSMVCLQQTINTYPTLKIFKNGRIFDG
QVYRGVKITDEITQYMIQLYEASVIYLNSEDEIQPYLENATLPVVINRGLTGLNETYQEV
ALDLAEDYVFLSLLDSEDKSLSIHLPNTTEPILFDGNVDSLVGNSVALTQWLKVVILPYF
TDIEPDLFPKYISSNLPLAYFFYTSEEELEDYTDLFTQLGKENRGQINFIALNSTMFPHH
VRFLNMREQFPLFAIHNMINNLKYGLPQLPEEEYAKLEKPQPLDRDMIVQLVKDYREGTA
KPIVKSEEIPKEQKSNVYKIVGKTHDDIVHDDDKDVLVKYYATWCIHSKRFAPIYEEIAN
VLASDESVRDKILIAEVDSGANDILSFPVTGYPTIALYPAGNNSKPIIFNKIRNLEDVFE
FIKESGTHHIDGQAIYDKLHQAKDSEVSTEDTVHDEL

YDR519W, 908 bp, CDS: 501-908 (SEQ ID NO 77) GGGGCAAATGATATCTTAAGTTTTCCTGTGACAGGATATCCAACCATTGCTTTGTATCCT GCCGGAAATAACTCTAAGCCTATTATCTTCAATAAAATTAGAAATTTGGAAGATGTTTTC GAATTTATCAAGGAATCAGGTACACATCACATTGACGGCCAGGCAATTTATGATAAATTG CACCAGGCCAAGGATTCTGAAGTGTCTACTGAAGATACCGTACATGATGAATTATAATCA ATAAATAAAGCATATAATGCACATTTTTAACATCTGATTACTCGCATCGTTTCTGGAA GAAAATAGCTAATATTCGTTATTTATGGCATCACGATTATTCTCACCAGTTACCCGTTTA TGCTCTTGAAGAGATTTAGCATTACTGCCAGCGCATCTTCAAATACAGGTTTATATGAGA CCCATTACTATAACCCTAAGAAGAGAAAAAGGAGTGCTTTCGTTTTCAATCACATTCTAG CCATTCTTGCAGGTTCCCTGTCAGATTTGGAAATCGGTATTATCAAGAGAATACCGGTAG AAGATTGCTTAATTAAGGCAATGCCAGGTGATAAAGTTAAGGTTCATTATACAGGATCTT TATTAGAATCGGGAACTGTATTTGACTCAAGTTATTCAAGAGGCTCTCCTATCGCTTTTG AACTTGGCGTTGGCAGAGTAATTAAAGGTTGGGATCAAGGTGTTGCCGGCATGTGCGTTG GCGAAAAAAGAAAGCTGCAAATTCCAAGTTCTTTGGCCTACGGAGAAAGAGGTGTCCCAG GCGTCATTCCTCCAAGTGCTGATTTGGTGTTTGATGTCGAATTGGTAGACGTGAAATCAG **CCGCCTAG**

YDR519W, 136 aa (SEQ ID NO 78) MMFNIYLFVTFFSTILAGSLSDLEIGIIKRIPVEDCLIKAMPGDKVKVHYTGSLLESGTV FDSSYSRGSPIAFELGVGRVIKGWDQGVAGMCVGEKRKLQIPSSLAYGERGVPGVIPPSA DLVFDVELVDVKSAA

CTGGTGCTAAACGTGCTCAATTCAGAAAGAAGAAGAAAGTTCGAATTAGGTCGTCAACCAG CCAACACAAAAATTGGTGCTAAGAGAATCCACTCTGTCAGAACTAGAGGTGGTAACAAGA AATACAGAGCTCTAAGAATTGAAACCGGTAACTTTTCTTGGGCTTCTGAAGGTATCTCCA AGAAGACCAGAATTGCTGGTGTTGTTTACCATCCATCCAACAATGAATTGGTTAGAACTA ACACTTTGACCAAGGCTGCCATTGTCCAAATTGATGCTACTCCATTCAGACAATGGTTCG AAGCTCACTACGGTCAAACCTTGGGTAAGAAGAAGAACGTCAAGGAAGAAACTGTTG CCAAGAGCAAGAACGCTGAAAGAAAGTGGGCTGCTAGAGCTGCTTCTGCCAAGATCGAAT CTTCCGTTGAATCTCAATTCAGCGCCGGTAGATTATACGCTTGTATCTCTTCCAGACCAG GTCAATCCGGTAGATGTGATGGTTACATCTTGGAAGGTGAAGAATTAGCTTTCTACCTAA GAAGATTGACTGCTAAGAAATAG

YER102W, 200 aa (SEQ ID NO 80)
MGISRDSRHKRSATGAKRAQFRKKRKFELGRQPANTKIGAKRIHSVRTRGGNKKYRALRI
ETGNFSWASEGISKKTRIAGVVYHPSNNELVRTNTLTKAAIVQIDATPFRQWFEAHYGQT
LGKKKNVKEEETVAKSKNAERKWAARAASAKIESSVESQFSAGRLYACISSRPGQSGRCD
GYILEGEELAFYLRRLTAKK

YER153C, 1265 bp, CDS: 501-1265 (SEQ ID NO 81) ACCCTATATGGGAGGACAACTCGCCCACTGTTTGGGTCGTGTTAGCGATAAGGTCCGAAG TAGAAGCGGAAAGAGAAGGCTGAAGAGGTTAATTCATCGATGGAAGGCAACTGGGTTT GGATTTCCGAGACATCGTTGGCATTTGGGCCCGTCGAATTAAATCTTTTGGCCTGAAAAG AGATCCATGACGGATGGGGCCGGGGCAATACTATGGTTCGAGCGGTGGCCAGTCTGGAAG AGGCAGCAAACCTTGACGTGACGAGTCGAGAGGTGAGTTTGAACATCGTCGGGGAGGTTA TTCTGTGGCTCCGCTTGTACGTGAACAGATACGTATAGAGGGCGAGCCACTGGTTAAATT TTTCATGGCTCGGATTACTTCCGTACTGCTGGCTAAAATCGAAATCTCGGCCTGCTGAGA GTGTTTTGAGCAATCAAGGGAACATCTGAACGTGGAAGAGCAGACGAGGCATTAGCTCGA ACATAAGAACGGAACACGTCATGTTGACTATCACGAAAAGACTGGTGACCACCGATGTGC GGTCGCGAATACTGTTAAGCAGTTTAAACGGGAAAATGTCCGATGCACTGGCGCTGCTGC GTCAGCAGCAGACCAGCGTGGATGTGGAGCTGCTGCACACGATGCTAGCGCGAGCCG CTGCGCTTGCCCATGCCGACACTATAGCATACATGTGGTATCAGCATGTGATGCCACGCC GGCTCTTCTTACCCGCGCAGTTCCTCCAGCACTACCAGGCGATGAATCGCGATCGTCGCA CCAGCCCAGAAGATGAACTGATTGAGTATGAGCTTAGACGGATTAAAGTCGAAGCGTTTG CGCGTGGCACAATGCACTCCACGGCGCTCAGGGAAAAGTGGAAGGTATTCTTGCAGGAGA TGGATACGCTACCAGGGCAGCCGCCATTAAGGCTGCGCGACTTCCCGCAAATGACCAAGG CTATGGGCATAGCATTGATGCAGCAAGATGAGCAGCAGCTGCCCTGGCGTTGTTTGGAC GGCATGTTCCCGGCCCAGCGCAGGCGCGACGTGTGCTGGCGGAGTTCCGTCAAAGTTATC GCGGGCTGCCGCTGCTGGATGCCGAACTAGTGATAAAGAGAAGAGGATTTGAAATCAACA CATAA

YER153C, 254 aa (SEQ ID NO 82)
MLTITKRLVTTDVRSRILLSSLNGKMSDALALLRQQQQTSVDVELLHTMLARAAALAHAD
TIAYMWYQHVMPRRLPVEGRLLCEMAGVALYQDRLFLPAQFLQHYQAMNRDRRTSPEDEL
IEYELRRIKVEAFARGTMHSTALREKWKVFLQEMDTLPGQPPLRLRDFPQMTKAMGIALM
QQDEQAAALALFGRQPLVIKNEWSLPLLLAGVLWHVPGPAQARRVLAEFRQSYRGLPLLD
AELVIKRRGFEINT

YFL014W, 109 aa (SEQ ID NO 84) MSDAGRKGFGEKASEALKPDSQKSYAEQGKEYITDKADKVAGKVQPEDNKGVFQGVHDSA EKGKDNAEGQGESLADQARDYMGAAKSKLNDAVEYVSGRVHGEEDPTKK

YFL015C, 995 bp, CDS: 501-995 (SEQ ID NO 85) GACCTTCAGCGTTATCCTTGCCTTTTTCGGCAGAGTCGTGGACACCTTGGAAGACACCCT TGTTGTCTTCTGGTTGAACCTTACCAGCGACCTTGTCGGCCTTGTCAGTGATGTATTCCT TACCTTGTTCAGCGTATGACTTTTGAGAGTCTGGCTTCAAAGCTTCAGAAGCTTTTTCAC ATAAGATCAAACGCAATTGAGGAAGTAGAACGCAATTCACCGTCCTATTTATACGTTTTA ATATAGATTTAGAGAAAGACCTTTCAGATCAAGAGGGGGACGACCGGAACCTCAAAGTTG ACCAAACGATTTTCCAGGGGCTGTAGATCTAGTTACTCTCCGTCTAGAGTGCTTCTGGTC TGTGTTTGTGGGTTGTATTAATGCTTGCGTATACCTTTCCTTCTTTCAATTTCTACGTCA ATGTTATTTTGTGCCGCCCCCTGCAAGTTGCAACATATCCCCTTAACAGATGCCAGCAAT ATTCTAGTCTTGCTATTTTTACCGCCTCTGGCTTTTTGGCTTCTAGTCCTTGTCCCAAGAG CCAAGGGCCCGTCAACACGTCGTCATTGCTACCGCCAGCTGGCACCCACACATCACCGAC CTTGGATTTGCGCGTCCCCTTTTTTTCTTCATTCTCTGACTCCCCCTACCTTCTCCCACT TTTCTGTGTATCAAGAGGAAAAGAAGGAGAAAAGGAGAAACTCCGAAAAATACCGAACAAG AGGGTAACAGAATGTGCATTTGGATGAGCGGGTAA

YFL015C, 164 aa (SEQ ID NO 86) MLAYTFPSFNFYVNGFFSFLFLFLFLFPSLLRFYVILCRPLQVATYPLNRCQQYSSLAIF TASGFWLLVLVPRAKGPSTRRHCYRQLAPTHHRPFFSIFGWAVSGIRPLPEIFTWICASP FFLHSLTPPTFSHFSVYQEEKKEKRRTPKNTEQEGNRMCIWMSG

YFR022W, 2702 bp, CDS: 501-2702 (SEQ ID NO 87) CTGCCTTCCGTACGTCACAACGCATACACAATATAGTTTATATAAACTCCTGCGTATAAT AATAGAACTCGCCTAAAGGGGAAATTTTCGATATAAAAATTCAAAAAAATGGCTTTCATG GATCGAGTATTTGTTGTCGAAAAAGGATCACTGGAGTGACGTTACTACGCTACGAAGCC TCCTTCCGGCTTAGCCCTGTTGATTACGAATTTGGATCAGTTGGTATTTGATTCCTCGGA AGAGTTAACTTCACGCGGGTAAATCACTTGTGATGCGGTATATTCTCTATACGGCTAATA GATGAATCAGGGTGTTTTAAAGTGCGTATAAACCCTTTTTGCTATTTTCGTTTATATAATT GGCGTTGATAAAGAGCCAATATCTATTGTTGCTACATAGAGGCAGCTCTCTTAGCAAAAT AAAAATACAAAAAGTTCGACATGGGCTTCAGTAGCGGTAAATCAACTAAGAAAAAGCCTC TGCTTTTCGATATCAGACTTAAAAATGTTGACAACGATGTAATACTCCTCAAAGGTCCTC CAAACGAGGCCCCCTCGGTGCTTTTATCTGGTTGCATCGTTTTATCGATTAACGAACCCA TGCAGATCAAAAGCATATCATTGAGACTTTATGGGAAGATACAAATAGACGTACCATTAG AGAGGCCCCAGGACGCTAGTTCTTCGTCGTTGTCTTCATCGCCGCCAAAGATCAGAAAGT ACAACAAAGTTTTTTATAATTACGCATGGGATAATGTTAACCTCAAGGAGTATCTGAGTG GTTTAAGAGGGCAATCTGGCCTTGCGGGCAGTAGCTCATCAAGTAATATCTTGGGCACTC GCCAAAGAGCTCAGTCCACAAGTTCCTTGAAGTCTTTAAAGGGGTCCTCCTCACCCTCTT CATGTACTTTAGATAAGGGCAACTACGATTTTCCCTTTAGTGCTATTTTGCCTGGTTCGT TACCAGAGAGCGTAGAATCTTTGCCAAATTGCTTCGTGACATATAGCATGGAATCCGTTA TTGAACGCAGCAAAAATTATAGTGATTTGATCTGTAGGAAAAATATTAGAGTTCTGAGAA CCATTTCACCCGCAGCAGTGGAGTTATCAGAAACTGTTTGTGTAGATAACTCATGGCCCG ACAAAGTGGATTATTCTATTTCAGTACCCAACAAAGCCGTAGCTATTGGTTCAGCCACCC TATTATTGAGAATTATCAATATTGTGACCCCTTCCCTCCAGTAATTTCTGAAAATAGGC AAGTGACAGAACTAAATCTTGAAGATCCCTTGAACGAGTCATCTGGAGAATTTAATGGTA

AGATTGATACCATCCTGCAAATCCCGAACAGCTTATCAAACTGTGTGCAAGATTGTGATG TCCGCTCTAACATTAAGGTTCGCCATAAGCTCAAATTTTTCATCATCCTAATTAACCCAG ATGGTCATAAATCTGAGTTAAGAGCGTCCTTACCGATTCAACTTTTTATTTCACCATTTG TGGCACTTTCAATAAAACCATTGTCATCCTCGAATTTGTATTCGCTTTTTTAGCACCACTA ACCAGAAAGACGAAAACTCATCACAAGAAGAGGAAGAGGAATATCTGTTTTCTAGATCAG CATCAGTCACAGGGTTGGAATTATTAGCGGATATGCGTAGCGGTGGCTCTGTTCCTACCA TTTCAGACTTGATGACGCCCCCAAATTATGAAATGCACGTATATGATCGTCTTTATAGCG GTTCTTTCACTCGCACGCTGTGGAAACGTCTGGAACATGTACTCCTTTGGGAAGCGAAT GTTCGACTGTCGAGGATCAGCAACAGGATTTAGAAGATTTACGTATACGGTTGACAAAAA TTAGAAATCAACGTGACAATCTAGGGCTACCACCGTCTGCCTCGTCTGCCGCCTTCCA GATCGCTATCTCCATTACTAAACGTTCCAGCACCAGAGGATGGCACGGAGAGAATCTTAC CTCAGAGTGCTCTTGGTCCCAATAGTGGCTCTGTGCCAGGAGTACATAGTAACGTATCAC CTGTTTTACTTTCAAGATCCCCAGCCCCAAGCGTGTCAGCCCATGAAGTGTTACCAGTGC CCTCGGGCTTAAATTATCCAGAGACTCAAAACCTGAACAAGGTTCCATCGTATGGCAAGG ATGTGCAACCAAGAAAACCCAGTAGGGTACATTCCAGGAACTCTTCGACAACATTGTCAT CTTCTATACCAACTAGCTTTCATTCCTCTAGTTTTATGAGTAGCACTGCTTCCCCTATTT CCATAATTAATGGCTCTAGAAGTAGTTCTAGTGGGGTATCTCTTAATACACTTAATGAGT TAACTTCGAAAACTTCGAATAACCCATCCAGTAATAGTATGAAAAGGTCACCAACAAGAC GGAGGGCTACTTCTTTAGCTGGGTTTATGGGAGGTTTTCTATCAAAGGGTAACAAACGAT

YFR022W, 733 aa (SEQ ID NO 88)
MGFSSGKSTKKKPLLFDIRLKNVDNDVILLKGPPNEAPSVLLSGCIVLSINEPMQIKSIS
LRLYGKIQIDVPLERPQDASSSSLSSSPPKIRKYNKVFYNYAWDNVNLKEYLSGLRGQSG
LAGSSSSSNILGTRQRAQSTSSLKSLKGSSSPSSCTLDKGNYDFPFSAILPGSLPESVES
LPNCFVTYSMESVIERSKNYSDLICRKNIRVLRTISPAAVELSETVCVDNSWPDKVDYSI
SVPNKAVAIGSATPINISIVPLSKGLKLGSIKVVLFENYQYCDPFPPVISENRQVTELNL
EDPLNESSGEFNGNGCFVNNPFFQPDHSFQDKWEIDTILQIPNSLSNCVQDCDVRSNIKV
RHKLKFFIILINPDGHKSELRASLPIQLFISPFVALSIKPLSSSNLYSLFSTTNQKDENS
SQEEEEEYLFSRSASVTGLELLADMRSGGSVPTISDLMTPPNYEMHVYDRLYSGSFTRTA
VETSGTCTPLGSECSTVEDQQQDLEDLRIRLTKIRNQRDNLGLPPSASSAAASRSLSPLL
NVPAPEDGTERILPQSALGPNSGSVPGVHSNVSPVLLSRSPAPSVSAHEVLPVPSGLNYP
ETQNLNKVPSYGKAMKYDIIGEDLPPSYPCAIQNVQPRKPSRVHSRNSSTTLSSSIPTSF
HSSSFMSSTASPISIINGSRSSSSGVSLNTLNELTSKTSNNPSSNSMKRSPTRRATSLA
GFMGGFLSKGNKR

YGL011C, 1259 bp, CDS: 501-1259 (SEQ ID NO 89) AGACAATAAAATATGGAAAATAAAACGCTTAGCACAGCAGTCAATGAAATACTCTGATAT ATTTTGACTCTGTGGAGCATACAGCTACCACTAAATAGGATTGTGGGGACAAATATGGAA TGGATCAAAACGTTCTTAGGATTGTGGTGGTAAAACTTGTAAAATCCAAGCTGAGATCTT AAATCCAGCAAACCTTCGCCCATATTTATTCTTTTATAACAGAAGAAGAGACTATATTCT GATTTACCTTGGCATTCCTTTTTCCCCATCCTCTTATAATGGTAATCGCGATCCTTAATTA TGATATCACAATAGACGAAGGGCACACACCAATTTGCCACCGTAAGGATAGAGTAAGTTA AATGGCTAACTCATTATAATCTTCATGCTAAATCATATAAGGGCAGAGACGAAGCAAAGC GAAAAAACATATTACAATCATGTCGGGTGCTGCTGCTGCTGCTGCTGCTGGTTATGACA GGCACATCACTATCTTTTCCCCCGAGGGTCGTTTATATCAAGTAGAATATGCCTTTAAAG CGACTAATCAAACTAACATAAACTCACTAGCGGTCAGAGGTAAAGATTGTACAGTGGTGA TAAGTCAGAAAAAGGTCCCTGATAAACTGTTGGATCCAACTACTGTTTCGTATATTTTTT GTATTTCAAGAACAATTGGTATGGTAGTGAACGGACCAATACCGGATGCAAGAAATGCGG CCCTAAGAGCCAAGGCTGAGGCTGCAGAATTCCGTTATAAATATGGTTATGATATGCCAT GCGATGTATTGGCTAAGAGAATGGCTAACCTTTCCCAAATCTATACTCAAAGAGCATATA TGAGACCATTAGGTGTTATACTCACATTTGTTTCGGTAGATGAAGAATTGGGTCCCTCCA TTTACAAAACTGACCCTGCAGGTTATTACGTTGGCTACAAAGCTACTGCGACAGGACCAA AACAACAGGAGATCACAACAAACTTAGAAAACCATTTCAAAAAGAGTAAAATCGACCATA TTAATGAAGAATCATGGGAGAAGGTGGTAGAATTTGCTATTACTCATATGACTGCCAC TGGGTACCGAATTTTCAAAGAATGACTTGGAAGTCGGTGTCGCTACAAAGGACAAATTCT TTACCTTGAGTGCTGAGAACATCGAAGAAAGGCTAGTAGCAATTGCTGAACAAGATTAA

YGL011C, 252 aa (SEQ ID NO 90)
MSGAAAASAAGYDRHITIFSPEGRLYQVEYAFKATNQTNINSLAVRGKDCTVVISQKKVP
DKLLDPTTVSYIFCISRTIGMVVNGPIPDARNAALRAKAEAAEFRYKYGYDMPCDVLAKR
MANLSQIYTQRAYMRPLGVILTFVSVDEELGPSIYKTDPAGYYVGYKATATGPKQQEITT
NLENHFKKSKIDHINEESWEKVVEFAITHMIDALGTEFSKNDLEVGVATKDKFFTLSAEN
IEERLVAIAEQD

YGL031C, 968 bp, CDS: 501-968 (SEQ ID NO 91) CCAAGTTAAGCAAGACACCAAGACAATAACTTGAGAGGTATGTCCCTATATGATGATGAT TCATAATTAATGGCGACCGAGGGCAGCGTTGTGCTAGAAAGCAATGTATTAATATATGAG AGAGCTTCAGATAGCCAATACACCGGAATTTAGACTTTGACAGGATTGTGGCTTGTTCCA GTATAACTTATAATATATGTCAACCTTTGAGCAGGAAACCCAATGAAAATGCTTCATTAC ATATATACGATATGGAGAAGCATGAAAAATAACAGCGTGAGATGTTATCCATGTTGCAAG AACCTAGTAAAATGAATTCTGAATTTGCAAAAAGTCCATATTTCCACGTTCTCCTCTTCC TGGATTAATATAGTGATAAAATGAAGGTTGAAATCGATTCTTTTTCAGGTGCCAAAATCT ACCCAGGCAGAGGTACCTTGTTTGTCCGTGGTGACTCCAAAATCTTCAGATTCCAAAACT CCAAATCTGCCTCTTTGTTCAAGCAAAGAAGAACCCAAGAAGAATCGCTTGGACTGTCT TATTCAGAAAGCATCACAAGAAGGGTATCACCGAAGAAGTTGCTAAGAAGATCTAGAA AAACCGTTAAGGCCCAAAGACCAATTACCGGTGCTTCTTTGGACTTGATCAAGGAAAGAA GATCTTTGAAGCCAGAAGTTAGAAAGGCTAACAGAGAAGAAAAATTGAAGGCCAACAAAG AAAAGAAGAAGGCTGAAAAGGCTGCTAGAAAAGGCTGAAAAGGCTAAGTCTGCTGGTACTC AAAGTTCTAAGTTCTCCAAGCAACAAGCTAAGGGTGCTTTCCAAAAGGTTGCTGCTACTT CTCGTTAA

YGL031C, 155 aa (SEQ ID NO 92) MKVEIDSFSGAKIYPGRGTLFVRGDSKIFRFQNSKSASLFKQRKNPRRIAWTVLFRKHHK KGITEEVAKKRSRKTVKAQRPITGASLDLIKERRSLKPEVRKANREEKLKANKEKKKAEK AARKAEKAKSAGTQSSKFSKQQAKGAFQKVAATSR

YGL032C, 87 aa (SEQ ID NO 94) MQLLRCFSIFSVIASVLAQELTTICEQIPSPTLESTPYSLSTTTILANGKAMQGVFEYYK SVTFVSNCGSHPSTTSKGSPINTQYVF

TGCTTCGAATGACAACGCCTTTTTGATATATAATATCCAATTTCATTATAGGGAAATTTT CAACTCTTACCCGCCCCACTGTGCTGATATGACCAAGTGATCACTCGATGATGGGACTAC GTATTGAAAAATATTGAATGAAAAATTACTCAAGCAGCAGAACATTCACAGTGTAGTCAG TCCGCATAAGAGCATTCATCATGGATAGTAAGGAAGTACTGGTACATGTTAAGAATCTAG AAAAGAACAAAAGTAATGATGCTGCAGTTCTAGAAATCTTACATGTCTTGGATAAAGAAT TCGTCCCCACTGAAAAGTTACTGAGAGAAACAAAAGTTGGTGTGGAAGTCAACAAGTTTA AAAAATCCACTAATGTAGAGATCAGCAAACTCGTGAAGAAAATGATTAGCTCTTGGAAAG ACGCAATTAATAAAAATAAGCGTTCCAGGCAAGCACAGCACCATCATCAAGATCATGCGC CAGGCAATGCAGAGACAAGACAACTGTAGGTGAGTCCGTGAATGGTGTTCAACAGCCGG CCTCCTCCCAGTCAGATGCCATGAAACAAGACAAGTACGTCAGCACTAAACCAAGAAATA GTAAGAACGATGGTGTGGATACAGCTATATACCACCACAAATTACGTGATCAGGTACTAA AAGCACTCTACGACGTTTTGGCCAAGGAAAGTGAGCATCCACCTCAATCTATTTTGCATA CTGCAAAGGCCATAGAAAGTGAAATGAATAAAGTTAACAACTGTGACACCAACGAAGCCG CTTACAAAGCCAGGTATCGTATAATTTATTCAAACGTCATATCAAAGAATAACCCAGATC TCAAACATAAAATTGCCAACGGTGATATAACACCTGAATTCTTAGCTACATGCGATGCCA AGGATCTGGCACCAGCGCCCTTAAAGCAAAAGATAGAAGAAATTGCCAAGCAAAACTTAT ACAACGCACAGGGTGCCACCATAGAAAGGTCAGTCACCGATAGATTTACATGTGGTAAAT GTAAAGAGAAGGTATCTTACTATCAATTGCAAACAAGATCTGCGGATGAACCATTGA CCACTTTCTGTACATGTGAAGCATGTGGTAACAGATGGAAATTCTCTTAG

YGL043W, 309 aa (SEQ ID NO 96)
MDSKEVLVHVKNLEKNKSNDAAVLEILHVLDKEFVPTEKLLRETKVGVEVNKFKKSTNVE
ISKLVKKMISSWKDAINKNKRSRQAQQHHQDHAPGNAEDKTTVGESVNGVQQPASSQSDA
MKQDKYVSTKPRNSKNDGVDTAIYHHKLRDQVLKALYDVLAKESEHPPQSILHTAKAIES
EMNKVNNCDTNEAAYKARYRIIYSNVISKNNPDLKHKIANGDITPEFLATCDAKDLAPAP
LKQKIEEIAKQNLYNAQGATIERSVTDRFTCGKCKEKKVSYYQLQTRSADEPLTTFCTCE
ACGNRWKFS

YGL102C, 929 bp, CDS: 501-929 (SEQ ID NO 97) TGTTACGATCAACATTCTTGTCCGTAATCAGCATGGTAGTTAAACCCATTCTGTACATAT GGTCAGATATACTTTCGCATGGGTCAATACCATGGTCAACCCAACCAGTTCTTTGCG TTTTCAAAAGTTGTATAATATTCAAAAACGCTAACTGATAATTTGGGTGAGGTTTCGAAA GAATTGCCAAAATCTCCCTAGGTATATTATCTTCTGGCTTCCAGATGTTAACTGCAGTCA TTTTGTTTTCCTGGTCTTTACCTCGAATAGGTTTTCTTGTTTTGTTATTTGTTTCTTT TTGGACCCTATGTTTATATATGGATTTTGAAAATCTTTTAAAAAAGCGATAAAAGCGTTG GGATCTGCCACTGGTAACTTCAAAATAGACAAGACGAAAAAAACGGTGAAAATGGGTGATA GAAATAATACAGAAGTAGATGTTGAATTAGATTAAACTGAAGATATATAATTTATTGGAA AATACATAGAGTTTTTGTTGATGCGCTTAAGCGATCAATTCAACAACACCACCAGCAGCT CTGATTTTTCTTCAGCCAACTTGGAGACGAATCTAGCTTTGACGATAACTGGAACATTT GGAATTCTACCCTTACCCAAGATCTTACCGTAACCGGCTGCCAAAGTGTCAATAACTGGA GCAGTTTCCTTAGAAGCAGATTTCAAGTATTGGTCTCTCTTGTCTTCTGGGATCAATGTC CACAATTTGTCCAAGTTCAAGACTGGCTTCCAGAAATGAGCTTGTTGCTTGTGGAAGTAT CTCATACCAACCTTACCGAAATAACCTGGATGGTATTTATCCATGTTAATTCTGTGGTGA TGTTGACCACCGGCCATACCTCTACCACCGGGGTGCTTTCTGTGCTTACCGATACGACCT TTACCGGCTGTACAAAAAAAAATATTGTAA

YGL102C, 142 aa (SEQ ID NO 98) MRLSDQFNNTTSSSDFFFSQLGDESSFDDNWNIWNSTLTQDLTVTGCQSVNNWSSFLRSR FQVLVSLVFWDQCPQFVQVQDWLPEMSLLLVEVSHTNLTEITWMVFIHVNSVVMLTTGHT STTGVLSVLTDTTFTGCTKKIL

YGL103W, 1461 bp, exon1: 501-549, intron1: 550-1060, exon2: 1061-1461 (SEQ ID NO 99)

AACAAGCTATAATATTGTTAAATATAGTTGATCAACAGCATTGTAATGATTACAAGAGAC GAGGTGGAATGAACCTTATGAAATGCGTATTATATATAAACTGTAATAAGAGCTAAGTTG AATTGAAATCTACGATACTTGATGTTGACATTATAGCACTAGTTCCCAGGAAACCCTTTC GAAAAACACAGCAAAAACAAGAGTACTGTAACCAATGTAACATCTGTACACCAGGGACCC ACACATTACCAAAATTATTTTTCTAATGCCTGTTATTTTTCCTCTTGGCGCGCGTGAATAGCCCGCAGAGACCCAAACCAATTTTCCTCGCAGTTTTTTCCTCTTTAA TGCGTGTTATTTTCCCCAGATAGATCAAACCCTTTCATCTGTATCCCGTATATTTTAAGATGGCG

AATCATCCAACTAATCAAGAATGCCTTCCAGATTCACTAAGACTAGAAAGCACAGAGGTC ACGTCTCAGGTATGTAGTTCCATTTGGAAGAGGGAATGAAAGAACCAAGACGGTGACTTT TTTTTTAGTGTTGTGCAACCAATATGTCGTGTGTATATCATGGTACAGGAGAATGTCAAT CAGCTAAGTGTACTCAACATATTTCTTTGTGTTTTGATTGCGAACTTTGTATTACCATCT CACTGTTGAGACGGCTTATTTGAGGTAATAGCTCGAGTAAATGTACTCTTCCATCGCAAA CTGAGCAAAAAGAAGTGTGCATAGCCTTTGTCATACTTCTCCTTTATTATACCATGATA TTCAGAACAGTCATACTGTCTACTCATTTTACGGCTATAAAAGGTAACTTTCATTTAGAT TATGGAAAGCACTAATTATCGCTGTATCAAATGGTTGTAGAGAGCGCAATTATGAAAAAG AGTTACCACGTTTCTTTTGTTTCGATAAAATGTCCAGTTGAAAACCTGTTTTACTAACGA TTTAAAAATTGTATTTCATTACAATATTTTTTTTTGTACAGCCGGTAAAGGTCGTATCGGT AAGCACAGAAAGCACCCCGGTGGTAGAGGTATGGCCGGTGGTCAACATCACCACAGAATT AACATGGATAAATACCATCCAGGTTATTTCGGTAAGGTTGGTATGAGATACTTCCACAAG CAACAAGCTCATTTCTGGAAGCCAGTCTTGAACTTGGACAAATTGTGGACATTGATCCCA GAAGACAAGAGACCAATACTTGAAATCTGCTTCTAAGGAAACTGCTCCAGTTATTGAC ACTTTGGCAGCCGGTTACGGTAAGATCTTGGGTAAGGGTAGAATTCCAAATGTTCCAGTT ATCGTCAAAGCTAGATTCGTCTCCAAGTTGGCTGAAGAAAAAATCAGAGCTGCTGGTGGT GTTGTTGAATTGATCGCTTAA

YGL103W, 149 aa (SEQ ID NO 100) MPSRFTKTRKHRGHVSAGKGRIGKHRKHPGGRGMAGGQHHHRINMDKYHPGYFGKVGMRY FHKQQAHFWKPVLNLDKLWTLIPEDKRDQYLKSASKETAPVIDTLAAGYGKILGKGRIPN VPVIVKARFVSKLAEEKIRAAGGVVELIA

YGL130W, 1880 bp, CDS: 501-1880 (SEQ ID NO 101) TTTTGGTACTTGAATTTCTCGTTTCTACTAGCTGGATTGCTTGTCCTTTTACAATTCCTG GGAGTTTGGCTATTGCTACCCTTGGTCTTAGCACCACTTTTTTCCGCTATTTGTATTTGT TGAACTAATTTAGTATCTATTTCCATTTCATTATAATTCACGTTTTTAGCAGCCTCTCTT CTTCTAGGTAATTGGAAATCTTCTTTTAGGCATAGCGTGACCAGCTGAAAGGCAGATG ATCTCAATATGTCCCGATAGGCCAATTTTGCCACCAGATAGTTCGATGGCATTTTATTTT TAGTCCTTTTGAAAGCAATATCATAAAATATATATAGTTCTCCATGATGTTCGGGTCAGT CGACCGCTAATTTAACAAATATGGTTTTAGCAATGGAAAGTAGAGTGGCACCGGAAATTC CTGGGCTCATTCAACCTGGGAATGTCACGCAAGACTTGAAGATGATGGTCTGTAAATTAT TGAATTCCCCAAAACCTACGAAAACATTCCCTGGTTCCCAGCCTGTGTCCTTTCAGCATT CTGATGTGGAAGAGAAGCTGCTTGCGCATGATTACTACGTTTGTGAGAAAACAGATGGTC TGCGGGTGTTGATGTTTATAGTGATAAATCCTGTGACGGGTGAGCAAGGATGCTTTATGA TTGATAGGGAAAATAACTATTATCTGGTTAATGGATTTAGGTTTCCCAGATTACCCCAAA AGAAGAAGAAGAGCTGCTAGAGACTCTTCAAGATGGCACCTTATTAGATGGTGAACTTG TCATACAAACTAACCCAATGACAAAATTACAAGAGTTGCGTTATTTAATGTTCGATTGTC TTGCTATCAATGGTAGATGTCTCACACAATCACCAACAAGTTCTAGACTAGCCCACCTTG GAAAAGAATTTTTTAAACCATACTTCGATTTAAGAGCAGCGTACCCTAATCGTTGTACTA CTTTTCCGTTCAAAATTTCCATGAAACATATGGATTTCAGTTACCAATTAGTAAAAGTTG CTAAAAGTTTAGATAAACTACCACATCTTTCTGATGGTCTGATATTTACTCCTGTGAAGG CACCTTACACTGCCGGCGGAAAAGATTCATTGTTATTAAAATGGAAGCCAGAACAAGAAA ACACCGTGGACTTCAAATTGATTTTAGATATCCCAATGGTGGAGGATCCTTCTTTGCCTA AAGATGATCGGAACAGGTGGTATTACAATTATGACGTTAAGCCAGTTTTCAGCTTATATG TCTGGCAAGGCGGAGCTGATGTCAATTCACGTTTAAAACATTTCGACCAGCCTTTCGATA GGAAGGAATTTGAAATATTAGAAAGAACATACAGAAAATTTGCAGAGTTGAGCGTTTCAG ATGAGGAATGGCAAAATTTGAAGAACCTAGAACAGCCATTAAATGGTAGAATAGTAGAGT GCGCAAAAAACCAAGAGACTGGGGCGTGGGAAATGTTAAGATTCAGGGATGATAAGTTAA ATGGTAATCATACATCGGTGGTCCAGAAAGTTTTGGAGAGTATCAACGATTCAGTTTCAT TGGAGGACCTCGAGGAAATTGTTGGTGATATTAAAAGGTGCTGGGACGAGAAAAGAGCAA ATATGGCTGGTGGTAGTGGGAGACCACTACCGTCTCAAAGTCAAAATGCGACATTATCTA CCTCTAAGCCAGTCCATTCACAGCCCCCAAGTAATGATAAGGAGCCAAAATATGTAGACG AGGATGATTGGTCGGATTAG

YGL130W, 459 aa (SEQ ID NO 102) MVLAMESRVAPEIPGLIQPGNVTQDLKMMVCKLLNSPKPTKTFPGSQPVSFOHSDVEEKL LAHDYYVCEKTDGLRVLMFIVINPVTGEQGCFMIDRENNYYLVNGFRFPRLPQKKKEELL ETLQDGTLLDGELVIQTNPMTKLQELRYLMFDCLAINGRCLTQSPTSSRLAHLGKEFFKP YFDLRAAYPNRCTTFPFKISMKHMDFSYQLVKVAKSLDKLPHLSDGLIFTPVKAPYTAGG KDSLLLKWKPEQENTVDFKLILDIPMVEDPSLPKDDRNRWYYNYDVKPVFSLYVWQGGAD VNSRLKHFDQPFDRKEFEILERTYRKFAELSVSDEEWQNLKNLEQPLNGRIVECAKNQET GAWEMLRFRDDKLNGNHTSVVQKVLESINDSVSLEDLEEIVGDIKRCWDERRANMAGGSG RPLPSOSONATLSTSKPVHSOPPSNDKEPKYVDEDDWSD

YGL147C, 1076 bp, CDS: 501-1076 (SEO ID NO 103) CAATATTATAGTTACTACCTATTTGATTATTAAGATCAAAAGTAATCCTTCATCTCATAT CAAAAAGAAAGGTTTGTAAAAGAGCATTGGGCAGAGAGTATTTGTCCTGCGTATAGAGGA TTTCCAGAAATGTTTGGGTTTATTTTTTAATTTTTTGAAACATTTTTTTCATCCTTTCTC ATTTTGTCATTTCATTTTCTGTGGAAAATTTCACTGACGCGAAGAAGCGATGAAATTTC GAGGTCAGAGGCAATGTGGCAGAGACGCTGGCGCGCCTGTATTGTATAATAGTATATTTT ACACTCAATTCAATTTTTGATATTAAATTAGTGTGTAAAAAGCTTCTGAAATCAAGAAG CCCGTACCAGAAGTTCAATCATGAAATACATCCAAACTGAACAACAAATCGAAGTCCCAG **AAGGTGTCACTGTCAGCATCAAGTCCAGAATCGTCAAGGTTGTTGGTCCAAGAGGTACTT** TGACCAAGAACTTGAAGCACATTGATGTTACCTTCACCAAGGTCAACAACCAATTGATCA AGGTTGCTGTTCACAACGGTGGCAGAAAGCACGTTGCTGCTTTGAGAACCGTCAAGTCTT TGGTTGACAACATGATCACTGGTGTCACCAAGGGTTACAAGTACAAGATGAGATACGTCT ACGCGCATTTCCCAATCAACGTCAACATTGTTGAAAAGGATGGTGCCAAATTCATTGAAG TCAGAAACTTTTTGGGTGACAAGAAGATCAGAAACGTTCCAGTTAGAGATGGTGTTACTA TCGAATTTTCCACCAACGTTAAGGACGAAATTGTCTTGTCAGGTAACTCTGTCGAAGACG TTTCCCAAAACGCTGCTGACTTGCAACAAATCTGTCGTGTCAGAAACAAGGATATCCGTA AATTTTTGGACGGTATCTACGTTTCTCACAAGGGTTTTATTACTGAAGATTTATAA

YGL147C, 191 aa (SEQ ID NO 104) MKYIQTEQQIEVPEGVTVSIKSRIVKVVGPRGTLTKNLKHIDVTFTKVNNQLIKVAVHNG GRKHVAALRTVKSLVDNMITGVTKGYKYKMRYVYAHFPINVNIVEKDGAKFIEVRNFLGD KKIRNVPVRDGVTIEFSTNVKDEIVLSGNSVEDVSQNAADLQQICRVRNKDIRKFLDGIY VSHKGFITEDL

YGL213C, 1694 bp, CDS: 501-1694 (SEQ ID NO 105) AATCAAAACGATCGTTATACAATTCATTGAGGAACCTCTCTAGTCCGATCCGTCTTTCAT CGATCATTTCCGGATCATCATATCTTCTTTGCCACCTCCTGTCCAATACACCGGGCTTTT CAGGGAAGTCATATGGGATGGTGCTTCCTACATCTCTCCAATCGTGTCTTCAGTTTCC AAAACTCGGAATACCTTTTGTAAAGGCGCTTGTTTGGTGTACTAACACCGTATAAAACAT ACTTGGGGTTGATTTTAACATCGTCCACCTTGATTCTTAACTTTTCACTCATTTTCCCTA CAGAATTAGCTGCCATCAATATCAATTATCAACCCTTATATGACTTTATTGTTTTTGTTT GAAGGAAAAATTAGGCGATATTAAAACAAATCTAAAATAAAGACAAGAAACGAAAAAGAG GTTAATCAAGTATTGGAAAAATGTCCAAAGTGTTTATTGCCACAGCAAATGCAGGTAAAG CTCATGACGCTGATATTTTCTCGGTTTCTGCTTGCAATTCATTTACGGTAAGTTGTTCAG GTGACGGTTACTTAAAGGTGTGGGATAATAAGCTGTTAGATAATGAAAATCCAAAAGATA AGTCATATTCTCACTTTGTCCATAAGTCCGGATTGCACCATGTCGATGTCTTGCAAGCTA TTGAGAGAGATGCATTTGAATTATGCCTTGTTGCTACCACTTCATTTTCTGGCGATTTAC TCTTCTATCGTATCACTAGAGAAGATGAGACTAAAAAAGTTATATTCGAGAAATTGGATC TTCTAGACTCAGACATGAAAAAGCATTCCTTTTGGGCATTAAAATGGGGTGCCTCAAATG ACAGACTACTTTCCCATAGGCTGGTTGCTACAGACGTCAAAGGGACCACTTACATTTGGA AGTTTCACCCGTTTGCAGATGAGTCAAATTCTTTAACACTAAATTGGAGCCCCACGTTAG AATTACAAGGCACTGTCGAATCGCCTATGACTCCAAGTCAATTTGCCACTTCTGTGGATA TCTCTGAACGAGGACTAATTGCCACAGGTTTTAATAATGGAACAGTACAAATTTCAGAAC TATCTACATTACGCCCGTTGTACAATTTTGAATCTCAGCATTCTATGATTAATAATTCGA ATTCCATCAGATCGGTGAAATTTTCTCCTCAAGGATCCTTATTAGCCATTGCTCACGATT CAAATTCATTTGGTTGCATCACTCTATATGAAACTGAATTTGGTGAAAGAATAGGCTCCT TATCCGTACCAACCCATAGCTCGCAGGCAAGTCTGGGTGAATTTGCACATTCTAGCTGGG TCATGAGTCTATCGTTTAATGATTCTGGTGAAACATTATGCAGTGCCGGATGGGATGGTA AATTGAGATTTTGGGATGTAAAAACAAAGGAAAGAATCACTACATTGAATATGCATTGTG

YGL213C, 397 aa (SEQ ID NO 106)
MSKVFIATANAGKAHDADIFSVSACNSFTVSCSGDGYLKVWDNKLLDNENPKDKSYSHFV
HKSGLHHVDVLQAIERDAFELCLVATTSFSGDLLFYRITREDETKKVIFEKLDLLDSDMK
KHSFWALKWGASNDRLLSHRLVATDVKGTTYIWKFHPFADESNSLTLNWSPTLELQGTVE
SPMTPSQFATSVDISERGLIATGFNNGTVQISELSTLRPLYNFESQHSMINNSNSIRSVK
FSPQGSLLAIAHDSNSFGCITLYETEFGERIGSLSVPTHSSQASLGEFAHSSWVMSLSFN
DSGETLCSAGWDGKLRFWDVKTKERITTLNMHCDDIEIEEDILAVDEHGDSLAEPGVFDV
KFLKKGWRSGMGADLNESLCCVCLDRSIRWFREAGGK

YGL235W, 1037 bp, CDS: 501-1037 (SEQ ID NO 107) CTGGTTCCAACCATATCTTATGGGAAGATCTATCAGGAAACCTTAGAATCTTAGCTTCGA TGGAGGGACAATAGCGGGGGCCTTTGATGGTCGTGTCCTGAATATGAATGGATTGATGCA AGTTATTGCGCAAAAAGTCGTGCATTTGAGGTGTGGTATGTGTGCCAAAGCAATCCAGTT GCTTCGTGGGTTCGACTGACACGGTTTCATTCAGAAAACTCATAGGGACAGGCAACGCAT CTCCCTTCTGGACCTCCAGAGCGCTGAAATCAATGGATTCCTTGGCCAGCCTAGCCGGAG TGCCTGTTTTCAAACGCCCTAACTGAAAGCCCACCTCATTTTGTAGAGTATTGCTGATCC CATATGTTGGCTGCCAATTCTTCCTGCTGCAATACGCTTGTCGCCGATGTGAATTT CTGCACTGAGAAACGTACCTGTAGTGATTATGACCTGATCTGCCCCAACCTGGGTACCGT CATCCAGAACCACACCTTTGATGACCTTGTGGCCACATCCGGGGTCATACAAGATCAAGT CAGCAACTTTGTTCTGCAGCAGAGACAAGTTGGGGTGTGCTTTCTTGTCGGAAAGTTCCC TTTGCATGTATTTCTTATATAACTCTCTGTCTATCTGGGCTCTGGGCCCCCACACAGCAG GACCCTTGCTTCTGTTCAGCATTTTGAATTGCACTCCAGCGAGATCAGTTACTTTGCCCA TCAGCCCATCGAGAGCGTCGATTTCCTTTACAAGGATGCCCTTACCCACTCCACCAATAG AGGGGTTGCACGAACACTTACCAATATCTGTTAACGATGGTGTAATGAGAGTAGTATGCG CACCAGTCCTAGATGACGCAGCTGCAGCTTCGCAGCCTGCATGTCCAGCACCGATGACCA CGACCTGTGTCTTGGTTGTGGGAAGCTTGTCAAAGAAGATATGGTCAACCGCCTCC TGAGGACCTGTAAGGGAAATGAAGTACACGAAGACGCCAAGGTTGTTACACGCAGCATCG TTCTTTGGGGCGTTTAG

YGL235W, 178 aa (SEQ ID NO 108) MTLWPHPGSYKIKSATLFCSRDKLGCAFLSESSLCMYFLYNSLSIWALGPHTAGPLLLFS ILNCTPARSVTLPISPSRASISFTRMPLPTPPIEGLHEHLPISVNDGVMRVVCAPVLDDA AAASQPACPAPMTTTCVLVVGWKLVKEDMVNRLLRTCKGNEVHEDAKVVTRSIVLWGV

YGL260W, 76 aa (SEQ ID NO 110) MEMLLFLNESYIFHRLRMWSIVLWHSCVFVCAECGNANYRVPRCLIKPFSVPVTFPFSVK KNIRILDLDPRTEAYC

YGR085C, 1025 bp, CDS: 501-1025 (SEQ ID NO 111) TCCTTACTTTAGTCTATTATCAATATCTCTTCCCCCTCTAAATATGTACTCTTTATTT

TTTTTAATTGTGAAGGAACAATTCAAGTTAGAACTCTTTTGATAGGAAACATTATTTCCT GTCGTATAGACATCTATATATAACAAGCACAGAACCGTCTAATTGGTATTTTTCAGGACA TTTTAAACATCCGTACAACGAGAACCCATACATTACTTTTTTAATATTCTTTTTGTTTT CACCGCCTTCTTTTTATTTTATCCGAAGATCTTTTGGAACCCGCTCTGCGAATAGCGAA GCTAGGATACCAAATTGAAACTTGGACATAACTCATCATTAAAGAAGTATACTGTTAAGA GAGGCATTCATTTCGTGTATTATAACGTTTAGCATCAGTTACCCTTGAAAGCCCAACATA TACAAAAATACGCGTCCAAGATGTCTACTAAAGCCCCAAAACCCTATGCGTGATTTGAAGA TCGAGAAATTGGTCTTGAACATCTCCGTTGGTGAATCTGGTGACAGATTAACCAGAGCCT CCAAGGTTTTAGAACAATTATCTGGTCAAACTCCAGTTCAATCCAAGGCCAGATACACTG TCAGAACTTTCGGTATCAGAAGAAACGAAAAAATTGCTGTTCACGTTACCGTCAGAGGTC CAAAGGCTGAAGAAATTTTGGAAAGAGGTTTGAAGGTCAAGGAATACCAATTGAGAGACA GAAACTTCTCTGCTACCGGTAACTTCGGTTTCGGTATTGACGAACACATTGACTTGGGTA TCAAGTATGACCCATCCATCGGTATTTTCGGTATGGATTTCTATGTCGTCATGAACAGAC CAGGTGCTAGAGTCACTAGAAGAAGAGATGTAAGGGTACTGTTGGTAACTCCCACAAGA CAACTAAGGAAGACACCGTCTCTTGGTTCAAGCAAAAGTACGACGCTGATGTGCTCGATA AATAA

YGR085C, 174 aa (SEQ ID NO 112) MSTKAQNPMRDLKIEKLVLNISVGESGDRLTRASKVLEQLSGQTPVQSKARYTVRTFGIR RNEKIAVHVTVRGPKAEEILERGLKVKEYQLRDRNFSATGNFGFGIDEHIDLGIKYDPSI GIFGMDFYVVMNRPGARVTRRKRCKGTVGNSHKTTKEDTVSWFKQKYDADVLDK

YGR118W, 1258 bp, exon1: 501-565, intron1: 566-885, exon2: 886-1258 (SEQ ID NO 113) AGCCATGTCGGTCGCACTAGACTTTTCTTCTCACTGTCACTTACCTGTTTGAAATCATGT CCTTTTTTTTTTTGCCATTCTTATACATTTTCTTTCCTTCTGAAATTAACTGTACACCCA TACCCTATATACACCCATACCCTATTTTTAAATATAAAAAGTAAACTTCATTTTGAAAGA CCACTCTGCATCAGCACGCGGGCTCTGGAAGGAAGAAATGACGTTTCGGCGGAATACCCT TTCAGAAGGTCTGCTCTTGTGGCTGGTTCATGGGAGACACCCAGCGGAGCTCCTCCCGAG AAAGGCCCCTTCATCTCTGCCGATTGCTGACGGAAAGCAGTAGCGGAGGTTTGAGTTCTC TACGCCGAGAGTACACTGCCGTAATATCACAATGTTTCGACTAACGGTTACAGTACGTTA AATTAGATACTGCCTATGAATTGACATATTAGATAATGTCAAATTTTACAAAAACCTAAG ACAACAGGAAATAAACAAAGATGGGTAAAGGTAAGCCAAGAGGTTTGAACTCTGCTAGAA AACCCCCTATTGTGATATCGTTTTAGGTGAAGGAAATGTTGTGAGCTCTGGAGTGATAAA TTTATCAAGTAACATATCCTGGCGCAAATCAGTTTGGAGAGGCTTAAAATGACACGTCAC AGTGATAAAAAGTAATGAATAGTGAACGGTCAGCTTCGGCCATTCTTCCCAATCTATAGT GTGGAAAATAAACCTTTTCTTCCCAAAATAACTCAGAAAGTCACAGGAGGCCGTTTTTTA CAACGGAATCATTTTTTACTAACAGTTTTTTTTTTTATTATTATAGCCGTTGGGCCGAAAA CAACTACAAGAAGAGATTGTTGGGTACTGCCTTCAAGTCTTCTCCATTCGGTGGTTCTTC TCATGCCAAGGGTATCGTCTTGGAAAAATTGGGTATCGAATCCAAGCAACCTAACTCTGC TATCAGAAAGTGTGTTAGAGTTCAATTAATCAAGAACGGTAAGAAGGTCACTGCTTTCGT TCCAAACGATGGTTGTTTGAACTTTGTCGACGAAAATGATGAAGTCTTGCTAGCAGGTTT CGGTAGAAAGGTAAAGCTAAGGGTGATATTCCAGGTGTTAGATTCAAGGTCGTTAAGGT CTCTGGTGTCTCCTTGTTGGCTTTGTGGAAAGAAAGAAGGAAAAGCCAAGATCATAA

YGR118W, 145 aa (SEQ ID NO 114) MGKGKPRGLNSARKLRVHRRNNRWAENNYKKRLLGTAFKSSPFGGSSHAKGIVLEKLGIE SKQPNSAIRKCVRVQLIKNGKKVTAFVPNDGCLNFVDENDEVLLAGFGRKGKAKGDIPGV RFKVVKVSGVSLLALWKEKKEKPRS

CTTCTTGAAAGAAATATCAGTATTACAATCATAACAACAACCAAAAGAAAATAACTAATA GACCCCATTACAATATAGAAATGTTTTCCATATTCAATTCACCATGTGTTTTTGAACAGC TGCCATCTTTTAGTCAGCCCCTACATTCGCGTTATTTTGATTGCAGTTCTCCAGTGAGCT ATTATCCAGAATGTAAAAGGAGGAAAGCAATAAAAGCTAACCTAAGAGCTCCAAAAAAA GCGATGCAAATTGTTCAGAACCTTTGAGGTATGCACTTGCTGAAACACCCAAATGGTTATA CATTAAGCTTGTCTAAGCGGATTCCATATGAACTTTTTTCAAAGTACGTTAATGAGAAAT TAGGTGAGCTAAAGGAGAACCATTACAGACCAACTTACCATGTTGTCCAAGATTTTTTTG GAAACCAGTATTATGTTGAAGATGAAGCGGATGAAGATGCTCTATTGAGATCTGCATTGA AAGATCTGGATTTTAGAGCCATAGGAAAGAAATTGCTAAGGATCTTTTCCAAGACTACG AAATAGAATTGAATCATAGAGGTGATGAATTGAGCATATTGAGTAAGAAGGATAAAATCT TTAAGGAATTCTCTCTAGACCAAGTGTTTGAAGATGTTTTTTGTTATTGGCTGTGGAGTTG AAAACATAGATGATGGCTCGAGAGAAAAATATGCACTTTTAAAGATTGGTTTAGTTAAGC ATGAGGAAGAATTTCCGAAGGTGGCATCAACGAACCAAAGATGCCAATAATTGAATCCA AAATAGACGAGTCTCACGATGATGTTAACATGTCTGAATCTTTGAAGGAGGAAGAAGCGG AGAAAGCGAAAGAACCACTAACCAAAGAAGACCAAATAAAAAATGGATAGAGGAAGAAA GATTGATGCAGGAGAAAGCAGAAAATCAGAACAGGAAAAAGCTGCCAAGGAAGATGAAG AAAGGCAAAAGAAAGAAGGAAGCCAGATTGAAGGCAAGGAAAGAATCTTTGATAAATA AGCAAAAAACCAAGAGGTCCCAGCAAAAAAAATTGCAAAATTCCAAATCATTGCCTATCT CTGAGATTGAGGCCAGCAATAAAAATAATAATAGCAATTCTGGTTCAGCAGAAAGTGATA ATGAAAGTATAAACAGTGATTCTGATACGACTTTGGATTTCTCTGTGTCTGGTAATACAC TAAAAAAACACGCTTCACCCCTATTAGAAGACGTTGAGGATGAGGAAGTTGACAGATACA ACGAGTCCCTAAGCAGATCTCCCAAGGGAAACTCTATTATTGAGGAGATATAA

YGR142W, 410 aa (SEQ ID NO 116)
MFSIFNSPCVFEQLPSFSQPLHSRYFDCSSPVSYYPECKRRKAIKANLRAPKKSDANCSE
PLRYALAETPNGYTLSLSKRIPYELFSKYVNEKLGELKENHYRPTYHVVQDFFGNQYYVE
DEADEDALLRSALKDLDFRAIGKKIAKDLFQDYEIELNHRGDELSILSKKDKIFKEFSLD
QVFEDVFVIGCGVENIDDGSREKYALLKIGLVKHEEEISEGGINEPKMPIIESKIDESHD
DVNMSESLKEEEAEKAKEPLTKEDQIKKWIEEERLMQEESRKSEQEKAAKEDEERQKKEK
EARLKARKESLINKQKTKRSQQKKLQNSKSLPISEIEASNKNNNSNSGSAESDNESINSD
SDTTLDFSVSGNTLKKHASPLLEDVEDEEVDRYNESLSRSPKGNSIIEEI

YGR236C, 890 bp, CDS: 501-890 (SEQ ID NO 117) CAAAAAAGTTTTCGGATGAACCGGATTAATACAAGTAAAATCAGCAAAGATATAGAAGAC AAAATAAGCGTGAAAACAATCATAAACCACTCACAACGGGGGTTTTCAGCTGTTACTCCT CCATACATACATTTGATAAAGATATAATGTTATATTTCTTTTCGTAATTTTGTTTTACT TCGGTTTGCTCTATAGATTTCATCAGCCGCACCGAAAAGGGAGATCAATAAGGTACCCTT TAAAAGGGATAAGAAGCCTACATCACCCCAATAAATGGAGTAATGGCCAGCATTGGATGA AGAGAAGAATTACGGGATACTGGGATAACACTGTTAAAAAATGCTTCGCGACGTGAGGGT CTTCTTCATATAAATTGAACTGCCAAATCTCTTTCACATTATCCAGGATAGTTTGGAATG TGTGTTACTGAAGGATCAGAATCAATAAATACAATCAATACAAATATTTAGCGCATAAAA TTCAAACAAAGTTTACTGAAATGAAGTTAGATTCAGGAATATACTCAGAGGCACAAAGAG TTGTGAGAACTCCAAAGTTTAGATATATTATGTTAGGGCTGGTGGGCGCTGCTGGTAC CGACCGCATACATGAGGAGAGGCTATACGGTTCCTGCACATAGCTTAGACAACATCAACG GCGTAGACAACTAAGGCGTCTGTTATGGGTACAGAACAGAGAGCAGCTATGACGAAGG GTAAGAGTTTACAAGAGATGATGGATGATGATGAAGTAACGTATTTGATGTTCCTCTTCA ATCATGTAAGGGAATTTGTACTTGGTTCCCTGCATTTATGTTCTTTGCATTTTCG CATTTAATCATAGTACGACAAACGGGGAAGGGGATTGTGATTTTACATAA

YGR236C, 129 aa (SEQ ID NO 118) MKLDSGIYSEAQRVVRTPKFRYIMLGLVGAAVVPTAYMRRGYTVPAHSLDNINGVDTTKA SVMGTEQRAAMTKGKSLQEMMDDDEVTYLMFLFNHVREFVLGSLHLCSLHFVFAFNHSTT NGEGDCDFT

YGR277C, 1418 bp, CDS: 501-1418 (SEQ ID NO 119)
AATCTTTGCGATTGAATTGCTGCACGAACATTAACATTAGTTCTTTTTGCTAAAGTTTCTC
CAATATCTGGAATATCAGAATTTAGCAAGGCAATCAAAGCGGATAAAGCAGGGATTAGCC
TGCCATTCTGTTTGTTCAGAGTAAAATCCACAACATTTTTACAAATTATGTTGCGGCCAA
TAAGTATATTGACTTGAAATAAGTCTCTGTGCGATTCCTGTAAGTTGTCCATTGTTAAAT
TGGATATTATGGGTGAAACGTGTGACCTTATCATTTCCCAGTTTTCTCTCTGAAATTTAA

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TGTCTTCATCCTGTATGGTAGCGGTAGACATGCTGGTTTGTAGCCTTTTTATTCCTTTTT AGGTTTCTTACTCACAATGCCAAAATAAATATCAGTGTAATATAATTTTTCAAGAGTACG TAATGGAAAAAGATAAAATAAGGACCGTCATAAAAAGAGACGTGATTAAACCTAAAAAT CTAAAGTAAAGAAGTGTAAGATGGTTGAGGAAAATTCCAGAGTTTTGATTGTTCTTCCTT ATACACCGCCTAGTGCTACTTTGCAGAGGATTATAGGGCAAACTATTCCGTTCTTAAGAG AATGTCAAAGTCAACTAGACATCGTGATTGTACCTGAATTCAAAACCTCATTCCAGTTGG ATTCTGCGCTAGGGAAGATGTACAGTATTACCAGGGATGTCCTTTTGGGCTATGGAATGA TCAACAGCGGAATCAACATATTCAACAATATTCATTTCGTCGAGAGTAATTTGCAAT GGAAAGTGGTTTTATTGCCACAGGAATCCACTTTTGAAACTTGGAAGCTAGAGTTGGGAC AAGGACAATACCATAGTATAGAACATTATGCATTACACGATAATATAATGGAAGAGATAG AAGGTCCCAAAGATGCTAACAAATTTCATGTCACCGCATTGGGCGGAACGTTCGACCACA TTCACGATGGACATAAAATATTGTTGAGCGTCTCTACATTCATCACGTCACAAAGGTTAA CTTATGATACACGATGCAGGCACGTACATCAATTCATCAAGTTGTTAAAACCGGATCTCT CCGTAGAACTAGTTCCCTTAAGGGACGTGTGCGGCCCCACAGGGAAAGTACCCGAGATAG AATGTTTAGTTGTGAGTAGAGAAACCGTCAGTGGGGCAGAGACTGTGAATAAGACTAGGA TTGAAAAAGGCATGAGCCCATTGGCAGTACATGTGGTTAATGTACTTGGAGGAAGGGAGG AAGACGGCTGGAGCGAGAAGTTAAGCAGCACGGAAATCAGACGCCTACTTAAGTCCTCTG CTTCGCCAACGTGCACTCCACAAAACCCTTGCGTATAA

YGR277C, 305 aa (SEQ ID NO 120)
MVEENSRVLIVLPYTPPSATLQRIIGQTIPFLRECQSQLDIVIVPEFKTSFQLDSALGKM
YSITRDVLLGYGMINSGINIIFNNIHFVESNLQWKVVLLPQESTFETWKLELGQGQYHSI
EHYALHDNIMEEIEGPKDANKFHVTALGGTFDHIHDGHKILLSVSTFITSQRLICGITCD
ELLQNKKYKELIEPYDTRCRHVHQFIKLLKPDLSVELVPLRDVCGPTGKVPEIECLVVSR
ETVSGAETVNKTRIEKGMSPLAVHVVNVLGGREEDGWSEKLSSTEIRRLLKSSASPTCTP
QNPCV

YGR284C, 1433 bp, CDS: 501-1433 (SEQ ID NO 121) AGAGAGCCATCCGTAACTCTGCTAAGGAAGCTGACTACTTTGGTGATGCTGACAAGGCCA CCACGATTGACGAACAAGTTGGTTTGATCGTTGACAGTTTGAATGACGAAGAGTTAGTGT CCACCGCCGATAAGATCAAGGCCAATGCTGCTGGTGCCAAGGAAGTTTTGAAGGAATCTG CAAAGACTATTGTCGATTCTGGCAAACTACCATCCAGCTTGTTGTCCTACTTCGTGTGAA TACCGTAAGAAATGGAATAGAATATATACGAATGTATACGAATATTATAGAGAACGTTCT CTTTTATTTCTATAATGAATAGGTTCGGGTAACGGTTCCCTTTTTAGGTATTTCTAGAAG ATGAGAGAAGAGGGAATAATGAGAAAGGCGAAAAATAAAGGACACCTTTAACGAAAGATC AAAGGTGTCCTTATTTACTTACAATAGCTGCAATTAGTACGACTCAAAAAAAGTGAAAAC AAAACTGAAAGGATAGATCAATGTCTTACAGAGGACCTATTGGAAAATTTTGGCGGTATGC CAATGTCATCGCAAGGACCATACTCTGGCGGTGCACAATTCAGATCAAACCAGAACC AATCCACTTCTGGCATCTTAAAGCAATGGAAGCATTCTTTTGAAAAGTTTGCCTCCAGAA TTGAGGGGCTCACTGACAATGCAGTTGTTTATAAATTGAAGCCTTACATTCCAAGTTTGT CAAGATTTTTCATTGTGGCCACCTTTTATGAAGATTCGTTTAGGATCTTATCACAATGGT CAGATCAAATTTTTTATCTGAATAAGTGGAAGCATTACCCATACTTCTTTGTCGTTGTGT TTCTAGTGGTTGTTACCGTTTCCATGTTGATTGGCGCCAGTTTGTTAGTTTAAGAAAGC AAACCAATTATGCCACCGGTGTGTTATGTGCTTGCGTTATTTCTCAAGCATTAGTTTATG GGTTGTTTACGGGTTCATCATTTGTCCTAAGAAACTTTAGTGTTATTGGTGGGTTGTTAA TTGCATTCAGCGATTCAATTGTTCAAAACAAGACAACATTCGGTATGCTTCCTGAATTAA ACAGCAAAAACGACAAAGCGAAGGGTTACCTGTTGTTTGCTGGTAGAATTTTAATTGTTT GCACAATATGTTTCGCCATTGGTTACAAGACAAAATTCGCATCCATTATGTTGGGTTTGA TACTAACTTTTTACAATATCACGCTAAACAACTACTGGTTTTATAACAATACTAAGAGAG ATTTCTTGAAGTATGAGTTTTACCAGAACTTAAGCATCATTGGTGGGCTTCTATTAGTTA CTAATACTGGCGCTGGTGAATTATCCGTTGATGAAAAGAAGAAGATTTACTAG

YGR284C, 310 aa (SEQ ID NO 122)
MSYRGPIGNFGGMPMSSSQGPYSGGAQFRSNQNQSTSGILKQWKHSFEKFASRIEGLTDN
AVVYKLKPYIPSLSRFFIVATFYEDSFRILSQWSDQIFYLNKWKHYPYFFVVVFLVVVTV
SMLIGASLLVLRKQTNYATGVLCACVISQALVYGLFTGSSFVLRNFSVIGGLLIAFSDSI
VQNKTTFGMLPELNSKNDKAKGYLLFAGRILIVLMFIAFTFSKSWFTVVLTIIGTICFAI
GYKTKFASIMLGLILTFYNITLNNYWFYNNTKRDFLKYEFYQNLSIIGGLLLVTNTGAGE

LSVDEKKKIY

YGR285C, 1802 bp, CDS: 501-1802 (SEQ ID NO 123) CATTTAGTTCTGATTACAGCAGAAATCGTAGCGCGATGAGACATTTCATCAAATGGCCTT TTTTTTTGGGCAATTTTTTTATATCTTGAAATGATAGTTGCCTTGTACTTTCAACCGTT AACTATAAATATGTCAAAGAAACCATACAATCATAGATTTATAACTATCTTTTGGATGAC ATTAATGAACATAACGCTCCTAATACAAATGTCCAAAAAATATTACCCGCAAATACGAAT CTTTTTTTTTCTCGATGAAATTTTGCAAAGAGTTCGAAATTTTTATTTCAAGAGCTGGT AGAGAAAATTTCATAAGGTTTTCCTACCGATGCTTTTATAAAATCTTCGTTTTGTCTCAC ATATACCAACAAGAGTAACGATGTTTTCTTTACCTACCCTAACCTCAGACATCACTGTTG AGTTCTTTTTGCAACATGCTCAAAGAACTTTGAGAAACCACACCTGGTCTGAATTTGAAA GAATTGAAGCTGAAAAGAACGTCAAAACCGTTGATGAATCCAATGTCGACCCAGATGAGT TGTTATTCGACACTGAATTGGCCGATGAAGATTTACTGACTCATGATGCTAGAGACTGGA AAACTGCCGATTTGTATGCTGCTATGGGTTTGTCTAAGTTGCGTTTCAGAGCTACTGAAA GTCAAATCATCAAGGCTCACAGAAAACAAGTTGTCAAGTACCATCCAGACAAGCAATCTG CTGCTGGTGGTAGTTTGGACCAAGATGGCTTTTTCAAGATTATTCAAAAGGCCTTTGAAA CTTTGACTGATTCCAACAAGAGAGCTCAGTACGACTCATGTGATTTTGTTGCCGATGTTC CTCCTCCAAAGAAGGGTACCGATTATGACTTTTATGAAGCTTGGGGCCCCGTTTTCGAAG CTGAAGCTCGTTTTTCTAAGAAGACTCCTATTCCTTCTCTAGGTAACAAAGATTCTTCCA AGAAGGAAGTTGAACAATTCTATGCTTTCTGGCACAGATTTGACTCCTGGAGAACCTTTG AGTTCTTGGACGAAGATGTCCCAGATGACTCTTCTAACAGAGACCACAAGCGTTACATTG AAAGAAAGAACAAGGCCGCAAGAGACAAGAAGAAGACTGCTGATAACGCTAGATTGGTCA AACTTGTTGAAAGAGCTGTCAGTGAAGATCCCCGTATCAAAATGTTCAAAGAAGAAGAGAGA AGAAGGAAAAGGAAAGAAAATGGGAAAGAGAGCCGGTGCCAGAGCTGAAGCTGAAG CTAAGGCCAAGGCCGAAGCTGAAGCGAAGGCTAAAGCTGAATCTGAAGCCAAGGCTAACG CCTCCGCAAAAGCTGACAAAAAGAAGGCTAAGGAAGCTGCTAAGGCCGCCAAGAAAAGA ACAAGAGCCATCCGTAACTCTGCTAAGGAAGCTGACTACTTTGGTGATGCTGACAAGG CCACCACGATTGACGAACAAGTTGGTTTGATCGTTGACAGTTTGAATGACGAAGAGTTAG TGTCCACCGCCGATAAGATCAAGGCCAATGCTGCTGGTGCCAAGGAAGTTTTGAAGGAAT CTGCAAAGACTATTGTCGATTCTGGCAAACTACCATCCAGCTTGTTGTCCTACTTCGTGT

YGR285C, 433 aa (SEQ ID NO 124)
MFSLPTLTSDITVEVNSSATKTPFVRRPVEPVGKFFLQHAQRTLRNHTWSEFERIEAEKN
VKTVDESNVDPDELLFDTELADEDLLTHDARDWKTADLYAAMGLSKLRFRATESQIIKAH
RKQVVKYHPDKQSAAGGSLDQDGFFKIIQKAFETLTDSNKRAQYDSCDFVADVPPPKKGT
DYDFYEAWGPVFEAEARFSKKTPIPSLGNKDSSKKEVEQFYAFWHRFDSWRTFEFLDEDV
PDDSSNRDHKRYIERKNKAARDKKKTADNARLVKLVERAVSEDPRIKMFKEEEKKEKERR
KWEREAGARAEAEAKAKAEAEAKAKAESEAKANASAKADKKKAKEAAKAAKKKNKRAIRN
SAKEADYFGDADKATTIDEQVGLIVDSLNDEELVSTADKIKANAAGAKEVLKESAKTIVD
SGKLPSSLLSYFV

YHR010W, 136 aa (SEQ ID NO 126) MAKFLKAGKVAVVVRGRYAGKKVVIVKPHDEGSKSHPFGHALVAGIERYPLKVTKKHGAK KVAKRTKIKPFIKVVNYNHLLPTRYTLDVEAFKSVVSTETFEQPSQREEAKKVVKKAFEE RHQAGKNQWFFSKLRF

YHR021C, 1299 bp, exon1: 501-503, intron1: 504-1053, exon2: 1054-1299 (SEQ ID NO 127) TTACTTACGTCTATTATAACCTTCCGCGTAAAAAAGAAATATTGACATCCTTTCTTGTAT TTAGCCCATACATTTTCACCCATGCACCATTGGATTATAAAGAAAAAAATTTAATAAAAA TCTGCCGGGGAAATTTCAGAAGAAAAAAGGAAGGTGTGTTCGCATTTAACACGGGCCACC ATAAACTTTTGTTTGCCACCCATCTAGACGGGATCCGCCCCGCCCAAGGCTCTCTTCCTC TAGCTAGGCAATGTGGCTCTCGGAAAGGAAACTCCCACCAGGACGTGGTGGGAAATGCAG AAAAGTTCTATATAGCATTTGCTTTTATTTAGAGAATACGAAAACACACCAGATAATTAG TGCATATATATAGATCAATATGGTATGTGAAAGAGATATTAAACATAAGATGTGAAGGA AACAGAAGAACAATATTTGAGGAATGAATTCGGATGAAATTCTAGTAGAAGAAAAAG CCTAAAATAAAAAGAAAGAAAGGAAAATAAAGCAGTAATCAACCTCTGACATTTGATAGG AGTATGCGTTTCCGCAAAATCAACAAATCATGCATTAAACTGGTAACGGAGACTTTAAAG ACGTGCAAAGAAAGCAATTAATTTTTAGATAGGGAATTGAAAGGCTCTGTATAGCAGAAA ATTTGAGATCTACTGTGGAGATAAGCATATGGTGTTGAGTTATGGGTAATCTAACAATAA TAGAAACTTATAGCAGTTGAAGATGGCGGATCATGATGCCGGATACTGCTGGGTAATGAT TTATCCTTCTTTTTTGGAGCACAAATGCTCACTTTTTCCTGTCTCCTCTAACTTTTCTG CTTTCGTTTCGTTTCTATTTATTTCATTACAGGTTTTAGTTCAAGATTTGTTGCACCCA ACTGCTGCTTCTGAAGCCAGAAAGCACAAGTTAAAGACTTTGGTTCAAGGCCCAAGATCC TACTTCTTGGATGTCAAATGCCCAGGTTGTTTGAACATCACCACTGTTTTTTCTCATGCT CAAACTGCTGTCACTTGTGAATCATGCTCTACTGTCTTATGTACTCCAACCGGTGGTAAG GCCAAATTATCTGAAGGTACTTCTTTCAGAAGAAAGTAA

YHR021C, 82 aa (SEQ ID NO 128) MVLVQDLLHPTAASEARKHKLKTLVQGPRSYFLDVKCPGCLNITTVFSHAQTAVTCESCS TVLCTPTGGKAKLSEGTSFRRK

YHR141C, 106 aa (SEQ ID NO 130) MVNVPKTRKTYCKGKTCRKHTQHKVTQYKAGKASLFAQGKRRYDRKQSGFGGQTKPVFHK KAKTTKKVVLRLECVKCKTRAQLTLKRCKHFELGGEKKQKGQALQF

YHR217C, 962 bp, CDS: 501-962 (SEQ ID NO 131) TCCATGGTGCACAGTATCTTAACTATCTGCTTAGTCGAGGAGAACCAGGATTCTGTTCGT TGCTCAGCCGCTTCGTGGATATTCTCTTGGATACTTTAAACATGGACCTACGTTCCGCTC TCGAAAAGACCAATATAATAAAAAGTTATAAATTACATTTCCTTATTAGGTATACGACCT AACTTCCCCCAAAAATGTATTACCCCGCCGAATAAGAAAACAGACCCATTCACCCACGAC GTATCAAGTTACTTCCTTGGTGCAATGTCCCACTATAAAAAAATTCCTTGACGCTAGATC GTTGGACTAAAATCTGCGTCACAATCGCCTAAACAGGAAATATTGCCTATTTTCGTACAA GGTTACTTCCTAGATGCTATATGTCCCTACGGCCTTGTCTAACACCATCCAGCATGCAAT ACCTGTCTCTTAACCTACCCTCACATTACCCTACCTCCCCACTCGTTACCCTGCCCCACT TCATAACCGTTACCCTCCAATTACCCATATCCAACTCCACTACCATTACCCTGCTATTAC CCTACCATCCACCATGTCCTACTCACTGTACTGTTCTACCCTCCATATTGAAACGTT AA

YHR217C, 153 aa (SEQ ID NO 132) MSLRPCLTPSSMQYSDIYIHTPHPHPHPHPHTPTHTHPHTPTPTPTPHPHPHTTPTPTPTPHHTTLSNLSLNLPSHYPTSPLVTLPHSTIPLPTTIHLSTYYYHPPPIITVTLQ LPISNSTTITLLLPYHPPCPTHCTVVLPSILKR

YIL112W, 3752 bp, CDS: 501-3752 (SEQ ID NO 133) TTCCATAGGGCTTATTTTCCAGTTGATGGAATGGGAGGTTGCTCTTAACGCGAAGACTAA TTCCGTATTTCTTCGCTTTGTTTCATGCTCTGTTCTGAGCTTTTAGTTTCTCTTATTGAG AGCCTTTTCCAAATCAAGGCTCAGGAAGTGACTCGTCCTTAGAAGAACAAGGTTTGGATT TGGTAGGGTTCTTGTACGAAGTTCTCAATATAATTTGCGCATTTACTGTACGGTTCATAC TAGTTTATTCCGGGTAACAAGTTTTCTTGTGATGCTAAATCAATGTGTATATTGAGAAAA CTATGTAGTAAGTTACACAAAGCAACAAAGGATATTATTATATGTGACAGAGAAGAATTG CTGTAGAGATTCATGACAATATGAATGAGACTACTACAAAACAGCCGCTAAAGAAAAGGT CCCTGAGCAGCTATCTTTCAAACGTGAGCACGAGACGGGAGGAGCTGGAAAAGATTTCTA AACAAGAAACATCCGAAGAGGAAGATACTGCCGGCAAGCATGAACAAAGGGAAACACTGT CGGAAGAAGTAAGTGATAAGTTTCCAGAAAATGTTGCATCGTTTCGCTCACAGACTACAA GCGTTCATCAAGCCACCCAAAATAACCTGAATGCAAAGGAATCCGAAGACCTGGCCCATA AGAATGATGCGAGTTCACACGAAGGAGAGGTTAATGGGGACAGCCGTCCGGACGATGTTC CTGAAACGAATGAAAAAATAAGCCAAGCAATACGAGCGAAAATTTCGTCATCATCATCAT CACCCAATGTACGTAATGTTGATATCCAAAACCATCAACCTTTTTCGAGAGACCAACTTC GAGCGATGTTGAAAGAACCAAAAAGGAAAACTGTTGATGATTTCATAGAAGAAGAGGGGTT TGGGAGCTGTTGAAGAAGAGGATTTAAGTGATGAGGTACTTGAAAAAAATACAACAGAAC CAGAAAATGTGGAAAAAGATATAGAGTATAGCGACTCAGATAAGGACACAGACGATGTGG

GAAGCGATGATCCCACGGCACCCAACTCACCAATAAAACTTGGTCGTCGCAAACTGGTTA GAGGTGACCAACTTGATGCAACAACAAGTTCCATGTTTAATAACGAATCAGATTCTGAAT TATCAGATATCGATGATAGCAAGAATATTGCTTTATCCAGTAGCCTATTTAGAGGCGGTT CTTCACCTGTGAAAGAGACAACAACCTTTCAAATATGAATTCTTCACCAGCACAAA ATCCAAAAAGGGGTTCTGTCTCCAGGAGTAATGATAGTAACAAGAGTTCTCATATAGCTG TTTCCAAGCGCCCCAAACAGAAGAAGGGCATATATAGGGATTCTGGTGGTAGAACAAGAC TACAGATTGCCTGTGACAAGGGCAAATATGATGTGAGAAAAAGATGATTGAAGAAGGAG GTTACGATATTAATGACCAAGACAATGCTGGTAATACAGCATTGCATGAAGCGGCGTTGC AAGGTCATATTGAGATTGTGGAACTGTTGATAGAAAATGGTGCAGATGTAAATATCAAGT CTATTGAAATGTTCGGCGATACTCCCTTGATCGATGCTTCCGCCAATGGACACTTGGATG TTGTCAAGTATCTTCTTAAAAACGGTGCGGACCCAACTATACGTAACGCTAAAGGGTTAA CTGCGTTTGAATCTGTCGATGATGAATCTGAATTTGATGATGAAGAAGACCAAAAGATTT TGCGTGAAATAAAAAAGGTTGAGTATAGCCGCTAAAAAATGGACTAACAGAGCAGGAA TTCATAATGACAAATCTAAAAATGGCAATAATGCTCACACAATAGATCAGCCACCTTTTG ATAATACCACAAAAGCCAAAAACGAAAAGGCCGCTGACTCACCTTCAATGGCTTCCAATA TTGATGAGAAAGCTCCGGAAGAGGAATTCTATTGGACAGATGTTACTTCTAGAGCGGGAA AAGAAAAACTGTTTAAAGCTTCGAAGGAGGGACATTTACCATACGTTGGTACGTATGTAG AAAATGGTGGTAAGATAGACTTAAGGTCATTTTTCGAAAGCGTTAAGTGTGGCCATGAAG ATATTACAAGTATCTTTTTGGCATTCGGATTTCCCGTAAATCAAACTTCAAGGGATAATA AAACATCCGCTTTAATGGTAGCTGTAGGTCGTGGCCATCTTGGAACTGTTAAACTGCTAT TAGAGGCAGGTGCAGATCCAACCAAAAGAGATAAAAAGGGTCGTACCGCTTTGTACTATG TAAATAACTATTTGAAGAAGCACTCTGAAGATAATAATGATGATGATGATGATGATGATA ATAATAATGAAACATATAAACATGAAAAAAAGAGAGAGAAAACGCAATCACCCATATTAG CAAGCCGAAGAAGTGCCACTCCTAGAATTGAAGACGAAGAGGACGATACGAGGATGCTCA ATCTGGCAGACGATGACTTTAATAACGATCGTGATGTCAAGGAATCTACAACTTCGGATT CGCGCAAGAGATTGGATGACAATGAAAATGTTGGTACTCAATACTCATTGGACTGGAAAA AACGTAAAACAAATGCCTTGCAAGATGAAGAAAAATTAAAAAGTATCTCACCACTCTCTA TGGAACCTCATTCTCCAAAGAAGGCAAAATCTGTAGAGATAAGTAAAATACATGAAGAAA AAAAGAAAAGAAAAAAGAACAGGAACTACTACAAAAGCTGGCCGAAGATGAGAAAAAAA GGATCGAAGAACAGGAGAAGCAGAAAGTCTTAGAAATGGAAAGATTGGAAAAAGCTACTT TAGAGAAAGCAAGAAAAATGGAAAGGGAAAAAGAAATGGAAGAAATCTCTTATAGAAGGG CAGTAAGGGACTTATATCCGTTAGGACTGAAGATTATTAACTTCAACGATAAACTTGATT ACAAAAGATTTTTGCCGCTATATTATTTTGTAGACGAAAAAAACGATAAATTTGTGCTCG CTTCTGAGAAGATTCCCGTCGATCCCTCGCACCTGACTCCATTGTGGAATATGTTGAAAT TCATTTTCCTGTATGGAGGTAGTTATGATGATAAAAAGAACAACATGGAAAATAAAAGAT ATGTTGTAAACTTTGATGGGGTTGATTTGGACACAAAGATTGGGTATGAGCTTTTGGAGT ACAAAAATTTGTTAGTTTGCCCATGGCGTGGATTAAATGGGATAACGTTGTTATTGAAA ACCACGCAAAAAGAAAAGAAATTGAAGGAAATATGATTCAAATATCAATAAACGAATTTG CACGATGGAGAAACGATAAGCTGAACAAAGCGCAGCAGCCGACGCGCAAACAGCGTTCTC TAAAAATACCTCGAGAGTTACCGGTTAAATTTCAACACCGTATGAGCATATCCTCCGTCC TCCAGCAGACATCCAAAGAACCATTTTGGTAA

YIL112W, 1083 aa (SEQ ID NO 134)

MNETTTKQPLKKRSLSSYLSNVSTRREELEKISKQETSEEEDTAGKHEQRETLSEEVSDK FPENVASFRSQTTSVHQATQNNLNAKESEDLAHKNDASSHEGEVNGDSRPDDVPETNEKI SQAIRAKISSSSSSPNVRNVDIQNHQPFSRDQLRAMLKEPKRKTVDDFIEEEGLGAVEEE DLSDEVLEKNTTEPENVEKDIEYSDSDKDTDDVGSDDPTAPNSPIKLGRRKLVRGDQLDA TTSSMFNNESDSELSDIDDSKNIALSSSLFRGGSSPVKETNNNLSNMNSSPAQNPKRGSV SRSNDSNKSSHIAVSKRPKQKKGIYRDSGGRTRLQIACDKGKYDVVKKMIEEGGYDINDQ DNAGNTALHEAALQGHIEIVELLIENGADVNIKSIEMFGDTPLIDASANGHLDVVKYLLK NGADPTIRNAKGLTAFESVDDESEFDDEEDQKILREIKKRLSIAAKKWTNRAGIHNDKSK NGNNAHTIDQPPFDNTTKAKNEKAADSPSMASNIDEKAPEEEFYWTDVTSRAGKEKLFKA SKEGHLPYVGTYVENGGKIDLRSFFESVKCGHEDITSIFLAFGFPVNQTSRDNKTSALMV AVGRGHLGTVKLLLEAGADPTKRDKKGRTALYYAKNSIMGITNSEEIQLIENAINNYLKK HSEDNNDDDDDDDNNNETYKHEKKREKTQSPILASRRSATPRIEDEEDDTRMLNLADDDF NNDRDVKESTTSDSRKRLDDNENVGTQYSLDWKKRKTNALQDEEKLKSISPLSMEPHSPK KAKSVEISKIHEETAAEREARLKEEEEYRKKRLEKKRKKEQELLQKLAEDEKKRIEEQEK

QKVLEMERLEKATLEKARKMEREKEMEEISYRRAVRDLYPLGLKIINFNDKLDYKRFLPL YYFVDEKNDKFVLDLQVMILLKDIDLLSKDNQPTSEKIPVDPSHLTPLWNMLKFIFLYGG SYDDKKNNMENKRYVVNFDGVDLDTKIGYELLEYKKFVSLPMAWIKWDNVVIENHAKRKE IEGNMIQISINEFARWRNDKLNKAQQPTRKQRSLKIPRELPVKFQHRMSISSVLQQTSKE PFW

YIL115C, 4883 bp, CDS: 501-4883 (SEQ ID NO 135) TTTCAATGCGCTACAACTGACTGAACCAGTCCACAAATTTGGCTGGTCTCTATCGTTCTC GCCCTGAGAGATTTTATTTTCTTATAAATTTTACTAAATAAGGATTTGTACTTTTGATAG AGTTTTTTTTTTTTCTGACGTTTGTTTAGTTAATATTATATAATAGTATTTAGGAAACTA GGTGGGAGGGACATCGCAACTTTTATCGTGACCTACGACCAGTGTTTTTTCAATTGTTT GATCAAAAGAGAAAAAAGACAAAGGACCGAAGGATAGTTGCACGCATAAACTGGAGAAA AAATTGTGTTTGACATCGGCGTTTAGGCTTGTTTGTTCTCACACATACGCTGCTTCAC ACCAATTCATATTTCTCAGGTTAATTTGTCTCCTCTCCAACTTCAATAACGATTTTGCGT GATTACAGAACCATTATAACATGTCTTCTTTGAAGGATGAAGTACCCACTGAGACTTCCG TGCCATTTGCATCTCTACAAAATCTCGATATTTCAAACAGTAAGTCTTTATTCGTTGCTG CCTCTGGTAGTAAGGCGGTGGTCGGCGAATTACAATTACTGAGAGATCATATCACCTCCG ACTCTACTCCGTTAACGTTCAAGTGGGAGAAAGAAATCCCAGATGTAATATTTGTGTGCT TTCATGGTGATCAGGTTTTGGTTTCAACCAGAAATGCATTATATTCGTTAGACTTGGAGG AATTGAGTGAATTTCGAACGGTCACTTCTTTTGAGAAGCCAGTTTTCCAATTGAAGAACG TTAATAACACTTTAGTAATTTTAAATTCAGTCAATGATTTATCAGCACTGGATTTAAGAA CAAAATCGACTAAGCAACTGGCACAAAACGTTACCTCTTTTGATGTCACAAATTCGCAGT TAGCAGTTCTACTAAAAGATAGAAGTTTTCAAAGTTTTGCATGGCGAAATGGCGAAATGG AAAAACAATTTGAGTTCTCTCTACCGTCAGAATTAGAAGAGCTTCCAGTAGAAGAATATT CCCCTTTGAGTGTTACCATTCTCTCTCCACAGGATTTTTTGGCGGTTTTTCGGTAATGTTA TATCAGAGACCGATGACGAAGTTTCATACGATCAAAAAATGTACATTATAAAGCACATAG ACGGCAGCGCCTCATTTCAAGAAACTTTTGATATTACACCTCCATTCGGGCAAATAGTAA GGTTCCCATATATGTACAAAGTTACCTTGTCTGGTTTAATTGAACCTGATGCAAACGTAA ATGTGCTAGCATCATGTTCAAGTGAAGTAAGTATATGGGACTCGAAACAAGTTATTG AACCTTCCCAGGATTCTGAACGAGCAGTATTGCCCATCAGTGAGGAAACAGATAAGGACA CAAATCCAATAGGTGTGGCAGTTGACGTCGTTACTTCAGGCACTATTCTAGAACCTTGTT CCGGTGTTGATACGATAGAGCGATTGCCGCTCGTTTACATATTGAATAACGAAGGTAGCT TACAGATAGTCGGGTTGTTTCATGTGGCAGCAATCAAAAGCGGCCATTATAGCATAAATC TGGAATCTTTAGAACATGAGAAATCTCTCTCTCTCCTACATCAGAAAAAATTCCTATTGCTG GACAGGAGCAGGAAGAAAAAAGAAAAATAATGAATCAAGTAAGGCTTTATCAGAGAATC CTTTCACATCAGCAAATACATCAGGCTTCACTTTTCTTAAAACACAACCAGCCGCTGCCA ATAGCCTGCAGTCTCAAAGTTCTTCAACCTTTGGTGCTCCCTCATTTGGATCATCCGCAT TTAAAATTGACTTGCCATCAGTCTCATCTACCAGTACTGGTGTAGCGTCCAGTGAACAAG ACGCAACAGATCCTGCTTCTGCTAAGCCAGTATTCGGCAAACCCGCGTTCGGAGCTATTG TTGGCTCTGGAAAGTCATCTGTTGAATCGCCTGCCTCCGGATCTGCCTTTGGTAAGCCCT CTGCATTTGGTAAGCCCTCTTTTGGTACTCCTTCCTTTGGCTCTGGAAATTCATCTGCTG AGCCGCCTGCTTCCGGATCTGCCTTTGGTAAGCCCTCTTTTGGTACATCTGCATTCGGAA CTGCATCAAGTAACGAAACTAACTCTGGATCCATATTTGGAAAGGCTGCATTTGGTTCAT CATCTTTTGCACCCGCCAACAATGAACTTTTCGGATCAAACTTTACTATTTCAAAACCTA CAGTTGACAGCCCAAAGGAGGTAGATTCAACGTCACCTTTCCCATCTTCTGGCGATCAAA GTGAAGATGAGTCTAAGAGTGATGTAGACTCTTCTTCGACACCTTTTTGGTACGAAACCTA ACACCTCTACGAAACCAAAGACCAATGCCTTTGATTTTGGGAGTTCTTCCTTTGGATCTG GATTTTCAAAGGCTCTGGAATCTGTTGGTTCCGATACAACTTTTAAATTCGGTACTCAGG CTTCACCTTTCTCTCACAGTTAGGAAACAAATCACCATTCAGTTCCTTCACAAAAGATG ATACTGAAAATGGATCTTTAAGTAAGGGCTCTACCAGTGAAATCAATGACGATAATGAAG AACACGAAAGCAATGGTCCCAACGTAAGCGGTAATGATTTGACAGATTCTACGGTTGAGC AAACATCTTCTACTAGATTACCGGAAACTCCCTCGGATGAAGATGGTGAAGTTGTCGAGG TTGACATGGCTGGTTTAAAAAATCCTGTATTTGGAAATCATGTCAAAGCAAAATCCGAAT CGTTTGGTAACTCCACAATGAATAAAAGTAATACATCTACGGTTTCACCAATGGAAGAAG

AAAATTTGAACATGGCAAAATAG

CTGATACTAAAGAAACTAGTGAAAAGGGCCCCATAACCTTGAAGAGTGTGGAGAATCCGT TTCTACCAGCGAAAGAAGAAGAACTGGAGAAAGTTCTAAAAAGGATCATAACGATGACC CAAAAGATGGTTATGTATCAGGAAGTGAAATATCTGTAAGGACTTCTGAAAGTGCTTTTG ATACCACAGCAAACGAAGAAATTCCAAAGTCACAGGACGTGAACAATCATGAAAAAAGCG AAACAGACCCAAAATATAGTCAACATGCTGTGGTTGATCACGATAACAAGTCTAAAGAAA TGAATGAAACTTCGAAGAATAATGAAAGGAGCGGTCAACCAAATCATGGTGTCCAAGGAG ATGGAATAGCATTGAAAAAAGACAATGAAAAAGAGAATTTTGATTCAAATATGGCAATAA GCAGTGAAGTTAAAGAATCAGATGATAACATGTCACTCAACAGTGACCGGGATGAAAGTA TATCTGAGTCCTACGATAAACTGGAAGATATTAATACTGATGAGCTACCTCATGGTGGAG AAGCTTTTAAAGCACGTGAAGTGAGCGCTTCCGCTGATTTTGATGTACAAACTTCATTAG AAGACAATTATGCTGAATCTGGCATACAGACAGACCTTTCAGAAAGTTCCAAGGAAAATG CAGTCGACAATGGTCTGCAAACTGAGCCTGTTGAAACATGTAATTTTTCTGTTCAAACAT TTGAAGGTGACGAAAATTATTTAGCAGAGCAATGCAAACCAAAGCAATTGAAAGAATATT ACACAAGTGCAAAAGTATCAAATATTCCTTTCGTTTCACAAAATTCTACGTTAAGGTTGA TTGAGAGTACATTTCAGACGGTCGAAGCTGAGTTTACTGTTCTGATGGAAAACATCCGGA ATATGGATACTTTTTTTACTGATCAATCGAGCATCCCTTTGGTGAAGCGTACAGTGCGGT CTATCAATAATCTGTATACTTGGAGAATACCAGAGGCTGAAATTCTATTAAATATTCAGA ATAATATCAAGTGTGAACAAATGCAAATAACAAATGCTAACATTCAAGACCTGAAGGAAA AAGTTACAGATTATGTCAGGAAAGATATTGCACAAATAACTGAAGATGTAGCCAATGCAA AAGAGGAGTATCTGTTTTTAATGCATTTTGATGATGCTTCGAGTGGATACGTTAAAGATC TCAGCACGCATCAATTTAGAATGCAAAAGACATTACGTCAAAAGCTATTCGATGTCCC CCAAAATTAATCATACTGAAGAGTTGCTGAACATTTTAAAATTGTTCACTGTAAAGAATA AGAGATTGGACGATAATCCATTAGTGGCAAAACTAGCTAAAGAATCTCTTGCACGTGACG GTTTACTAAAAGAAATCAAATTATTGCGTGAGCAAGTGAGTAGGTTACAATTGGAGGAGA AAGGTAAAAAGGCTTCGTCGTTCGATGCATCCTCTTCAATAACAAAGGACATGAAAGGAT TTAAAGTAGTAGAAGTTGGGTTGGCCATGAATACGAAAAAGCAAATTGGTGATTTCTTCA

YIL115C, 1460 aa (SEQ ID NO 136) MSSLKDEVPTETSEDFGFKFLGQKQILPSFNEKLPFASLQNLDISNSKSLFVAASGSKAV VGELQLLRDHITSDSTPLTFKWEKEIPDVIFVCFHGDQVLVSTRNALYSLDLEELSEFRT VTSFEKPVFQLKNVNNTLVILNSVNDLSALDLRTKSTKQLAQNVTSFDVTNSQLAVLLKD RSFQSFAWRNGEMEKQFEFSLPSELEELPVEEYSPLSVTILSPQDFLAVFGNVISETDDE VSYDQKMYIIKHIDGSASFQETFDITPPFGQIVRFPYMYKVTLSGLIEPDANVNVLASSC SSEVSIWDSKQVIEPSQDSERAVLPISEETDKDTNPIGVAVDVVTSGTILEPCSGVDTIE RLPLVYILNNEGSLQIVGLFHVAAIKSGHYSINLESLEHEKSLSPTSEKIPIAGOEOEEK KKNNESSKALSENPFTSANTSGFTFLKTQPAAANSLQSQSSSTFGAPSFGSSAFKIDLPS VSSTSTGVASSEQDATDPASAKPVFGKPAFGAIAKEPSTSEYAFGKPSFGAPSFGSGKSS VESPASGSAFGKPSFGTPSFGSGNSSVEPPASGSAFGKPSFGTPSFGSGNSSAEPPASGS AFGKPSFGTSAFGTASSNETNSGSIFGKAAFGSSSFAPANNELFGSNFTISKPTVDSPKE VDSTSPFPSSGDQSEDESKSDVDSSSTPFGTKPNTSTKPKTNAFDFGSSSFGSGFSKALE SVGSDTTFKFGTQASPFSSQLGNKSPFSSFTKDDTENGSLSKGSTSEINDDNEEHESNGP NVSGNDLTDSTVEQTSSTRLPETPSDEDGEVVEEEAQKSPIGKLTETIKKSANIDMAGLK NPVFGNHVKAKSESPFSAFATNITKPSSTTPAFSFGNSTMNKSNTSTVSPMEEADTKETS EKGPITLKSVENPFLPAKEERTGESSKKDHNDDPKDGYVSGSEISVRTSESAFDTTANEE IPKSQDVNNHEKSETDPKYSQHAVVDHDNKSKEMNETSKNNERSGQPNHGVQGDGIALKK DNEKENFDSNMAIKQFEDHQSSEEDASEKDSRQSSEVKESDDNMSLNSDRDESISESYDK LEDINTDELPHGGEAFKAREVSASADFDVQTSLEDNYAESGIQTDLSESSKENEVQTDAI PVKHNSTQTVKKEAVDNGLQTEPVETCNFSVQTFEGDENYLAEQCKPKQLKEYYTSAKVS NIPFVSQNSTLRLIESTFQTVEAEFTVLMENIRNMDTFFTDOSSIPLVKRTVRSINNLYT WRIPEAEILLNIQNNIKCEQMQITNANIQDLKEKVTDYVRKDIAQITEDVANAKEEYLFL MHFDDASSGYVKDLSTHQFRMQKTLRQKLFDVSAKINHTEELLNILKLFTVKNKRLDDNP LVAKLAKESLARDGLLKEIKLLREQVSRLQLEEKGKKASSFDASSSITKDMKGFKVVEVG LAMNTKKQIGDFFKNLNMAK

YIL148W, 1321 bp, exon1: 501-508, intron1: 509-942, exon2: 943-1321 (SEQ ID NO 137)
TCGATCAACTCTATCCAACAATTCTATAATATCCACTGTTCATTAACGAATATTGGTCTT

TTTCCCTTATGGTGAAGTAAATTTTCCATGCAATATCCGGGTAAGCTATCGACAAGTTTA TTGACTGCAATTTGAGTTTATTACATCCGTACATTACTAAGATGTATGGTTTTTCTATTT TTGTGCTCCGTGTCGATATTTCGTGGAGCAAACCAGAAAAGATGCGGAACCTCTTAGCAC TCCGCCTGGACATAGGCGGAGCATATTCCTCCTATGGGATGGGTTTTGTTGTACTCTTTT CTCTCTAGACAGGACCTCCGATTGCCTCCCTGAGGGTGAGATGGTTTCCGGCCTCAGGAC AAATTAAAGGTAGTTGAATCTCTATTTGTTGTTGTTATTACCGCTTATTATCCCATAGTT GAGACGACCAAGATTCAAACATGCAAATGTATGCACCATATCCATTCTAAACATAGTTTT TCGAACGTTCAGAGCTTAAAGGGACAATTATTTTAGAAACTGAATTTTTACCCAGTGGAA TAACATCGTATCTGTAAAGTCTACAAAATTTTTTATCCATCAAAAATTAAAACAAAGAAA ACTGCCAAACTGAATATGAGGAACTTTCCTCTCTAGGAATGACTTAGTGAATGTACAGTG ACTTGTGGAAAATATGATTAGATTTTGAGCGGGTGATGCGACTTAACAGTCTCATTGCCT AAGAAATATCCAAATTTGTGGTTCATGCTCTCCCCCAAGATATGACGATGAGAGCTCGTT TAAAATTTTGTCTTCCGAACAGTTATGAAAAAACTATTACGTGTTTTTATGATATCC TTACTAACTTGTCATTTTTTATAAAATTATTTTTTTAACAGTTTTGTCAAGACTTTGAC TGGTAAGACCATCACTTTGGAAGTTGAATCTTCTGACACTATTGACAATGTCAAGTCAAA GATTCAAGACAAGGAAGGTATCCCACCTGACCAACAAGATTGATCTTTGCTGGTAAGCA ATTGGAAGACGGTAGAACCTTGTCTGACTACAACATTCAAAAAGAATCCACTTTGCACTT AGTCTTGAGATTGAGAGGTGGTATCATTGAACCATCTTTGAAAGCTTTGGCTTCCAAGTA CAACTGTGACAAATCTGTTTGCCGTAAGTGTTATGCTAGATTGCCACCAAGAGCTACCAA CTGTAGAAAGAGAAAGTGTGGTCACACCAACCAATTGCGTCCAAAGAAGAAGTTAAAATG

YIL148W, 128 aa (SEQ ID NO 138) MQIFVKTLTGKTITLEVESSDTIDNVKSKIQDKEGIPPDQQRLIFAGKQLEDGRTLSDYN IQKESTLHLVLRLRGGIIEPSLKALASKYNCDKSVCRKCYARLPPRATNCRKRKCGHTNQ LRPKKKLK

YIL150C, 2216 bp, CDS: 501-2216 (SEQ ID NO 139) AATATTCAACCTGAAGTTGCAGTCAAAGCGGCGATTAACTTTTCCAACGTAACCGATCTA ACTAACAATAGCACCGATGGAGCAAAAATAACAGAAATTGGAAGTACATCTAAACGGCCA ATTGAGAGCGGTACATCTTCTGATCCAGACACCAAAAAGGTTAAAGAGAGTCCAGCAAAT GATCAAGCTTCCAACGAGTGATGTAATATTAAACAATGTAATTATATAAATATGAAACAT CTACATATTTTAAATGTCACTAATGTCATTACAGAGGACATAAAGTGATTTATGACACAT GTTTCTTGGATGCGCAAACCCACCTTTTCTAACACCACTAAGAAATATCAACTTTATAGG CCATCGAAGATAAAGGAACGTAAGTTTGTCAATTCAACCTCACATTTTCAACGCACATTA AGCACTTGGTTCGTGGAGAAATGAATGATCCTCGTGAAATTTTAGCGGTTGATCCGTACA ATAATATTACTTCTGATGAAGAGGATGAGCCAAGCCATCGCGAGAGAACTTGAATTTATGG AGGATCCTAATTTTGAAGCCATCGAGGTACCTCAATCTCCTACCAAAAACCGTGTGAAAG TGGGGTCTCATAATGCTACACAACAAGGCACAAAATTCGAAGGTTCGAATATTAATGAAG TAAGGTTATCTCAATTACAGCAGCAACCAAAACCACCAGCTAGTACAACCACATACTTTA TGGAGAAATTTCAAAACGCAAAGAAGAACGAAGATAAACAAATTGCCAAGTTTGAAAGCA TGATGAATGCAAGAGTACATACGTTCAGTACCGATGAGAAGAAATATGTGCCGATAATCA CAAACGAATTAGAAAGCTTTTCAAATCTTTGGGTTAAAAAGAGGTACATACCTGAAGATG ACTTAAAACGGGCTTTGCATGAGATCAAAATCCTTCGGTTGGGCAAACTTTTTGCTAAAA TTCGCCCACCTAAATTTCAAGAGCCTGAATACGCCAACTGGGCCACCGTAGGCCTCATTA GCCACAAATCGGACATCAAATTTACATCATCTGAAAAGCCAGTCAAATTCTTCATGTTCA CCATAACGGACTTTCAGCATACACTAGATGTTTATATCTTCGGGAAAAAGGGTGTAGAAA GATATTATAATCTTCGCCTGGGTGATGTGATAGCAATATTAAACCCAGAAGTACTACCAT GGAGACCCTCAGGGCGAGGAAATTTTATCAAATCCTTCAACCTTCGAATTAGTCATGACT TCAAATGTATCCTGGAGATAGGTTCAAGTAGAGATTTAGGTTGGTGTCCCATAGTGAATA AAAAGACTCACAAAAAATGTGGCTCTCCCATTAACATATCTCTTCATAAGTGTTGCGATT ACCATAGAGAAGTGCAATTTCGTGGAACAAGTGCTAAAAGAATTGAATTAAATGGTGGGT ACGCCTTGGGCGCCCTACGAAAGTGGACTCTCAACCAAGCCTATATAAGGCCAAAGGGG AAAACGGGTTTAATAATAATCAAAGGTACTCGTAAGCGCCTGTCAGAAGAGGGAAAGAC TTAAAAAGAGCTCTCACAATTTTACGAATAGTAATTCTGCCAAAGCATTTTTCGACGAGA AATTTCAGAATCCAGATATGCTGGCAAACTTAGACAATAAAAGAAGAAGGAAAATAATAGAAA CTAAGAAATCGACAGCACTGAGCCGCGAACTAGGCAAAATTATGAGAAGGAGGGAATCCA

YIL150C, 571 aa (SEQ ID NO 140)
MNDPREILAVDPYNNITSDEEDEQAIARELEFMERKRQALVERLKRKQEFKKPQDPNFEA
IEVPQSPTKNRVKVGSHNATQQGTKFEGSNINEVRLSQLQQQPKPPASTTTYFMEKFQNA
KKNEDKQIAKFESMMNARVHTFSTDEKKYVPIITNELESFSNLWVKKRYIPEDDLKRALH
EIKILRLGKLFAKIRPPKFQEPEYANWATVGLISHKSDIKFTSSEKPVKFFMFTITDFQH
TLDVYIFGKKGVERYYNLRLGDVIAILNPEVLPWRPSGRGNFIKSFNLRISHDFKCILEI
GSSRDLGWCPIVNKKTHKKCGSPINISLHKCCDYHREVQFRGTSAKRIELNGGYALGAPT
KVDSQPSLYKAKGENGFNIIKGTRKRLSEEEERLKKSSHNFTNSNSAKAFFDEKFQNPDM
LANLDNKRRKIIETKKSTALSRELGKIMRRRESSGLEDKSVGERQKMKRTTESALQTGLI
QRLGFDPTHGKISQVLKSSVSGSEPKNNLLGKKKTVINDLLHYKKEKVILAPSKNEWFKK
RSHREEVWQKHFGSKETKETSDGSASDLEII

YIL167W, 1133 bp, CDS: 501-1133 (SEQ ID NO 141) GACATTTTGAAAAATTACATTTATAGAAGTTTATTATAACGTAACAGTTAACAACAAAG GCTCATAGTCCGAGATCAATATAATAAATTATTCAAGGTTTAAGGAAGAAGTTACCATGG AAATGACTTACTATGAAAAGACACCTTTGATTCGTCAATTTTTGAACAATGGTAAGACAA ATTCGTGGTTTTACGTTAAGCATGAGATGTTACAACCAGGTGGAAGTTTCAAATCGAGAG GAATCGGGCATTTGATAAGGAAGAGTAATGAAGAAGCGCTAAGCGAGGGTTCTGGGAAGC CGATGCACTTAATTGCAGTGTAGTGGTTCCTAAAACTACAAAACCTAGAATGGTAAAGA AAATTCAAAGTGCAGGAGCCAAAGTCATTATCCATGGTGATCATTGGGGGGAAGCAGATG AATACTTGAGGCACGAATGAATGGCGCAAGAAAGCCAACATGGTTCGAAGACACTATATG TGCACCCGTTTGATAACGAGACAATTTGGGAAGGTCATTCTACGATTGTGGATGAAATCA TAGAACAATTGAAGGAAAATGATATATCCTTACCTAGGGTGAAAGCTTTGGTTTGTAGTG TTGGTGGTGGCCTATTTAGTGGCATAATTAAAGGCCTAGATAGGAATCAGCTTGCTG AAAAAATTCCGGTCGTTGCTGTAGAAACTGCCGGTTGTGACGTATTGAATAAGTCTCTCA AAAAAGGTAGTCCAGTTACTCTTGAAAAATTGACAAGTGTTGCAACTTCTTTGGCCTCCC CATACATAGCATCATTCGCGTTTGAGAGTTTTAACAAGTATGGATGTAAGTCTGTAGTTT TATCAGATCAAGACGTTCTGGCAACATGCTTGAGATATGCCGATGACTACAATTTTATAG TGGAACCAGCCTGTGGAGCATCCTTACATTTATGTTATCATCCAGAGATTCTTGAAGACA TTCTGGAACAAAAATATATGAGGATGATATCGTTATTATAATCGCATGCGGTGGATCAT GTATGACGTATGAAGACTTGGTGAAAGCGTCGAGCACATTAAACGTATCATAA

YIL167W, 210 aa (SEQ ID NO 142)
MAQESQHGSKTLYVHPFDNETIWEGHSTIVDEIIEQLKENDISLPRVKALVCSVGGGGLF
SGIIKGLDRNQLAEKIPVVAVETAGCDVLNKSLKKGSPVTLEKLTSVATSLASPYIASFA
FESFNKYGCKSVVLSDQDVLATCLRYADDYNFIVEPACGASLHLCYHPEILEDILEQKIY
EDDIVIIIACGGSCMTYEDLVKASSTLNVS

YJL034W, 2549 bp, CDS: 501-2549 (SEQ ID NO 143)
CCATGAACTCAGCATGTGCTACTCCAGTTAATGACTTGTTCGTATCGTTCATGCCATAAG
CCATCACCTGGCCAGTTGGCGTATGTACAAAGATGCAAGCTACCGGTGTCTCATCGTGGT
CAAGAGCGTATCTAGCCAAACGGACAGCTGTCCTCATATGTTTAATATGCTGCATAGTGT
GAGTCCTCTAGTTTTTACCGCAGCCACCAGCCGCTTCTCGAGCAAAGTGTAGATCCCATT
AGGACTCATCATTCATCTAATTTTGCTATGTTAGCTGCAACTTTCTATTTTAATAGAACC
TTCTGGAAATTTCACCCGGCGCGCGCACCCGAGGAACTGGACAGCGTGTCGAAAAAGTTGC
TTTTTTATATAAAGGACACGAAAAAGGGTTCTCTGGAAGATATAAATATGGCTATGTAATT
CTAAAGATTAACGTGTTACTGTTTTACTTTTTTAAAGTCCCCAAGAGTAGTCTCAAGGGA
AAAAGCGTATCAAACATACCATGTTTTTCAACAGACTAAGCGCTGGCAAGCTGCTGGTAC
CACTCTCCGTGGTCCTGTACGCCCTTTTCGTGGTAATATTACCTTTTACAGAAATTCTTTCC
ACTCCTCCAATGTTTTAGTTAGAGGTGCCGATGATGTAGAAAACTACGGAACTGTTATCG
GTATTGACTTAGGTACTACTTATTCCTGTGTTGCTGTGATGAAAAATGGTAAGACTGAAA
TTCTTGCTAATGAGCAAGGTAACAGAATCACCCCATCTTACGTGGCATTCACCGATGATG

AAAGATTGATTGGTGATGCTGCAAAGAACCAAGTTGCTGCCAATCCTCAAAACACCATCT TCGACATTAAGAGATTGATCGGTTTGAAATATAACGACAGATCTGTTCAGAAGGATATCA AAGGAGAAAAGAAGGTTTTTACTCCAGAAGAAATTTCTGGTATGATCTTGGGTAAGATGA AACAAATTGCCGAAGATTATTTAGGCACTAAGGTTACCCATGCTGTCGTTACTGTTCCTG CTTATTTCAATGACGCGCAAAGACAAGCCACCAAGGATGCTGGTACCATCGCTGGTTTGA ACGTTTTGAGAATTGTTAATGAACCAACCGCAGCCGCCATTGCCTACGGTTTGGATAAAT CTGATAAGGAACATCAAATTATTGTTTATGATTTGGGTGGTGGTACTTTCGATGTCTCTC TATTGTCTATTGAAAACGGTGTTTTCGAAGTCCAAGCCACTTCTGGTGATACTCATTTAG GTGGTGAAGATTTTGACTATAAGATCGTTCGTCAATTGATAAAAGCTTTCAAGAAGAGC AGGCTAAACGTGCCTTGTCCAGCCAAATGTCCACCCGTATTGAAATTGACTCCTTCGTTG ATGGTATCGACTTAAGTGAAACCTTGACCAGAGCTAAGTTTGAGGAATTAAACCTAGATC TATTCAAGAAGACCTTGAAGCCTGTCGAGAAGGTTTTGCAAGATTCTGGTTTGGAAAAGA AGGATGTTGATGATATCGTTTTGGTTGGTGGTTCTACTAGAATTCCAAAGGTCCAACAAT TGTTAGAATCATACTTTGATGGTAAGAAGGCCTCCAAGGGTATTAACCCAGATGAAGCTG TTGCATACGGTGCAGCCGTTCAAGCTGGTGTCTTATCCGGTGAAGAAGGTGTCGAAGATA TTGTŢTTATTGGATGTCAACGCTTTGACTCTTGGTATTGAAACCACTGGTGGTGTCATGA CTCCATTAATTAAGAGAAATACTGCTATTCCTACAAAGAAATCCCAAATTTTCTCTACTG CCGTTGACAACCAACCGTTATGATCAAGGTATACGAGGGTGAAAGAGCCATGTCTA AGGACAACAATCTATTAGGTAAGTTTGAATTAACCGGCATTCCACCAGCACCAAGAGGTG TACCTCAAATTGAAGTCACATTTGCACTTGACGCTAATGGTATTCTGAAGGTGTCTGCCA CAGATAAGGGAACTGGTAAATCCGAATCTATCACCATCACTAACGATAAAGGTAGATTAA CCCAAGAAGAGATTGATAGAATGGTTGAAGAGGCTGAAAAATTCGCTTCTGAAGACGCTT CTATCAAGGCCAAGGTTGAATCTAGAAACAATTAGAAAACTACGCTCACTCTTTGAAAA ACCAAGTTAATGGTGACCTAGGTGAAAAATTGGAAGAAGAAGAAACCTTATTAG ATGCTGCTAACGATGTTTTAGAATGGTTAGATGATAACTTTGAAACCGCCATTGCTGAAG ACTTTGATGAAAAGTTCGAATCTTTGTCCAAGGTCGCTTATCCAATTACTTCTAAGTTGT ACGGAGGTGCTGATGGTTCTGGTGCCGCTGATTATGACGACGAAGATGAAGATGACGATG GTGATTATTTCGAACACGACGAATTGTAG

YJL034W, 682 aa (SEQ ID NO 144)
MFFNRLSAGKLLVPLSVVLYALFVVILPLQNSFHSSNVLVRGADDVENYGTVIGIDLGTT
YSCVAVMKNGKTEILANEQGNRITPSYVAFTDDERLIGDAAKNQVAANPQNTIFDIKRLI
GLKYNDRSVQKDIKHLPFNVVNKDGKPAVEVSVKGEKKVFTPEEISGMILGKMKQIAEDY
LGTKVTHAVVTVPAYFNDAQRQATKDAGTIAGLNVLRIVNEPTAAAIAYGLDKSDKEHQI
IVYDLGGGTFDVSLLSIENGVFEVQATSGDTHLGGEDFDYKIVRQLIKAFKKKHGIDVSD
NNKALAKLKREAEKAKRALSSQMSTRIEIDSFVDGIDLSETLTRAKFEELNLDLFKKTLK
PVEKVLQDSGLEKKDVDDIVLVGGSTRIPKVQQLLESYFDGKKASKGINPDEAVAYGAAV
QAGVLSGEEGVEDIVLLDVNALTLGIETTGGVMTPLIKRNTAIPTKKSQIFSTAVDNQPT
VMIKVYEGERAMSKDNNLLGKFELTGIPPAPRGVPQIEVTFALDANGILKVSATDKGTGK
SESITITNDKGRLTQEEIDRMVEEAEKFASEDASIKAKVESRNKLENYAHSLKNQVNGDL
GEKLEEEDKETLLDAANDVLEWLDDNFETAIAEDFDEKFESLSKVAYPITSKLYGGADGS
GAADYDDEDEDDDGDYFEHDEL

GCAACGTACTGTCTTGTCAGTAAATCATGATACGTGTACATTAGTGCCCAAGAACAATA GTGCGGCAGGGTACGAGAGTATACCGGGGATCTTGAGGAAAGAAGCAATAATGCTGCTGA GATACTTTTATGTAAGACAAAATGAAAGGGCGCCAAAGCCACGGTCCAAGAGTGACAGAG TGTTGGATAAAAACACGTTTCCGCCTATGGAATGGTCAAAGTATCTTAATGAAGAAGCAT TCATTGAGACTTTTGGTGATGATTACAGGACTTGTTTTGCGAATAAAGTTGACTTGTCCA GTAATAGCGTCGATTGGGATTTGATTGACTCCCACCAAGATAATATAATCCAAGAACTGG AAGAACAATGCAAAATGTTTAAGTTTAATGTACATAAGAAATCTAAGGTTTGA

YJL035C, 250 aa (SEQ ID NO 146)
MQHIKHMRTAVRLARYALDHDETPVACIFVHTPTGQVMAYGMNDTNKSLTGVAHAEFMGI
DQIKAMLGSRGVVDVFKDITLYVTVEPCIMCASALKQLDIGKVVFGCGNERFGGNGTVLS
VNHDTCTLVPKNNSAAGYESIPGILRKEAIMLLRYFYVRQNERAPKPRSKSDRVLDKNTF
PPMEWSKYLNEEAFIETFGDDYRTCFANKVDLSSNSVDWDLIDSHQDNIIQELEEQCKMF
KFNVHKKSKV

YJL070C, 3167 bp, CDS: 501-3167 (SEQ ID NO 147) TCCCCTGATGGTCAAATACTGTGCATGGCATCCCGTGCAGTCAAGGATGCTTTGAGACTA GTTCATCTGCCTTCTTGTAGCGTGTTCAGCAACTGGCCTACCAGCGGGACGCCTTTGGGT AAAGTTACCAGTGTCGCATTTTCGCCATCTGGTGGGCTACTGGCCGTGGGTAACGAACAA GGTAAAGTGAGGCTCTGGAAATTAAACCACTACTAAATTTCCATTTATAGACAAACTTAG ATATTAAAAGCAATGTACAAATACATACACAAAATATCACTGTAAAAAAATTGCGAAGAA ACTTGAAATTGAATATGATTCTGCCCACTTTTTTCTTGCTGTCATTTATAGTCAGAAATG AAAAATTGTCCGAGAAATTAAATATAATATATGGAAAAAAAGGGGACATTGAGTTTAAAG AATTTGATTAAAATGTCCTCTCAATATCCTCTGTAAGAGTTATCTAAATCTCACTTTACT TATTCATCTCGCTGGGAATTATGCAGGCGGTAGAGAGAGGCCCTCGTTACTCTTTGACG AATATCAAAATTCTGTTACTAAGCCTAATGAGACGAAGAATAAAGAÁGCCAGGGTCTTGT CAGAGAATGACGGTGATGTCTCCCCATCTGTTTTGAAACAGAAGGAAATATCAGTCGATG ATATGGATATGATTTCTTTGCCCACGGAATTTGACAGGCAAATGGTTTTAGGTTCACCTA ATTATGGAAATGGAGAAAGTGACAGCTTTGTCTCATCGTACACGCCCTCAAATCTGAAAA CGGGTGAAGAACTAAAGATCTTTTCATTAATCCGTTTGAATTGGTTTCTCAAATGAGAA AAAGATACATTGCTGCTTCCAAACAAGATGGCATTTCAAACATAAAAAATGACACTGAAA AGTGGTTTTTATACCCAAAACCACTGCCAAAGTTTTGGAGATTTGAAGACGATAAACGAT TCCAAGATCCCTCTGACTCTGACTTAAATGACGATGGAGACAGTACTGGGACCGGAGCCG CTACACCGCACCGCCATGGCTACTATTACCCAAGTTACTTTACCGATCACTACTACTACT ACACAAAATCTGGTTTGAAAGGAAAAGGAAATATAAAAGTACCATACACCGGTGAATATT TCGATTTAGAGGATTACAAAAAACAATACATTTACCATTTAAGTAATCAGGAAAATACGC AAAACCCACTTTCACCTTATTCTAGTAAGGAGGAGTCACTAGAGGAAGAATTTTTAACAG TGTTTCAGTACCTAAACTCTAAGAAAGAAATTTTAGCTAATAAAAATGTTCCCTACAGAG ATTTTTATAATTCTCGTAAGGTAGATCGAGACTTGTCTTTAAGTGGTTGTATTTCTCAAC G1'CAATTGAGTGAATATATATGGGAGAAAATAAATTTAGAACCTGAAAGGATAGTTTATC AAGACCCGGAAACGTCAAGGAAACTCAGTTTGAGAGACATTTTTCAGTTTGGTTGTTCTT ATAGAAATATTTACCTAATAGATTACCATCTAACTCCTAACAAAGTAGCAAAGTTGGTCG GCAAAGAAATGAGGTTTTACCTATTAGCCAAAGTGTTTCTGGAGTTTGATAATTTCATTG AAGGTGAGTACCTAGCAGAAATTTTCATAAAATACGTTATTCATATCCTCGAAAAATCAA AGTACCAATTGGCCCAAGTATCAGTTAATTTTCAATTCTATTCCAGTGGTGAAGACTGGT ACAAGAAATTTTCTCAATGGTTGCTACGATGGAAGCTAGTATCGTATAATATCCGCTGGA ATATACAAATTGCCAGGATTTTTCCCAAACTATTCAAGGAAAATGTCGTGTCAAATTTCC AGGAGTTTTTGGATCTTATCTTCAATCCTTTATTCACTCTGGAAAAGGAGCAGTTACCAA CTATGGATCTGGTCATTAAAGAGTCGGATGAATATTACTGGAAAGAATTTACTGATATGA ATTGTAAGCCAAAATTTTGGACAGCACAGGGTGACAATCCAACTGTTGCGCATTACATGT ATTATATTATAAAAGTTTAGCGAAAGTTAATTTTCTGCGGTCACAAAATCTTCAAAATA CAATCACCCTAAGAAATTATTGTTCTCCACTATCCAGCAGAACTTCCCAATTTGGAGTGG ATTTATATTTTACAGATCAAGTTGAATCGTTAGTGTGCAACTTACTGCTTTGTAATGGTG TCTTTCAAATACCCATTTTAGCTGCGCCATTATCATCTGTTTCATTACTGAATTCGCAAA

YJL070C, 888 aa (SEQ ID NO 148) MQAVERRPSLLFDEYQNSVTKPNETKNKEARVLSENDGDVSPSVLKQKEISVDDMDMISL PTEFDRQMVLGSPMFFDLEDEENKIDPLPSVSHHYGNGESDSFVSSYTPSNLKTGEETKD LFINPFELVSOMRKRYIAASKODGISNIKNDTEKWFLYPKPLPKFWRFEDDKRFODPSDS DLNDDGDSTGTGAATPHRHGYYYPSYFTDHYYYYTKSGLKGKGNIKVPYTGEYFDLEDYK KQYIYHLSNQENTQNPLSPYSSKEESLEEEFLTDVPTFQEFRDDFAYIIELIQSHKFNEV SRKRLSYLLDKFELFQYLNSKKEILANKNVPYRDFYNSRKVDRDLSLSGCISQRQLSEYI WEKINLEPERIVYQDPETSRKLSLRDIFQFGCSSNDQPIAIGLKLIDDEFLDWYRNIYLI DYHLTPNKVAKLVGKEMRFYLLAKVFLEFDNFIEGEYLAEIFIKYVIHILEKSKYQLAQV SVNFQFYSSGEDWYKKFSQWLLRWKLVSYNIRWNIQIARIFPKLFKENVVSNFQEFLDLI FNPLFTLEKEQLPIDSSVNTDIIGLQFFLSNVCSMDLVIKESDEYYWKEFTDMNCKPKFW TAQGDNPTVAHYMYYIYKSLAKVNFLRSQNLQNTITLRNYCSPLSSRTSQFGVDLYFTDQ VESLVCNLLLCNGGLLOVEPLWDTATMIOYLFYLFOIPILAAPLSSVSLLNSOKSTFLKN KNVLLEHDYLKDQETAKINPSRDITVGEQRSYETNPFMKMFKMGLKISLSSKSILYNSSY TLEPLIEEYSVAASIYLLNPTDLCELSRTSVLSSGYEGWYKAHWIGVGVKKAPYFEENVG GIDNWYDTAKDTSIKHNVPMIRRRYRKETLDQEWNFVRDHFGVINSIW

YJL078C, 3146 bp, CDS: 501-3146 (SEQ ID NO 149) TTTTTCTTCGCACATGGCTGGTTCTGCTGGAGGCGGCTGGGTGTTTATAGTTACCGCAAT GCAGGTCGCTTCGTTTACTTTTCTCTGCGTGCTCGAGAACTGATAAATACTGGTTTAGGA AGCAACGCTACGCACTAGCTGTGTGTGCTTGCTCTTTGTGTTCGTCTTTCGTATATTGC GGGTTCCCGCGGTTAATTCAACAACAAATATGGTATCTAGGCAGGGACCCAGCAACGGAA GGATGTAATTGCTATATAGGGCCGATGAAACAGTTCTCATGTTTCAACTCGGTCGAAGAA TTCTCTAAAACATATTCTATACTTCAAAGTTTTTAGCTTCTTGCTTTTCGGTAGTTGCCA AACCAATATCGGCATAAAATTATAATTGCTGCACCCCTGCAACTCCAAACAACTTAAAAC **AACTTAAAACGAAAACGCTTATGCTGGAGTTTCCAATATCAGTTCTGCTAGGATGCCTAG** TAGCCGTCAAGGCACAAACCACGTTTCCAAACTTCGAGAGCGATGTGCTGAACGAGCATA ACAAGTTCAGAGCGCTACATGTTGACACAGCGCCGCTCACCTGGTCCGACACTCTGGCCA CCTATGCGCAGAACTACGCCGACCAATATGATTGTTCGGGTGTCTTAACGCATTCCGATG GCCCATATGGTGAGAACCTTGCCCTTGGTTACACAGACACGGGAGCGGTGGACGCCTGGT ACGGGGAGATAAGCAAGTATAATTATTCAAATCCCGGATTTTCTGAATCCACGGGTCACT TCACACAGGTGGTTTGGAAGTCAACCGCCGAGATTGGATGTGGTTATAAATATTGTGGTA CGACATGGAACAATTATATTGTGTGCTCCTACAACCCTCCTGGAAACTACCTGGGTGAGT TTGCAGAGGAAGTGGAACCACTTATAAGCACTGTTTCCTCGTCCTCATCCTCGTCCTCTT CTACCTCAACTACATCAGACACAGTCTCCACCATCTCATCCAGTATTATGCCCGCTGTAG CGCAAGGGTATACAACAACGGTATCGTCTGCGGCTAGCAGCAGTTCTTTAAAATCGACGA CCATAAACCCTGCCAAGACCGCTACCCTCACTGCGTCCTCTTCTACCGTAATTACTAGTA GCACAGAATCAGTTGGATCCTCCACTGTCTCATCAGCCTCAAGCTCTTCTGTCACTACTT CCTATGCTACCTCGAGTACCGTCGTCTCTAGTGATGCTACTTCATCCACTACCACCA CCTCATCGGTTGCTACATCGTCCAGTACCACTTCTTCCGACCCTACCTCGAGCACTGCTG CTGCTTCTTCTGATCCTGCCTCAAGTTCCGCTGCCGCTTCCTCCAGCGCGAGTACCG AGAACGCCGCTTCTTCTAGCAGCGCCATCTCGAGCTCTTCATCAATGGTTTCTGCTCCTT TGAGTAGTACTCTTACTACTTCCACCGCAAGCTCCAGAAGTGTAACTTCCAATTCAGTTA ATTCTGTTAAGTTTGCAAACACAACTGTGTTTTCTGCTCAAACAACCTCTTCTGTAAGCG CCTCATTATCATCATCTGTAGCTGCTGACGATATTCAGGGTAGCACTTCCAAGGAGGCCA CAAGCTCAGTTTCCGAACATACTAGTATAGTAACTAGTGCAACTAATGCTGCCCAATATG CAACGAGACTTGGGTCATCTTCCAGAAGTTCTTCCGGGGCCGTCTCTTCCTCAGCTGTGT CGCAATCTGTTCTGAATTCCGTTATAGCCGTCAACACCGACGTATCTGTAACCTCAGTTA GTAGCACAGCCCATACCACAAAGGACACCGCCACCACTTCAGTAACCGCCTCAGAAAGTA TCACTTCGGAAACTGCTCAGGCTTCAAGTTCAACAGAGAAGAATATTAGTAACAGTGCCG CCACATCGAGTAGCATTTACTCCAACAGTGCTTCTGTGTCAGGACACGGTGTAACATACG CTGCCGAATACGCCATTACATCCGAGCAATCCTCTGCGCTTGCCACATCTGTGCCTGCTA CAAATTGCTCTAGTATCGTGAAGACCACAACTTTAGAAAATTCGAGTACCACAACCATCA CAGCCATTACTAAGAGTACTACAACCTTGGCCACTACTGCTAACAACTCCACAAGGGCAG CTACCGCAGTAACCATAGATCCCACATTGGACCCTACCGACAACTCAGCTAGTCCAACCG ACAATGCTAAACACACCTCTACATATGGATCTTCTTCCACAGGCGCATCTTTAGATAGCT TACGCACAACCACCAGTATTAGTGTCTCAAGCAACACCACACAGTTAGTCTCTACCTGCA CTTCCGAGAGCGATTATTCCGATAGTCCTAGCTTCGCCATCTCCACTGCCACCACCACTG **AAAGCAATCTGATCACAACACCATCACAGCTTCTTGTAGTACGGATAGTAATTTCCCTA** CCTCCGCTGCTTCTTCTACAGATGAGACGGCCTTCACTAGAACAATCTCGACATCTTGTA GCACTTTGAACGGCGCCTCAACCCAAACCAGTGAGCTAACCACATCGCCTATGAAAACCA ACACGGTGGTTCCAGCTTCTTTCTTTCCCTTCAACTACAACCACTTGTCTAGAAAATGATG ACACTGCCTTTTCTAGTATCTACACTGAAGTCAACGCCGCAACTATCATTAACCCCGGAG AAACATCTTCTCGCCTAGCGATTTCGCCACATCTGAAAAGCCAAACGAGCCCACTTCTG TCAAATCCACCTCAAACGAAGGCACCTCTTCCACAACAACAACCTACCAACAGACTGTTG CTACACTGTATGCCAAGCCCTCCAGCACAAGCCTAGGTGCAAGAACAACTACTGGTAGCA ACGGTCGTTCAACTACCAGCCAACAAGACGGGTCTGCCATGCATCAGCCAACTTCCTCGA TCTACACTCAACTAAAAGAAGGCACATCAACCACCGCAAAACTTTCTGCATACGAAGGTG CTGCAACACCTCTTTCCATTTTCCAGTGCAATAGTCTAGCTGGAACGATTGCCGCTTTTG TCGTAGCTGTTCTGTTCGCCTTCTAG

YJL078C, 881 aa (SEQ ID NO 150) MLEFPISVLLGCLVAVKAQTTFPNFESDVLNEHNKFRALHVDTAPLTWSDTLATYAQNYA DOYDCSGVLTHSDGPYGENLALGYTDTGAVDAWYGEISKYNYSNPGFSESTGHFTQVVWK STAEIGCGYKYCGTTWNNYIVCSYNPPGNYLGEFAEEVEPLISTVSSSSSSSSSTSTTSD TVSTISSSIMPAVAQGYTTTVSSAASSSSLKSTTINPAKTATLTASSSTVITSSTESVGS STVSSASSSVTTSYATSSSTVVSSDATSSTTTTSSVATSSSTTSSDPTSSTAAASSSDP ASSSAAASSSASTENAASSSSSAISSSSSMVSAPLSSTLTTSTASSRSVTSNSVNSVKFAN TTVFSAOTTSSVSASLSSSVAADDIQGSTSKEATSSVSEHTSIVTSATNAAQYATRLGSS SRSSGAVSSSAVSOSVLNSVIAVNTDVSVTSVSSTAHTTKDTATTSVTASESITSETAQ ASSSTEKNISNSAATSSSIYSNSASVSGHGVTYAAEYAITSEQSSALATSVPATNCSSIV KTTTLENSSTTTITAITKSTTTLATTANNSTRAATAVTIDPTLDPTDNSASPTDNAKHTS TYGSSSTGASLDSLRTTTSISVSSNTTQLVSTCTSESDYSDSPSFAISTATTTESNLITN TITASCSTDSNFPTSAASSTDETAFTRTISTSCSTLNGASTQTSELTTSPMKTNTVVPAS SFPSTTTTCLENDDTAFSSIYTEVNAATIINPGETSSLASDFATSEKPNEPTSVKSTSNE GTSSTTTTYQQTVATLYAKPSSTSLGARTTTGSNGRSTTSQQDGSAMHQPTSSIYTQLKE GTSTTAKLSAYEGAATPLSIFQCNSLAGTIAAFVVAVLFAF

YJL179W, 109 aa (SEQ ID NO 152) MSQIAQEMTVSLRNARTQLDMVNQQLAYLDRQEKLAELTKKELESYPTDKVWRSCGKSFI LQDKSKYVNDLSHAETVLLDQRKTLKIKKNYLETTVEKTIDNLKALMKN

YJL180C, 1478 bp, CDS: 501-1478 (SEQ ID NO 153)

AATAGTTCTTTATCTTTAATGTTTTTTTTTTTTTGATCCAGAAGAACAGTTTCGGCATGTG ATAAATCATTAACGTATTTGGATTTATCCTGTAAGATAAACGATTTACCGCAAGATCTCC ATACTTTGTCCGTTGGATAAGACTCTAGTTCTTTCTTTGTCAATTCAGCAAGCTTTTCTT GTCTGTCCAAATATGCTAGCTGCTGATTGACCATATCCAATTGTGTCCTGGCGTTTCTTA ATTTAGTAAAGAGCTCTGTAGATAGTTCTTTAATTCCCATCTGCTCATCTGAGAAATTTC AAAAAATTAAGGTAAAGGAAAAGGCTAAATAAGAACAAAACACTTGAAGGCAAACGAAAC ACACGATTGAGAATAACACTCCTACGGAAACAAATAGATTGAGCAAAACTTCACAGAAGT TTTGGGAAAAGGTGTCACTAAATAGGGATGTTGAGAAAGGAAAGATTGCTCTACAATTAG ATGGCAGGACTATAAAAACTCCTCTAGGAAATGGAATTATAGTTGATAATGCAAAGTCTC TCTTAGCATACCTATTAAAACTGGAGTGGTCGTCCCTATCCAGTCTTTCCATCAAAACTC ACTCTTTGCCACTAACTTCATTAGTGGCAAGATGCATAGATTTACAAATGACAAATGAGC CTGGCTGTGACCCTCAATTAGTTGCAAAGATTGGAGGCAACAGTGATGTTATAAAAAATC AAGGAAGATTACGCAATGCGCAAAATGAGTTATATATACCCATCATCAAAGGAATGGAAG AGTTTTTACGCAACTTTTCATCCGAGTCTAATATTCGACTACAAATTTTAGATGCCGACA TCCATGGGTTACGAGGCAATCAGCAGTCGGATATCGTTAAGAATGCAGCAAAAAAATATA TGAGCAGCTTATCACCATGGGATCTTGCAATTCTTGAAAAAACTGTATTAACCACAAAGT CCTTCATTTGCGGCGTGCTATTATTAGAAAAATAAAAAGATACTGCGAACTTAATTCCCG CCTTGAAAACTGATATGGATAATATTGTACGTGCCGCCACCTTAGAAACAATCTTCCAAG TTGAAAAGTGGGGAGAGGTTGAAGATACTCATGACGTTGACAAAAGAGACATCAGAAGAA AAATTCATACTGCTGCGATTGCTGCTTTTTAAGCAATAA

YJL180C, 325 aa (SEQ ID NO 154)
MLPSLRKGCFIVNSIRLKLPRFYSLNAQPLGTDNTIENNTPTETNRLSKTSQKFWEKVSL
NRDVEKGKIALQLDGRTIKTPLGNGIIVDNAKSLLAYLLKLEWSSLSSLSIKTHSLPLTS
LVARCIDLQMTNEPGCDPQLVAKIGGNSDVIKNQLLRYLDTDTLLVFSPMNEFEGRLRNA
QNELYIPIIKGMEEFLRNFSSESNIRLQILDADIHGLRGNQQSDIVKNAAKKYMSSLSPW
DLAILEKTVLTTKSFICGVLLLENKKDTANLIPALKTDMDNIVRAATLETIFQVEKWGEV
EDTHDVDKRDIRRKIHTAAIAAFKO

YJL181W, 2336 bp, CDS: 501-2336 (SEQ ID NO 155) GCAAGTCAGTACGATGCATCCTTGGATCAAGAAGGTGAGTCTGGAAACGGTGCTTCTAAT GGCGATGTTTACCATTATAATGAAGGGGACTTGGCTGCCTCCTTCAAGGGATGTAGATCA AGAGGTACGTGTGCTAGTGAAATAGGTCACATGTACCAGAAAATCAAGAAATCTTAGATG TGTGTAATCTTGCAATTTAGTTTCAAACAAGATCCTTGTATTTATATAAACAAAGATATA ATTTTTAAAAAAAATTAGAAAAAGCAAATATAATTCAGGTCCCACTTGGAATAATGGCA TTCTTGGCTTTTTTTTTTTCATTTTCGTAAAGGGTCTTAAAAGGATTAAAAAATGCAGTA TTGAAATAAAGAACAATTACGAACGGTGAAGCTGCTATTTTGGTTATTATACCCTTCCAG GACAGTACGCGCAAACTATTATGGAGATATTCAAGGAAGAAGAAGAAGAAGCTTTTTCGG CGATAGAAGGTATAATATATGCCTGTGAGGTGTATGACCCTGTACCCCGTCATTTACATA AAAGCAAAACAAAGATCATCAATGCTGCTAAATTAATTATAGAAACGCATCTTTCATATT ATACAATACTCAATAACATTTCAGATATACAAGCCTATCTTCTACTTGGCTTAGGGATC TTGGAACGACAGGTCCATACCAAACAATTCTTTCAGAAAGTATTTCTCTCATGTTTGACC GTCTTTATCTCAGATTGAAAAGCTACCAGAAGCTCTTAAACGATGCAGGATTAAAGAATT TTTTTCAAGCTACGATTATGCTTTCGGGGTTGCATACAACCTTGTAAATTGCTCTGAAT ACAGGTATGACGAAGTTCATTACATATCGAACGGCACTTACTCATTAGTTGCATCGATGA AGATAGATCCTGCTGAAGTCATTAAAAGGGAACATTTTAGGCTTACAATTCCGAAATTTA ACATATCTAATATTAATTGAAATTTTTCATTTGCTCGATGGATTAGCATTTTTTAAGG TGAACCCTGATAGTTTATCTATATCTACAGCTTCAGCAGAAACAATCTTTCGCAGTATCT CCGAAGGTAATCATCAGGTCCTAGAATTGGGGAGAAGTTTAATGTTTCCATTGTTGAGGA CTGGAGATTTTGAAATCTGTCGTATTGACGACGCGGGAGCTGTCATAACATTTACAGAAG CGAAGGATGTAAAACTAGAAATAATCAGTCTGGATGAAGTTTCCTGGGTAATGCAGTGGA AATCTTGTCTTCAAAATTATGAGAGAGGGCAGCAAATGACAGTTCATTATCAAAACAC ACCTACAATTTAAGAAGGCCAACAATTTCAATGAAGATAATAATGGGCTAGGACTAATTG

YJL181W, 611 aa (SEQ ID NO 156)
MEIFKEEEEAFSAIEGIIYACEVYDPVPRHLHKSKTKIINAAKLIIETHLSYYTILNNI
SDIQAYLSTWLRDLGTTGPYQTILSESISLMFDRTVSIFRKCTIEGGFPHLIARLYLRLK
SYQKLLNDAGLKNFFSSYDYAFGVAYNLVNCSEYRYDEVHYISNGTYSLVASMKIDPAEV
IKREHFRLTIPKFNISNILIEIFHLLDGLAFFKVNPDSLSISTASAETIFRSISEGNHQV
LELGRSLMFPLLRTGDFEICRIDDAGAVITFTEAKDVKLEIISLDEVSWVMQWKSCLQNY
ERRAANDSSFIKTHLQFKKANNFNEDNNGLGLIVDRNIPTDDFTLASTNRQSPPPSNTGC
SLHRSKPLHIPLSSVIREDFYDSSLNERISKDGDSSCESFSGAESILSDYDFHDNEFFNN
QSPHYFSEHIDNNSREVVITDENTIISLENTQVSRWSNYSWQKISPHQLQVSIIQLRMGN
FIVAYDSDYNLHQFKIRLCDDIKCIQSTEQDIQIRVPLGAIMCSVTGILNIRTKDADKLL
RVLSFYTTDHTEAVSHSNNQDATASPLSSVSSAMDLKHSLQKCSSTIMPQELTQDVIGSK
SDLISNIRQKI

YJL187C, 2960 bp, CDS: 501-2960 (SEQ ID NO 157) TCTTGCAACCATCGTCCTCTAAGGAAAGAAATGTGGCACCTTTAAATAGGTTCCACCTCA CAGATGCCAACATGTGGGAGATAGGGGGCTATTCGCAATTTATTAACGTCTCTAGTACTG CGGGTGATAACGACGCGAAAAATATTTTTTCATTTTTCTTTTAACCATCACAATTTGCGA CGCGACGCGAAAAAAATGCAGAGAAGTAAAAGAATGCTGGATAAGAAATCAACAACAC TTGAACATTGGCGTGCCCCTGTGTATTAAGTAAAGGTTGTCCAAGAGGCTCTTTTTTGTA TGTATGCGTGTGTTAACTATCCTGCACATCATCTTGCGCAGTTAGTCCAATAAAAAAGGA TTACTACTGAACAGGTCTTACTATTTTTGATTGCGTAGTGCTGGGGAAAAGTAAACACAC ACAGGCGCACACGAGAACAGATGAGTTCTTTGGACGAGGATGAAGAGGACTTCGAAATGC TGGACACGGAGAACCTCCAGTTTATGGGGAAGAAGATGTTTGGCAAACAGGCCGGCGAAG ACGAGAGTGATGTTTTGCTATAGGGGGTAGCACCCCGACCAATAAACTGAAATTTTATC CATATTCGAACAAATTGACAAGAAGTACGGGGACCTTGAACCTGTCATTAAGTAATA CAGCTTTGTCAGAGGCTAACTCCAAATTTCTTGGGAAAATTGAAGAAGAGGAAGAAGAGG AGGAAGAAGGCAAGGATGAGGAAAGCGTGGATTCTCGTATTAAAAGGTGGTCTCCGTTCC ATGAAAATGAAAGTGTTACTACTCCTATTACAAAAAGATCTGCGGAAAAAACGAACAGTC CTATTTCTCTCAAACAATGGAACCAGCGATGGTTTCCGAAAAATGATGCTCGCACTGAAA ATACATCCTCATCCTCATATAGCGTCGCTAAACCTAACCAATCAGCCTTTACGTCTT CGGGCCTCGTATCTAAAATGTCTATGGACACTTCGTTATACCCTGCGAAATTGAGGATAC CAGAAACACCAGTGAAAAAATCACCCTTAGTGGAGGGAAGAGACCATAAGCATGTCCACC TTTCGAGTTCGAAAAATGCATCGTCTTCTCTAAGTGTTTCCCCTTTAAATTTTGTTGAAG ACAATAATTTACAAGAAGACCTTTTATTTTCAGATTCTCCGTCTTCGAAAGCTTTACCTT CCATCCATGTACCAACCATAGACTCATCCCCACTGAGCGAGGCAAAATATCATGCACATG ATCGTCACAATAACCAGACAAACATCCTGTCTCCCACTAATAGCTTGGTTACCAACAGCT CTCCACAAACATTGCATTCTAACAAGTTCAAAAAAATCAAAAGAGCAAGGAATTCGGTTA TTTTGAAAAATAGAGAGCTAACAAACAGTTTACAACAATTCAAAGATGATTTATACGGCA CTCAACCTTATCAATTTCGTGGACGCTATGACAATGACACTGACGAAGAGATCTCCACTC CAACAAGACGAAAATCTATTATTGGGGCAACATCTCAAACACATAGAGAAAGCAGACCAT TGTCACTCTCCTCTGCCATCGTGACAAACACAACAAGTGCAGAGACGCATTCCATATCTT CCACCGATTCTTCGCCGTTAAATTCCAAAAGGCGTCTAATCTCTTCAAATAAGTTATCAG CAAATCCAGATTCCCATCTTTTCGAAAAATTTACGAATGTGCATTCCATTGGTAAAGGCC CCATTAAACCAAACAAATATAATTCCTTGAAACGCATATTACTGGAAATTAAAATACTAA TCAGTTCCTGGAAGTTTCAAAATTCATACTATATTATGACAGAATTGTGCGAAAATGGTA ATTTGGATGGATTTTTACAAGAGCAAGTTATCGCAAAGAAAAAAGGTTGGAAGATTGGA GAATTTGGAAAATCATCGTGGAATTAAGCCTGGCTTTACGATTCATCCATGATTCTTGTC ACATTGTGCATCTGGACTTGAAACCCGCAAACGTCATGATCACATTTGAAGGTAACCTAA **AACTAGGTGACTTTGGAATGGCTACTCATTTACCGTTGGAGGATAAAAGTTTTGAAAATG** CAGATATTTTTTCCCTGGGTCTGATGATTGTTGAAATTGCAGCGAACGTTGTGTTACCTG ACAATGGCAACGCATGGCATAAGTTGAGATCGGGTGATTTATCGGATGCAGGAAGATTAA GTTCCACAGATATTCATTCTGAATCATTATTTTCAGACATTACGAAAGTAGATACAAATG ATTTATTTGATTTTGAAAGAGACAATATCAGTGGTAATAGTAACAACGCTGGCACCTCCA CTGTTCATAACAATAGTAATATCAACAACCCTAATATGAATAATGGCAACGATAATAATA ATGTCAATACTGCCGCTACCAAGAATCGTCTTATTTTGCATAAAAGTTCTAAAATTCCCG TAGAGCCCAATTATGAGAGAAGGCCCACGGCAAATCAAATCTTACAAACTGAGGAATGCC TGTATGTAGAAATGACACGCAATGCAGGTGCTATTATCCAGGAAGACGACTTTGGACCTA AGCCAAAATTTTTTATATGA

YJL187C, 819 aa (SEQ ID NO 158)
MSSLDEDEEDFEMLDTENLQFMGKKMFGKQAGEDESDDFAIGGSTPTNKLKFYPYSNNKL
TRSTGTLNLSLSNTALSEANSKFLGKIEEEEEEEEEGKDEESVDSRIKRWSPFHENESVT
TPITKRSAEKTNSPISLKQWNQRWFPKNDARTENTSSSSSYSVAKPNQSAFTSSGLVSKM
SMDTSLYPAKLRIPETPVKKSPLVEGRDHKHVHLSSSKNASSSLSVSPLNFVEDNNLQED
LLFSDSPSSKALPSIHVPTIDSSPLSEAKYHAHDRHNNQTNILSPTNSLVTNSSPQTLHS
NKFKKIKRARNSVILKNRELTNSLQQFKDDLYGTDENFPPPIIISSHHSTRKNPQPYQFR
GRYDNDTDEEISTPTRRKSIIGATSQTHRESRPLSLSSAIVTNTTSAETHSISSTDSSPL
NSKRRLISSNKLSANPDSHLFEKFTNVHSIGKGQFSTVYQVTFAQTNKKYAIKAIKPNKY
NSLKRILLEIKILNEVTNQITMDQEGKEYIIDYISSWKFQNSYYIMTELCENGNLDGFLQ
EQVIAKKKRLEDWRIWKIIVELSLALRFIHDSCHIVHLDLKPANVMITFEGNLKLGDFGM
ATHLPLEDKSFENEGDREYIAPEIISDCTYDYKADIFSLGLMIVEIAANVVLPDNGNAWH
KLRSGDLSDAGRLSSTDIHSESLFSDITKVDTNDLFDFERDNISGNSNNAGTSTVHNNSN
INNPNMNNGNDNNNVNTAATKNRLILHKSSKIPAWVPKFLIDGESLERIVRWMIEPNYER
RPTANQILQTEECLYVEMTRNAGAIIQEDDFGPKPKFFI

YJL188C, 102 aa (SEQ ID NO 160) MTKSLKHKYVLRLDVHLGSSPVSSLSVVTDSVVGSQSDPLWQWSVLLLSLSHFLLDSERL LSLIKRETYRAHTKCTIVKNVSNNVQTHQYDAFTDPRQYHLT

YJL189W, 1042 bp, exon1: 501-506, intron1: 507-892, exon2: 893-1042 (SEQ ID NO 161)
TATTCAAGAATTATTTCACATCTTCCAGCGAGTAAACATGCCGCTGGTAATCGCGCGTCC
TCAATATTTGAGTTTTTCAAATAGTGAGGTGTGGATGTATAGAGGAATTACACACTTTTA

TTGATTTTCAAAAAACTTATGGGCGTTTTAGGCTCCGGCTCAAACTACCACCACCACGCG GCAGGCCGAGGCAAACAGTACGCCTTGGCGGGGACGCCGAAGCGACTCCTTCTGTTCCAA ATACTTTCTACAATTTTTGGTACATTCATATTATACTGAAAAATTCGAAAAAGACAAGCAA ATAAACACAGATAGATCAACATGGCTGTATGTTAGAAAGATATTATAAATCCCAGTTAGA AATTTGGATTTGAAATAGAAGCAATGTGTAAAATATAGGGAAAGGATTAGGAGTGTTAAC CATACTAAAATTTTTCTTATCCGAAACAGAAATCTAAAGTCGCCACTACGCAGATTAAAA TATGGTCATAAACTGCTTATTCTGAGAACTTTTGGTGGTCCAGCGTGGTTTATGTCAGGT GGTATTGCCTTGGATCCGTGAATGCATCATATTGATGAGTTTGAACATTGTTACTAACAT TTTTTACAATTGTACACTTCGTATGTGCACGATATGTTTCCCTTTTAATTAGGCTCAAAA GTCTTTCAGAATCAAGCAAAAAATGGCTAAGGCTAAGAAGCAAAACAGACCATTGCCACA ATGGATCAGATTGAGAACCAACAACACTATCCGTTACAACGCTAAGAGAAGAAACTGGAG AAGAACCAAGATGAACATCTAA

YJL189W, 51 aa (SEQ ID NO 162) MAAQKSFRIKQKMAKAKKQNRPLPQWIRLRTNNTIRYNAKRRNWRRTKMNI

YJL190C, 893 bp, CDS: 501-893 (SEQ ID NO 163) TCTCGACAGCCCAAAAGCCGAATTGCGTTAGTTAGCCCACGCGCGAGCGTAAACGCAAGG ACCATTGAGCTTGGAACAGAAGGAGTCGCTTCGGCGTCCCCGCCAAGGCGTACTGTTTGC CTCGGCCTGCCGCGTGGTGGTAGTTTGAGCCGGAGCCTAAAACGCCCATAAGTTTTT TGAAAATCAAGCTAAAAAATGAAAAAAAAAAAAGTTAAATTGGTACTGTGCGCCCATAC ATCACATACTTAAAAGTGTGTAATTCCTCTATACATCCACCCTCACTATTTGAAAAACT CAAATATTGAGGACGCGCATTACCAGCGGCATGTTTACTCGCTGGAAGATGTGAAATAA TTCTTGAATATGGGTTTGCAGTTAGTCAATTTCAATCTAAATAATCTTAATCGACTATTC AATTCTTAAATTGTAAGGTTTTTTAATGGCCTTTCAGTTCTAGTATTTTTTTATAAAACAA GACCAACATACATATCCAAGATGACCAGATCTTCCGTTTTAGCTGATGCTTTGAATGCCA TTAACAACGCTGAAAAGACCGGTAAGCGTCAAGTTTTAATCAGACCATCCTCCAAGGTCA TTATCAAGTTTTTGCAAGTTATGCAAAAGCACGGTTACATTGGTGAATTTGAATACATCG ATGACCACAGATCTGGTAAGATTGTTGTTCAATTGAACGGTAGATTGAACAAGTGTGGTG TTATTTCCCCAAGATTCAACGTTAAGATTGGTGACATTGAAAAATGGACTGCCAACTTGT TGCCAGCCAGACAATTCGGTTACGTCATCTTGACCACCTCTGCTGGTATCATGGACCATG AAGAAGCCAGAAGAAAGCACGTTTCTGGTAAGATTTTGGGTTTCGTTTACTAA

YJL190C, 130 aa (SEQ ID NO 164) MTRSSVLADALNAINNAEKTGKRQVLIRPSSKVIIKFLQVMQKHGYIGEFEYIDDHRSGK IVVQLNGRLNKCGVISPRFNVKIGDIEKWTANLLPARQFGYVILTTSAGIMDHEEARRKH VSGKILGFVY

YJL197W, 4265 bp, CDS: 501-4265 (SEQ ID NO 165) ATTTAAGTGTCATGACTTTCTTAACGAGAGGTGTTCCAGCTTCTATTTTGGCTTTCCTAT GTGTCATTACTCTAGGTTATGGTATCATGGCATCTGTTGTCAAGGGTAACGCAACCTCTG TAATCCAACACTTCTGTTGTGTAGTCTAATGTTCGAAAAAAAGGTACGCTTCCCTGTTAT AATCAGGTATATTTCGTTATTATAAGCTAAAAGATTAAAAATTTTTCCACTTTCCTT GAAATTTGGTCGGTTCGTGGAAAAATATTATTACGTATTGAAGAAGTGCATGAAGATAAA AGATGGGATTACTGGAAAAATAAAGGGAGGAAAATCCTGCAGAACGTTGTTGTTTCAATC GAAGGTTTCTTCATTCGAAAATGGGTTCTTCAGATGTTTCAAGTCGTGAATGTTCATTGG TTTATAATGAAGATCCCGATTTCACCGATGGCACAACACCATGTGATCGGTTGGGAGTGG ACTTGATGAATGTTCTAGATGACAAGGATGAAATAAAGCAAGAGTCTGTCCCAGTCTCAG ATCGTGAAATTGAGGATACGGAATCCGATGCTTCCGCTGTTTCTTCATTTGCTAGCGCTA ATGAGTTAATAGCTGAGCCACACGCTGCAAGTGAAACTAATCTTGGAACTAATGGTCAAG ATGGAAGAAATGTCTTAGAACAACAAGAGACGTGGTTGCTAGACTAATAGAAGAAAACA AGGAAACGCAAAAAGAGGGTGATAAAGTCTGTATTGTCCCCAAGGTTTGGTACGATAAAT TTTTCGACCCCGATGTTACCGATCCTGAAGATATAGGCCCTATTAATACACGCATGATTT GCAGAGACTTTGAAAATTTTGTGCTTGAGGATTACAATAGATGTCCGTATCTGTCTATTG

CAGAGCCTGTTTTCAATTTTCTATCAGAAATTTACGGCATGACAAGTGGCTCTTACCCAG TGGTAACTAATTTGGTTATCAACCAAACCACAGGGGAGTTAGAGACAGAATACAATAAAT GGTTTTTCAGACTACATTACCTGACCGAAAAACAAGACGGGAGGAAAAGGAGGCATGGCC AGGACGATTCAATAATGTACCTCTCGATGTCTGCGTTGAATTTAGTACGTGATTTGGTTG AAAAGAGTATGAATCTGTTTTTTGAGAAAGCTGATCATCTAGACGTGAATGCGGTGGATT TTAAAATTTGGTTTGTGTCAGAGGGATCTGATATTGCCACAGATAGCAATGTTAGTACTT TTTTGAATTCTTCATATGÁAATAACTCCGCTTCAATTTCTCGAACTACCGATAAAGAAAC TACTAATACCAGACATGTTTGAAAACCGTTTAGACAAGATAACTTCAAATCCGAGTGACC TTGTCATAGAAATTAAACCTATAGAAGGGAATCACCATTGGCCTTCAAACTATTTTGCTT ATAATAAACTCGAACCAGCATCAGGTACTACTGGTTTGGTCAATTTGGGAAATACATGTT ACATGAATTCTGCGTTGCAATGCCTGGTACACATTCCGCAGTTGCGTGATTATTTCCTTT ATGATGGTTATGAAGACGAAATCAATGAAGAAAATCCTCTTGGGTACCACGGCTATGTGG CTAGGGCATTTAGTGACTTGGTTCAGAAGTTGTTTCAAAACAGGATGAGCATAATGCAAA GAAATGCTGCTTTCCCCCCTTCAATGTTCAAATCCACTATCGGGCACTTTAATTCGATGT TTTCTGGTTATATGCAACAGGATTCTCAAGAATTTTTAGCCTTCCTGTTAGACAGTTTAC ATGAAGATTTGAACAGGATAATAAAGAAAGAATACACAGAAAAACCATCATTATCTCCTG GTGATGACGTGAATGATTGGAATGTCAAGAAACTGGCAGACGATACTTGGGAGATGC ATTTAAAGAGAAATTGTTCCGTTATAACGGATTTATTTGTCGGGATGTACAAATCAACGC TATATTGTCCCGAATGTCAAAATGTTTCTATAACGTTTGACCCGTATAATGATGTTACAT TGCCGCTTCCGGTTGATACAGTGTGGGATAAAACTATAAAAATTTTTCCCATGAACTCTC CACCACTTCTTCTTGAAGTTGAGTTAAGCAAATCGTCCACTTATATGGACTTGAAGAATT ATGTTGGTAAAATGTCGGGCCTAGATCCAAATACACTATTTGGCTGTGAGATTTTCAGTA ATCAAATCTATGTTAACTATGAGTCAACAGAGTCGAATGCTCAATTTTTAACCTTGCAGG AATTGATCAAACCTGCTGATGACGTTATTTTTTATGAATTACCAGTAACAAATGACAATG AAGTAATTGTTCCCGTATTGAATACTAGAATTGAAAAAGGCTACAAAAATGCAATGTTAT TTGGAGTCCCTTTCTTTATTACGTTAAAAGAAGATGAATTGAATAATCCAGGTGCAATAA GAATGAAATTGCAAAACAGGTTTGTCCATTTAAGTGGTGGGTATATCCCATTTCCTGAAC CTGTAGGAAATCGAACCGATTTTGCTGATGCTTTTCCATTATTAGTAGAAAAATATCCAG AGGATAAATCCTTTTTTTCCATCAAGATTCTGTCTGTAGAAAAAGAGCAGCAATTTGCTA GTAATAACCGAACAGGGCCTAATTTCTGGACCCCTATCTCCCAGTTAAACCTTGACAAAG CTACAGATATAGACGATAAACTTGAAGATGTGGTGAAGGATATCTACAATTATTCATCCT TAGTAGATTGTGCTGAAGGGGTCCTTATGCAAGTGGATGATGAGGGAGATACCGAGGGTA GTGAAGCAAAGAATTTTTCCAAGCCCTTCCAATCGGGAGATGATGAAGAAAATAAAGAAA CTGTAACAAATAATGAAAATGTAAATAATACTAATGATCGGGATGAAGATATGGAACTAA CAGATGATGTTGAAGAAGATGCAAGTACAGAGCCAGAATTAACAGATAAGCCAGAGGCGT TTATTGTTGTGAGTGGAGCGAATTGGGTTCAAATGAGGCATTTTCCGATGATAAAATAT ATAACTGGGAAAATCCAGCTACTTTGCCTAACAAAGAGTTGGAGAACGCTAAGTTGGAAA GATCTAACGCTAAGGAAAGAACCATAACCTTGGACGATTGTCTCCAAATTATTTTCCAAAC CAGAAATACTAGGATTAACCGATTCGTGGTACTGCCCTACATGCAAGGAACATCGTCAGG CTACCAAACAAATACAACTTTGGAATACACCAGATATTCTGCTAATTCACCTTAAAAGGT TTGAAAGTCAAAGGTCTTTTAGCGATAAAATTGATGCCACGGTTAATTTCCCCATTACAG ATTTGGATCTGTCGAGGTACGTTGTCTATAAAGATGATCCCAGAGGTTTAATCTATGACC AGAATTTTGCCGACAATAAATGGTACTATTTTGATGATTCTCGAGTAACTGAAACTGCGC CAGAAAATAGTATAGCTGGATCGGCTTATTTGCTATTTTACATTCGCCGTCATAAAGATG GCAATGGATTAGGCAGCTCTAAACTACAGGAAATAATCCAAAAGTCACGCCACGGATATG ATGAGCGTATCAAAAAGATATACGATGAACAGATGAAGTTGTATGAATTTAATAAGACTG ACGAGGAGGAAGATGTTTCTGATGATATGATAGAATGTAATGAAGATGTGCAGGCCCCTG AATATAGTAATCGTAGTTTGGAGGTTGGGCATATTGAAACTCAGGACTGCAACGACGAAG ATGACAATGATGATGGTGAGAGGACAAATTCAGGTAGGAGAAAGTTAAGATTGTTGAAAA AAGTCTACAAGAATAATTCAGGCTTGGGTTCATCGAGTACGTCTGAAATATCTGAGGGAT GCCCAGAAAACGAAGTCGCTGATTTGAATTTAAAAAAATGGTGTGACACTAGAATCGCCAG AATAA

YJL197W, 1254 aa (SEQ ID NO 166) MGSSDVSSRECSLVYNEDPDFTDGTTPCDRLGVDLMNVLDDKDEIKQESVPVSDREIEDT ESDASAVSSFASANELIAEPHAASETNLGTNGQDGRNVLEQQRDVVARLIEENKETQKEG DKVCIVPKVWYDKFFDPDVTDPEDIGPINTRMICRDFENFVLEDYNRCPYLSIAEPVFNF

LSEIYGMTSGSYPVVTNLVINQTTGELETEYNKWFFRLHYLTEKQDGRKRRHGQDDSIMY LSMSALNLVRDLVEKSMNLFFEKADHLDVNAVDFKIWFVSEGSDIATDSNVSTFLNSSYE ITPLQFLELPIKKLLIPDMFENRLDKITSNPSDLVIEIKPIEGNHHWPSNYFAYNKLEPA SGTTGLVNLGNTCYMNSALQCLVHIPQLRDYFLYDGYEDEINEENPLGYHGYVARAFSDL VQKLFQNRMSIMQRNAAFPPSMFKSTIGHFNSMFSGYMQQDSQEFLAFLLDSLHEDLNRI IKKEYTEKPSLSPGDDVNDWNVVKKLADDTWEMHLKRNCSVITDLFVGMYKSTLYCPECQ NVSITFDPYNDVTLPLPVDTVWDKTIKIFPMNSPPLLLEVELSKSSTYMDLKNYVGKMSG LDPNTLFGCEIFSNQIYVNYESTESNAQFLTLQELIKPADDVIFYELPVTNDNEVIVPVL NTRIEKGYKNAMLFGVPFFITLKEDELNNPGAIRMKLQNRFVHLSGGYIPFPEPVGNRTD FADAFPLLVEKYPDVEFEQYKDILQYTSIKVTDKDKSFFSIKILSVEKEQQFASNNRTGP NFWTPISQLNLDKATDIDDKLEDVVKDIYNYSSLVDCAEGVLMQVDDEGDTEGSEAKNFS KPFQSGDDEENKETVTNNENVNNTNDRDEDMELTDDVEEDASTEPELTDKPEALDKIKDS LTSTPFAILSMNDIIVCEWSELGSNEAFSDDKIYNWENPATLPNKELENAKLERSNAKER TITLDDCLQLFSKPEILGLTDSWYCPTCKEHRQATKQIQLWNTPDILLIHLKRFESQRSF SDKIDATVNFPITDLDLSRYVVYKDDPRGLIYDLYAVDNHYGGLGGGHYTAYVKNFADNK WYYFDDSRVTETAPENSIAGSAYLLFYIRRHKDGNGLGSSKLQEIIQKSRHGYDERIKKI YDEQMKLYEFNKTDEEEDVSDDMIECNEDVOAPEYSNRSLEVGHIETODCNDEDDNDDGE RTNSGRRKLRLLKKVYKNNSGLGSSSTSEISEGCPENEVADLNLKNGVTLESPE

YJL198W, 3149 bp, CDS: 501-3149 (SEQ ID NO 167) TGTCGTATTTCCACTGATTTGGATGTATGTTGCATGGTGCTAGATTGTGAATAAATCATT TCCACTGGTTTCTAGCAGAGGTAAGAAAATCAGTAGTAGCGGCAGCAGCCAAGAAAAATG GCAGCCTGGCAAGCAGCGAAGGCCATCTGTGCTGCATTTCCACACTCCTTGTATGACTGC ATACGCATAAAGAGGTGCCTTGCTGTAGGCGTATATGATCCTAAGCAACAGAGAAACCAC GGTTCTCTTCTTATTTCGTTATTGTCTTCCCTTTTTACTATGGGTAAAGTCGCCC TTTGCGCTGCTTCTCGAAGAATGAATGGCTCACTGAAAAATTTTGATTCATCGATATAAA GAACACTGTTCACTTCGATGTCATCCGGCCAATAAAGTTGTTTTTAGGATAAACGAGTAA GTGGTAGCTGGTACAGGATCATGAGATTTTCACACTTCTTGAAGTACAATGCTGTCCCAG AATGGCAAAACCATTATATGGACTACAGCGAGCTGAAAAATCTTATTTACACGCTACAAA CAGATGAACTTCAGGTTGGTGATAACGAAGAAGGATTTGGCGCAGGAAAGAGCTCTAACA GTATGAACAAGATGCAGGCATCGTTGAGGAAACCATCGAGTTGCGAGAGTTGCCTACTG CTCAGACGGTCGCCAAACCTTCTCCTTTCAGAAGAATGAAGGAAAAGATATTTTACA AAAGAAGGTCGTCTTCCGCATCGTCTCCTCCACGGCCAACGAAAATCTGCAATTAG ACACTTATGATACGTTTGTTGGTGATTTAACAGCTGAAAAACAGAAAGTAGATGATTTTT ATAAGAGGACAGAAGTTCTACGACAAATTTGACGCGCTGGTGAAGGACCTGAAGA AAATCGGAGTTATAGAATACGATATCGACGATGATACTCTGTTTAACGAACCGATTGCCA GCACAAATGACGAAGTTCCCCCACTAGACTTGGATGATGACGAAGACGACGACGAATTTT ACGATGATCAATCTAATATTGAAGATAATACTGCTTTGCTGCATCATTCGCAGTATAACA TTAAGTCTCAGAAAAAATCGCTGTTGAAGAAGTCGATCGTAAACCTATATATCGATCTTT GCCAGTTGAAGTCGTTCATCGAATTGAACCGCATTGGGTTTGCAAAAATTACAAAGAAAT CAGACAAAGTTCTTCACTTGAATACAAGAACCGAACTGATCGAATCGGAGCAGTTTTTCA AAGACACATATGCATTCCAGGCAGAAACGATCGAATTGCTAAATTTCCAAAATTTCCCAGC AGTTGAAATCCTACCTGCATGACCACATTGTTTGGGAAAGAAGTAACACTTGGAAAGACA TGTTGGGACTGCTATCGCAAGCTGACGAGTTGACACCAAAGGAAACAGAATATAATGCAA ATAAGCTGGTAGGCAAGTTAGATTTGGAATACTACAGATGGCCACTACCCAGACCGATAA ACTTAAAATTCACTAGTATAAACAACGTTGCACTACCGAAATTATTTTTCACCAAGAAAG CATACAAGATTTACTTTATTATTCTAGTCACTGGACTCTTGTTAGGAATAAAGACCTTCA ACGACGCTGCTCAGCACCGCTGCATGGCCCTTGTCGAGTGTGTCGCCTTTTTTGTGGGCTA GTGAGGCCATCCCATTACACATTACAGCATTCCTTGTACCACTACTTGTAGTCCTTTTCA AAGTCCTAAAAACCTCCGACGGGGCTATAATGAGTGCTGCAAGCGCTTCATCAGAAATTT TGGCCGCCATGTGGTCTTCTACAATTATGATTCTGCTGGCAGGTTTTACTTTGGGTGAAG TACTTGCACAATATAACATCGCCAAAGTTCTTGCCTCGTGGTTGTTGGCCTTCGCTGGTT TTTCCAATGTCGCAGCACCTGTTCTAACATATTCGTTGTTATCTCCCCTATTGGATGCCA TGGATGCAGATAGCCCATTTGCGCAAGCATTGGTGTTAGGTGTAGCGTTGGCTGCAAATA TCGGTGGTATGTCTTCACCAATCTCTTCACCTCAAAACATCATTTCCATGTCGTACTTGA AACCCTATGGTATTGGCTGGGGCCAATTCTTTGCTGTTGCATTGCCATCTGGTATCCTGG

YJL198W, 881 aa (SEO ID NO 168) MRFSHFLKYNAVPEWONHYMDYSELKNLIYTLOTDELOVGDNEEGFGAGKSSNITDRFKN KFSFKNAKEDTSSGMNKDAGIVEETIELRELPTAOTVAAKPSPFRRMKEKIFYKRRSSSA SSVSSTANENLQLDTYDTFVGDLTAEKOKVDDFYKRTEAKFYDKFDALVKDLKKIGVIEY DIDDDTLFNEPIASTNDEVPPLDLDDDEDDDEFYDDQSNIEDNTALLHHSQYNIKSQKKS LLKKSIVNLYIDLCQLKSFIELNRIGFAKITKKSDKVLHLNTRTELIESEOFFKDTYAFO AETIELLNSKISQLVTFYARITDRPHNISHSKQELKSYLHDHIVWERSNTWKDMLGLLSQ ADELTPKETEYNANKLVGKLDLEYYRWPLPRPINLKFTSINNVALPKLFFTKKAYKIYFI ILVTGLLLGIKTFNDAAQHRCMALVECVAFLWASEAIPLHITAFLVPLLVVLFKVLKTSD GAIMSAASASSEILAAMWSSTIMILLAGFTLGEVLAQYNIAKVLASWLLAFAGCKPRNVL LMAMCVVFFLSMWISNVAAPVLTYSLLSPLLDAMDADSPFAQALVLGVALAANIGGMSSP ISSPQNIISMSYLKPYGIGWGQFFAVALPSGILAMLLVWILLFTTFKMNKTKLEKFKPIK TKFTVKQYYIITVTVATILLWCVESQIEGAFGSSGQIAIIPIVLFFGTGLLSTQDLNAFP WSIVILAMGGIALGKAVSSSGLLSTIAKALQKKIENDGVFAILCIFGILMLVVGTFVSHT VSAIIIIPLVQEVGDKLGNPKAAPILVFGCALLSSCGMGLASSGFPNVTAISKVDRKGDR YLSVMTFLTRGVPASILAFLCVITLGYGIMASVVKGNATSA

YJR049C, 2093 bp, CDS: 501-2093 (SEQ ID NO 169) ACTGCCATCTCCATTCTTTGAAAAGATTATTAAGTTCGTCGTTAAGTTCCGCAATCT GCATTTCATTTAAAGACGGATCATATATTCTTGTGCTTTTTTTGTTTTATCTCTTTACTTA CTTGTCGCTTCCATTCGTTGGCCTCTTTTATGGATTTTACCTTAGACACGTTCCTGGGCC GTACCAGAACTGAGTTGGCCTTATCTACATTTCTACTCATTTTGAATGCACAGGTATCTG ATTACTGATGTGGTGCGCCTTGCGATATAACGGTGTGTCACTTTTATTTGCTCTTTCATG CATCCTGAAATTATTTCACCGCACTACGCAAAGAGAACGGAGAAAAAGGTATAATAGGGC GTAGAGTAAAAGCTCTTGAGATGAAGGAGAATGACATGAATAATGGCGTAGATAAATGGC TAAATGAGGAAGATGGTCGAAATGATCATCATAACAACAATAATAACTTGATGAAGAAGG CCATGATGAACAATGAGCAAATTGATAGAACTCAGGATATCGACAACGCCAAAGAAATGT TGAGGAAAATATCAAGTGAAAGCAGCTCGCGCAGAAGCTCCCTGTTGAATAAAGATTCAT CTCTCGTGAACGGCAATGCAAACAGTGGCGGTGGTACGAGCATTAACGGAACAAGAGGAA GTTCTAAGAGTAGTAATACACACTTTCAGTATGCCTCCACGGCGTATGGTGTAAGAATGT TGAGTAAAGATATATCTAATACCAAAGTGGAACTGGATGTGGAAAATTTGATGATTGTTA CGAAACTCAACGATGTCTCACTGTATTTCTTAACAAGAGAGTTGGTAGAATGGGTTTTGG TACATTTTCCACGTGTGACTGTTTATGTGGATTCCGAATTGAAAAACAGCAAAAAATTTG CCGCTGGCGAGTTATGTGAAGATAGTAAATGTAGAGAATCAAGGATCAAGTATTGGACAA AGGATTTCATCAGGGAACATGATGTTTTCTTCGATTTGGTAGTGACTTTGGGTGGCGACG GTACTGTTCTTTTGTAAGTTCCATTTTTCAGAGACATGTACCACCCGTTATGTCGTTTT CATTAGGGTCTCTAGGATTTTTAACAAATTTTAAGTTTTGAACATTTCAGGGAGGATTTAC CTCGGATTATGAATCATAAAATCAAGACAAATTTACGGTTGAGGTTGGAGTGCACAATTT ATCGTAGACACCGCCCTGAAGTAGACCCCAAACACGGGGAAGAAATATGTGTGGTGGAAA TGATTGCTGCTACTCCGACTGGGTCCACGGCCTATTCTTTGAGTGCAGGTGGGTCATTGG TATGCCCAACCGTCAATGCAATCGCTTTAACACCCATTTGTCCACATGCATTGAGTTTCA GACCCATCATCTTACCAGAAAGTATAAATTTAAAAGTGAAAGTCTCGATGAAGTCAAGGG

YJR049C, 530 aa (SEQ ID NO 170)
MKENDMNGVDKWVNEEDGRNDHHNNNNNLMKKAMMNNEQIDRTQDIDNAKEMLRKISSE
SSSRRSSLLNKDSSLVNGNANSGGGTSINGTRGSSKSSNTHFQYASTAYGVRMLSKDISN
TKVELDVENLMIVTKLNDVSLYFLTRELVEWVLVHFPRVTVYVDSELKNSKKFAAGELCE
DSKCRESRIKYWTKDFIREHDVFFDLVVTLGGDGTVLFVSSIFQRHVPPVMSFSLGSLGF
LTNFKFEHFREDLPRIMNHKIKTNLRLECTIYRRHRPEVDPNTGKKICVVEKLSTHHI
LNEVTIDRGPSPFLSMLELYGDGSLMTVAQADGLIAATPTGSTAYSLSAGGSLVCPTVNA
IALTPICPHALSFRPIILPESINLKVKVSMKSRAPAWAAFDGKDRIELQKGDFITICASP
YAFPTVEASPDEFINSISRQLNWNVREQQKSFTHILSQKNQEKYAHEANKVRNQAEPLEV
IRDKYSLEADATKENNNGSDDESDDESVNCEACKLKPSSVPKPSQARFSV

YKR094C, exon1: 501-508, intron1: 509-876, exon2: 1255 bp, 877-1255 (SEQ ID NO 171) AGGTTGTGTTCTTCAATGATGGGCAATGCAATTTGGCGTTAAGCGCCTGAGCAATAAGGT AACAGCGAAATTTATGACATATTATTTCGAACCTTTTACAAACTAGTAGATTTAGTGATT TATTACCTATTGGCATTCATTTGTGTTCTATATGTGGATGAGGATAGCCGCCTTTCTTCT CATCGGAGGCCATATCATCTTTCGACAATCCTTTTTAAATACTATTTCCATCCGTGCCTC TTTTCATGTTTTTCAGATTCTGAAGTACCGCAATAGGATATGGCGGATAATCCGCCATAT GATCCGCCTCATACTAGCCATTACCCATCTATCCCAGGCATTATGGGTATGCAACTCATA ATCTCAAATACACAAATAAGAGCAACCTTATATATCACTTTTTCCCGTTCAGCAAGAGGT AAAGCCACCAAAGGTTCAAAATGCAAATGTATGTTACGGCGAATACAGAATACTATGTTC GAAATAATATGAGGATTATACGATAGCAAAAAAGCCATAAACGAAAGACATAAATGGAAA ATGATTGACAAGCTCACAATTTATTAAACAAGTAGCAATTGAGAAAAACTATTACTCGCG GCAAGCTTCTGAGTTTACATTAAATCTGTAGAGCAAATTGAAAATGTCGCATATGTGCTG AAGGGTTTGTTTGTTCCATCTTATTTTGCATAACATAGTTATATTTACTTGGTCGCATAA TTACTCCATAAATGAACTTATTCCAATTTTGTACAGCTTCGTTAAGACTTTGACTGGTAA GACCATCACTTTGGAAGTTGAATCTTCTGACACCATTGACAATGTCAAGTCCAAGATCCA AGACAAGGAAGGTATCCCACCTGACCAACAAAGATTGATCTTTGCTGGTAAGCAATTGGA AGACGGTAGAACTCTATCTGACTACAACATCCAAAAGGAATCCACTTTACATTTGGTCTT GAGATTAAGAGGTGGTATCATTGAACCATCTTTGAAAGCCTTGGCTTCCAAATACAACTG TGACAAATCTGTTTGTCGTAAATGTTACGCCAGATTACCACCAAGAGCTACCAACTGTAG AAAGAGAAAGTGTGGTCACACCAACCAATTGCGTCCAAAGAAGAAGTTGAAATAA

YKR094C, 128 aa (SEQ ID NO 172) MQIFVKTLTGKTITLEVESSDTIDNVKSKIQDKEGIPPDQQRLIFAGKQLEDGRTLSDYN IQKESTLHLVLRLRGGIIEPSLKALASKYNCDKSVCRKCYARLPPRATNCRKRKCGHTNQ LRPKKKLK

YLR040C, 1175 bp, CDS: 501-1175 (SEQ ID NO 173)
AGCTCTCAAACAACTAATACTATAAGTTCAAGTACAAGCACAGGAGGTGTAGGTTCAGTC
AAGCCATGTCTTTACTTCGTTTTAATGTTAGAAACAATCGCTTATTTGTTTTCTTAAACA
AATATATTAGGTTCAAGGTCTTCGCAGGTGTAAGAAAACCCGTGGTCTCCATATTCTTAA
GTATGATAAATAAAAAAAAACTTAATAAATTATTAATTGCTTCAAACCTTTTTCTTTTT
TAGTTTTTAATATTTCAAACGTTATCTTCATTGAACGCCCAAATAGGGAAAAATCCTGGC
AAATTTTTATTGCTGTCATCCAAGGCTATGCTAGAAAATTCAAGAGCTTGGATGATTTA
AAAAGACACTCTCAATCGAGAAAGTTTATTCTTTGTTATTCTGCTTTACCTGATCATATT
CCGGCGTATTGTTTCTAATCAAGTGATTTCGATATCCAGTTACGAACCATTTACAACATT
CCTGAAAATATTGCGTATCAATGATATTTGCTCCTTCTTCTCCCTCATTAAAAATATTC
TCCTGGTAAGCTTTCTAATCAGCCACAGTTTTGCTGCCAAAACTTTAACGTCTAGTTCCA
ATGACGATACACTTGCCAGGTCCGCAGCTGCAGATGCAGACCATTCTTCATGGAGT

YLR040C, 224 aa (SEQ ID NO 174) MIFAPSFSLIKNILLVSFLISHSFAAKTLTSSSNDDTLARSAAADADMAFFMEFLNDFDT AFPQYTSYMMQNHLTLPQPVADYYYHMVDLASTADLQSDIAQSFPFTQFQTFITAFPWYT SLLNKASATTIYLPQHFITGETEATMTNSSYASQKNSVSNSVPFSTANAGQSMISMANEE NSTTALISASNSSSTSRTSQSQNGAHAKSLYFPMALFGIFAVAL

1618 bp, exon1: 501-590, intron1: 591-949, exon2: 950-1618 (SEQ ID NO 175) GCACCCTTTTTCTTTTCAATAACAAAAAAGAGCTTGGGCATTACGTTTTCAACACTTTT AATATTTCCCTTTTTACATCCGTACATATAAAATGTAAACCCATGCATTCATGACAATTT TACCTATTTCTTAAAGGCCTTTGTCACTTCTTTATGGGAATGGCGCTACTTTAATTTTCC GCCTACTTTGAAAAATTTACCAAGGCGAAATTGAGTGCGCTAGGCGGAAGTTCCAGGGCA GAGGAGCTGGAAAGATGGAATGGAAGGACTGCAACACTCAGTAAGAAGGTTCGTGGTAGG GAACATCACCTTCTCTAGTTCCTGTAAAAATAATATGATCAAGTTTGAATCCTCGTATTG AAAAATCGCGAGTTATTAAGTGTGTAATTTAGAATACCGAAATAGCACAAGAAGAGATAA GATAAGATACTGATAGGATAATGTCTTTACCAGCTACTTTTGATTTGACTCCAGAGGATG CCCAACTTTGTTGGCCGCTAACACCCATTTAGGTGCTAGAAACGTTCAAGTATGTACAC ATATCCCATACGATTATGTTCTATAGATGATAATAGGTCTCGAAAAGAATATGTCCCCGA TTTAATCATATTTGGAGGTCAGAGGACCAAAGGTAATTTCAGAGGAATTTTGAACACGCC GGGTTTAGAAGATTTCACTTCTTAGTGAGGGTAAGGAGAAACTCAATAAG AATATACATCCTCGACTGTCTCAAAGATTATGAACTCCGATGAAACAGTAAAACGTCAAA AAATTCCACGGGATATAATTCGGTACTTTATTGGATATGGAAGAAAACATTATATATGCA ACCATACGTTTTCAATGCTAGACCAGATGGTGTTCACGTTATCAATGTTGGTAAGACCTG GGAAAAGTTGGTTTTGGCTGCTAGAATTATTGCTGCCATTCCAAACCCAGAAGATGTTGT TGCCATCTCTTCCAGAACCTACGGTCAAAGAGCTGTCTTGAAATTTGCTGCTCACACTGG TGCTACTCCAATCGCCGGTAGATTCACTCCAGGTTCTTTCACTAATTACATCACCCGTTC TTTCAAGGAACCAAGATTGGTTATTGTTACCGACCCAAGATTAGACGCTCAGGCCATTAA GGAAGCTTCTTACGTTAACATTCCAGTCATTGCTTTGACTGATTTGGACTCCCCATCTGA ATTTGTTGATGTCGCCATCCCATGTAACAACAGAGGTAAGCACTCCATCGGTTTAATCTG GTACTTGTTGGCTAGAGAGTTTTGAGACTAAGAGGTGCTTTGGTCGACAGAACTCAACC ATGGTCCATCATGCCAGATTTGTACTTCTACAGAAACCCAGAAGAAGTTGAGCAAGTTGC TGAAGAAGCTGCTGCCGCTGAAGAAGGTGAAGAAGAAGAAGTTAAGGAAGAAGTCACTGA AGGTCAAGCTGAAGCTACTGAATGGGCTGAAGAAAATGCAGACAACGTTGAATGGTAA

YLR048W, 252 aa (SEQ ID NO 176)
MSLPATFDLTPEDAQLLLAANTHLGARNVQVHQEPYVFNARPDGVHVINVGKTWEKLVLA
ARIIAAIPNPEDVVAISSRTYGQRAVLKFAAHTGATPIAGRFTPGSFTNYITRSFKEPRL
VIVTDPRLDAQAIKEASYVNIPVIALTDLDSPSEFVDVAIPCNNRGKHSIGLIWYLLARE
VLRLRGALVDRTQPWSIMPDLYFYRNPEEVEQVAEEAAAAEEGEEEEVKEEVTEGQAEAT
EWAEENADNVEW

GGAGTTTGGCTTCCCTCTATTTGTATATTGATCGCCATCCCTACGAAGTTATTGGGAACG CGGCTACACTTAGAAAGAAATGACATTTGCTGTCTTATAAAAGGACTTGACAGACCAAAG ACGCGTATAATACACCAAGAATGGCCTTATTGGAGAAGTTGCATCGAAGGATTGTTGATA TGGGGCTTGTCCCGCGTATAATCGCCTTATTACCAGTTATTCCATGCTATGCGCTCTAT CTGAGAATGCATTGATGCCTTCACAAGCGTATAGTTACTTTAGAGAATCTGAATGGAACA TTTTGAGGGGCTATCGATCTCAAATTAAAGAAATGGTAAACATGACTTCTATGGAAAGAA ACAATTTGATGGGTTCTTGGTTACAAGAATTTGGTACTAAGACTGCTATTTACGAAAATG AACAATATGGAGAAACATTGTACGGTGTAATGCACGCTCCTAGGGGTGATGGAACAGAAG CGATGGTGCTTGCCGTTCCATGGTTTAATTCAGATGATGAATTCAATATTGGCGGCGCAG CTTTGGGTGTATCTTTAGCAAGATTTTTCTCACGTTGGCCAGTATGGTCCAAGAATATAA TTGTTGTCTTCAGCGAAAATCCTCGTGCAGCATTAAGATCATGGGTTGAGGCATACCATA CTTCCTTAGATTTGACTGGTGGTTCCATTGAAGCTGCTGTTGTGTTTGGATTATTCGAGTA CGGAAGATTTCTTCGAGTATGTAGAAATCTCATACGACGGTCTGAATGGTGAGCTGCCCA ATTTGGATCTTGTCAACATCGCTATATCCATTACGGAACATGAAGGTATGAAAGTTTCTT TGCACGGTCTACCCAGTGATCAGTTAACTAATAATAATTTCTGGTCAAGATTAAAAATAT TATGCCTGGGAATAAGGGATTGGGCGTTGTCCGGTGTTAAAAAGCCCCCATGGTAACGAGG CATTTAGCGGCTGGAGGATTCAATCTGTAACATTGAAAGCACATGGAAACAGTGGTCATG ATATTACTACATTTGGACGTATACCCGAAGCAATGTTTCGCTCTATTAATAACCTTTTGG AAAAATTTCACCAATCGTTCTTCTTTTATTTGTTATTAGCACCACGTCAGTTCGTATCCA TTAGTAGTTATTTGCCAAGCGCTGTGGCTTTATCTATAGCATTCGCCATAAGTTCATTAA ATGCATTTATAAACAATGCTTATGCAAATATATCCTTATTTTCCGAGTATAATTTGGTAG CGTTGTTGGTTTGGTGCATTGGTGATATCATTTGTTGTTTCACAAGCGTTTCTTC TAATACCTTCATCGGGATTATTGATGACAATTAGCATGGCATCTTGTTTTTTACCTTTGA TACTTTCCAGAAAAATTCACATCTCAGAACCACTATCATACAGGTTGAAAAATGTTGCTT TTTTATATTTCAGTTTGGTTTCAACATCTTTGCTAATGATAAACTTTGCAATGGCTTTAC TGATCGGCACATTGGCATTTCCTATGACATTTGTGAAGCCATTGTTGAAAGTTCTAGCG AACATGAGGTGACAACTCAATCCTCTAACCCAATAAAAACTGAGCCGAAAGATGAGATAG AGCTCGTCGAGAATCACATGGATACAACGCCAGCAACCCCCCAACAACAGAAACAAAAAC TGGATTTGAAATGTTGGAGTTGGTTTGTACTTTGTATAGGTTGGCTTCCATGTTGGCTAT GTTAG

YLR088W, 614 aa (SEQ ID NO 178)
MALLEKLHRRIVDMGLVPRIIALLPVISMLCALFGFISIAILPMDGQYRRTYISENALMP
SQAYSYFRESEWNILRGYRSQIKEMVNMTSMERNNLMGSWLQEFGTKTAIYENEQYGETL
YGVMHAPRGDGTEAMVLAVPWFNSDDEFNIGGAALGVSLARFFSRWPVWSKNIIVVFSEN
PRAALRSWVEAYHTSLDLTGGSIEAAVVLDYSSTEDFFEYVEISYDGLNGELPNLDLVNI
AISITEHEGMKVSLHGLPSDQLTNNNFWSRLKILCLGIRDWALSGVKKPHGNEAFSGWRI
QSVTLKAHGNSGHDITTFGRIPEAMFRSINNLLEKFHQSFFFYLLLAPRQFVSISSYLPS
AVALSIAFAISSLNAFINNAYANISLFSEYNLVALLVWFVSLVISFVVSQAFLLIPSSGL
LMTISMASCFLPLILSRKIHISEPLSYRLKNVAFLYFSLVSTSLLMINFAMALLIGTLAF
PMTFVKTIVESSSEHEVTTQSSNPIKTEPKDEIELVENHMDTTPATPQQQKQKLKNLVLL
ILTNPFISITLFGLFFDDEFHGFDIINKLVSAWLDLKCWSWFVLCIGWLPCWLLILASSF
ESKSVVVRSKEKQS

ATTTCTCTGATCTCTCATTTTCTGTTGTACAGCAGTGGGACAGTAGAGCCATTGAAAAAA CTACAATCATATCTTGTATGCGGCCCGCAAACCAAGAGATTTATCCTTTGAGACATTGTG AGACCCTCCGTTCGCAACCGTGCTCTCTGTTTTCATCACTATATGCACGCTCTTTTCCAAA GCTCCTGCACTTTGCACGCGGGGGCCATCGCCGGCTTCCATATGTACGGCTGCCACA CCTAA

YLR159W, 114 aa (SEQ ID NO 180) MKFQYALAKEQLGSNSRSGVKKLISKHHWLPEYYFSDLSFSVVQQWDSRAIEKTTIISCM RPANQEIYPLRHCETLRSQPCSLFSSLYARSFQSSCTLHVAEPSPGFHMYGCHT

YLR167W, 959 bp, CDS: 501-959 (SEQ ID NO 181) ATCAAAAGAGTGTTTCAAGTAAGTAAAAACATTTGAGCCTCCCCATTTGTTGAAAGGAGA GAAATTAAACTTGGTTGGGGTTAATTATTTGATGGGTATATTAATTTGCAACCGCAAGGT ATCGATAATAATATTCTACAAAACCTTTATCAATAGTGGTGAAGTCTTTAGTGCGATCT ACCTGGGGTTAATGAACGAGAAGTTCTTGAGATATCTTTCCTGTTTACCTCCGTGCATCC GGGCGCACTTTTTCAAGCGGTGGGAACTCATCAAAATGAAAAACTAGATACTTTTAGACT TATTAAATGGTTTAAATATTTTGAGATGTTCGTTATATCAGAAACTTCCTTACTTCTATC TTTTATTCCAATACAAAGAAGTCACAAGATTACTTGGTAAGAAGAAGCAGTTAATTTTT AATTTTGCCGACAAGCCAAGATGCAAATTTTCGTCAAGACTTTAACCGGTAAGACTATTA CCCTGGAAGTTGAATCTTCTGACACTATTGACAATGTCAAGTCCAAGATCCAAGACAAGG AAGGTATTCCACCTGACCAACAAGATTGATCTTTGCTGGTAAGCAATTGGAAGATGGTA GAACTTTGTCCGACTACAACATCCAAAAGGAATCTACTCTACACTTGGTCTTGAGATTGA GAGGTGGTGGTAAGAAGAAGAAGAAGAAGGTCTACACCACCCCAAAGAAGATCAAGCACA AGCACAAGAAGGTCAAGTTGGCTGTCTTGTCCTACTACAAGGTCGATGCTGAAGGTAAGG TTACCAAATTGAGAAGAGAATGTAGCAACCCAACTTGTGGTGGTGGTGTTTTCTTGGCTA ACCACAAGGACAGATTGTACTGTGGTAAGTGTCATTCCGTCTACAAGGTTAACGCTTAA

YLR167W, 152 aa (SEQ ID NO 182) MQIFVKTLTGKTITLEVESSDTIDNVKSKIQDKEGIPPDQQRLIFAGKQLEDGRTLSDYN IQKESTLHLVLRLRGGGKKRKKKVYTTPKKIKHKHKKVKLAVLSYYKVDAEGKVTKLRRE CSNPTCGAGVFLANHKDRLYCGKCHSVYKVNA

YLR232W, 848 bp, CDS: 501-848 (SEQ ID NO 183) AGCCACCAATTCCACCAGGCCCGGCATTCAAGTACTTGTAAGAACACCAACAGGCAAAGT CAACACCCCAATCATGAAGTTGCAATGGGACGTTCCCTACAGCGTGTGCTAAATCCCATC CAACCAATATGTCGGGGAATTGGTGGGCAAATGAGGTGATTCGGCCAATATCGAAATATT GCCCCGTGTAATACTGAACACCTGACAAACAGACCAGCGCCAATTCATCTTGATTTACCT CTATGGTATCCAGGATATCTTGAGTTCTGATATAAGTCTCTCCCTCGCGTGGCTCGATCT GAATAAAAACATTCTCAGGTTCCGAAATTCCATGAATTTTGCACTGGTTGTAGAAAGCAT AATAGTCTGATGGAAAGGAGCCCTTTTCAAAAAGGATCTTGAATCTTTTCTCAGTAGGTT TATAAAACGTAATTAACAATGAATTCAAATTTGCAGTGAGACTATTCATTACTGCAACTT CATTTTCTTGAGCACCCACGATGGGGGCTAGTAGTGGAAGAATAGGTAAGTCAATGCTGA CCCAAGGCACCTTTCCTCTGGCTTCTTCAGGATGTTTGAAATGCGATTCCACAGCACAAT CGCTCCACGCATCTAGCTCAGCATTAATTGAATTCCTAGTTGACTTCGGCATCAAACCTA AAGAATTCCCGCATAAGTACGTCACAGGCTTATCGTCGGACGATAGTCCCATGGATTTAA ATGTAGGGATGTTGAATTCATCCCTCAGAGATTCCGGATATTCTCCGTCTAATTCCAAAG CTTTCTCCATAATTACCAGTTTGTTTCTTTTTTCCACAGAATATTTAGGCTTAATATGTA **CGTATTGA**

YLR232W, 115 aa (SEQ ID NO 184) MGASSGRIGKSMLTQGTFPLASSGCLKCDSTAQSLHASSSALIEFLVDFGIKPKEFPHKY VTGLSSDDSPMDLNVGMLNSSLRDSGYSPSNSKAFSIITSLFLFSTEYLGLICTY

GTGATTTTCGCGTTCACGCCATTATCCAATGTCAAAAAGGATAATGGAAATGTTAACATG CCTGTATGATCCGACCGTTTTTAGCAAACTTATCAGGGGAAAAAGTATATTCCATTAAAT GACACATGCCACCATAGATAATGGATAATGAAGAAGTTAACGAAGAATGTATGAGATTAT TTTTCAAGAACGCTCGTGCGCATCTGGATAAACATCTAACATCAAGGTTGACATGCGATG AAAATGCATATATCACGTTCAGATGCTTCCTGGATGGAATACATCGCAAATCTACTAGGT TTCTCGAAGAGCTACTTTTGAAACAAGAAAATATGTACCATAATAACAATTACGAACGCA TAAATGATTCCGTGATACCATTGGTTCTGAAACTTTTATGGCTTCAAATTCACGAACCTA CACTCCAATGGTTTGAGCACTGGTTCCATGATATCATGCGACTAAGTAACAGAAGAAAGT TCAGAGTTTTTAGAATTTTTCAAAAAAAAATGATTCAATTTTTCAAAATTACACACAGGT ATTACTATGACATCATCGAACACCTATGCGCAAAGTACGATATGAATTCCGTTATTTCAA ATGCTCTCTCGCGAAGTTGAATTTAATGCAATACACAGATGGACTTTCAACTCATGAGA **AAATTATCTTAAACACGAGTAATCCACTGACGTTTTCCATTGTAATCTCACTACAAAGAT** GCGTGATTAATCTAGGTTCCACACATTTTTATAAAACACTACTAAACAAGCCGTCTAACA AACCCAAGAGTGTGGAAGGTTTTGAGAAGTCTATTAGGTACTTGAATATTGCCTCACTCT ATCTCCCAGCCGTTGGAGATACTTATTTTCAACGAGCGAAAATTTACTTGATCACTGGGA AATTCTCACTGTATTTCTTTGAATTAGTAAGAGGGGCATTGGTAAGGATTCCGTCTAAAT GTGCGTTAAACAATTTGAAAGATTTCATTTTGACTCCTGATTTTCCGGAAAGAAGACGTC TGATGAAAAATTGGCAATTCTTGTGTCAAAAGATCTCAAAGGTGAGAAATCATTCTTTG AAGGTCAAATTGTTTTGCAATTTCTATCGATAGTAGAACACACTTTGGTTCCACAGTCAT GGAACGCATCACGTGCTTCTAATTGTTGGTTATTGAAAGAGCATTTACAAATGGCTGCAT TAAAGTATCATTCAGGTAATATTAATGTTATACTTGAAAACTTGGCTGCCACAATGGGAA GTTTCGATCTTATGTTTACAACTCGAAAAAGTAAGGAACAAAAGAACAAACTCAAATATG CAGATTTGAGTGAGCGCCAGGTTTTTTTTTTTAGACTTGAGCTTTGATTTTATTGCTAATA TCATAGACGTCGTCATCAAACCCTCCTGGCAAAAAAACATGGAAGACTTTCGATATCTAG CCATTATTCGTTTGCTTATGTGCTGGATTAAGTCATATAGATCTATTTTGCAGTACACTC ACAGACACAGGAAGTTTTGCACTTCATTCGCCTTGTTGCTGAACGACTTGATAAATAGTC CACTGAATTGTTCAGGAAATATATAGCCACAGGCCGAAAAGAAGCTATCTTTTAGAG AAGATATTATTTTCAGGGAATTTTCTTGCATTAACTTTGCACTAACAGATTTTAATGACG ATTATGTGTATGATTCTCCCGACATGATTAATAATATAATTGGATGCCCTACATTGACTA **AAGTGCTTTCTCCAAAAGAAGAATGTGTTCTGCGAATTAGATCAATAATATTTTCTGGCA** TGAAATTTTTAGAGAAAAATGACACCGGCGTCATATGGAATGCCAGCAAATATAAGTTTG ATTTAATAAGCCCAAATATTAAAATAAAACGCCAAATAGCATTATCGGAAATTTCCTCCA AAATAAATGTAAAAACACAACAGGAAAGAGTAGTCTCTTCGAGAAAAGTTGAGGCCAAAA GAGATGAACAACAGCGCAAAAGAGCCGGGAAAATAGCTGTGACAGAACTGGAAAAACAAT TTGCAAATGTCCGGAGAACAAAAAATTGTCTCCGCTCCCAGAAAAAGATGGCGTTTCTT CTGAGTTGGTAAAACATGCTGCTTCACGAGGGAGAAAAACTATCACTGGCCCACTATCCT CTGATTTTCTCTCATATCCAGACGAAGCAATTGATGCTGATGAGGACATCACCGTCCAAG TGCCAGATACTCCTACTTGA

YLR233C, 699 aa (SEQ ID NO 186)
MDNEEVNEECMRLFFKNARAHLDKHLTSRLTCDENAYITFRCFLDGIHRKSTRFLEELLL
KQENMYHNNNYERINDSVIPLVLKLLWLQIHEPTLQWFEHWFHDIMRLSNRRKFRVFRIF
QKKMIQFFKITHRYYYDIIEHLCAKYDMNSVISNALFAKLNLMQYTDGLSTHEKIILNTS
NPLTFSIVISLQRCVINLGSTHFYKTLLNKPSNKPKSVEGFEKSIRYLNIASLYLPAVGD
TYFQRAKIYLITGKFSLYFFELVRGALVRIPSKCALNNLKDFILTPDFPERRRLMKKLAI
LVSKDLKGEKSFFEGQIVLQFLSIVEHTLVPQSWNASRASNCWLLKEHLQMAALKYHSGN
INVILENLAATMGSFDLMFTTRKSKEQKNKLKYADLSERQVFFLDLSFDFIANIIDVVIK
PSWQKNMEDFRYLAIIRLLMCWIKSYRSILQYTHRHRKFCTSFALLLNDLINSPLNCSGN
IYSHRPKRSYLFREDIIFREFSCINFALTDFNDDYVYDSPDMINNIIGCPTLTKVLSPKE
ECVLRIRSIIFSGMKFLEKNDTGVIWNASKYKFDLISPNIKIKRQIALSEISSKINVKTQ
QERVVSSRKVEAKRDEQQRKRAGKIAVTELEKQFANVRRTKKLSPLPEKDGVSSELVKHA
ASRGRKTITGPLSSDFLSYPDEAIDADEDITVOVPDTPT

AAAAACGGTCGGATCATACAGGCATGTTAACATTTCCATTATCCTTTTTGACATTGGATA ATGGCGTGAACGCGAAAATCACATTGATAAAAAAAAGCAGTTTGGCGAATTAGTAACTGT AAGGTGTATTATAGACAATAATGAAAGTGCTATGTGTCGCAGAGAAAAATTCTATAGCGA AGGCAGTTTCACAGATCCTAGGAGGAGGCAGATCAACTTCAAGGGATTCCGGCTACATGT ATGTAAAGAACTATGATTTCATGTTTAGTGGGTTCCCGTTTGCCAGAAATGGGGCTAACT GCGAAGTTACCATGACTAGTGTTGCAGGGCACCTAACAGGCATTGATTTCAGCCATGATT CGCATGGGTGGGGAAAATGCGCCATCCAAGAGTTATTTGATGCGCCACTGAACGAGATTA TGAATAACAACCAAAAAAAGATAGCAAGCAACATCAAGCGAGAAGCGAGGAATGCAGACT ATCTGATGATATGGACAGATTGCGACCGGGAAGGAGAGTACATCGGTTGGGAGATATGGC AGGAGGCCAAGAGGCAACAGGCTCATACAAAATGATCAAGTATACCGGGCAGTCTTTT CGCATCTCGAAAGACAACACATATTAAATGCAGCACGAAACCCAAGTCGATTGGATATGA AGAGTGTGCACGCTGTAGGCACGCGGATTGAAATCGATCTTCGAGCAGGTGTTACATTCA CCAGACTCTTAACAGAAACGCTACGAAATAAACTGAGAAACCAAGCCACCATGACCAAGG ATGGTGCAAAACACCGCGGTGGTAACAAGAACGACTCACAAGTCGTATCGTATGGTACAT GCCAGTTTCCAACGCTCGGCTTTGTAGTAGACAGGTTTGAAAGAATACGAAATTTTGTTC CCGAAGAGTTCTGGTATATCCAATTGGTAGTCGAAAACAAAGACAACGGCGGAACAACAA CGTTCCAGTGGGACAGGGCCACTTGTTCGACCGGCTGAGCGTGTTAACGTTTTACGAGA CATGCATCGAAACCGCCGGCAATGTTGCTCAAGTAGTAGACTTGAAATCAAAGCCAACAA CGAAATACAGACCTTTACCTCTGACCACAGTGGAGCTACAAAAAAACTGCGCCCGGTACC TGCGTCTGAACGCCAAACAATCACTAGACGCAGCAGAAAAGCTATACCAAAAGGGGTTCA TATCGTATCCAAGAACAGAGACTGATACTTTCCCACACGCAATGGACCTAAAATCCTTGG TCGAAAAGCAAGCTCAATTGGACCAACTCGCTGCAGGCGGCAGAACCGCCTGGGCATCGT ACGCGGCATCGCTGCTCCAACCCGAAAACACAAGTAACAATAACAAGTTCAAGTTTCCAC GAAGCGGCTCCCATGACGACAAAGCGCATCCACCAATCCACCCCATCGTAAGTCTGGGGC CTGAAGCAAATGTTTCGCCAGTGGAAAGAAGAGTATACGAGTACGTGGCCAGGCACTTTT TGGCATGCTCAGAGGACGCCAAGGGCCAATCGATGACCCTTGTGTTGGACTGGGCCG TTGAACGTTTCTCAGCTTCAGGTCTCGTAGTCCTAGAGAGAAATTTCCTCGATGTTTACC ACATCGCGAAGGCCGAAATGAAGGCGGGCACTACGGCGCCCCAAGCCGATGACTGAGA GTGAACTCATTCTCCTCATGGATACAAACGGCATTGGCACAGACGCCACCATTGCGGAGC ACATAGACAAGATCCAAGTACGTAATTACGTTAGGAGCGAGAAAGTAGGCAAGGAAACCT ACTTACAACCCACGACCTGGGTGTCTCACTAGTGCACGGCTTCGAGGCCATCGGCCTCG AAGACTCCTTTGCAAAGCCCTTCCAGCGCAGAGAAATGGAGCCAAGAACCTCAAGAAAATCT GCGAAGGTCATGCCTCCAAGACTGATGTTGTAAAGGACATAGTCGAGAAGTATAGGAAGT ACTGGCACAAGACGAATGCCTGCAAGAATACTCTCTTGCAAGTTTATGACCGTGTCAAGG CATCCATGTAA

YLR234W, 656 aa (SEQ ID NO 188)
MKVLCVAEKNSIAKAVSQILGGGRSTSRDSGYMYVKNYDFMFSGFPFARNGANCEVTMTS
VAGHLTGIDFSHDSHGWGKCAIQELFDAPLNEIMNNNQKKIASNIKREARNADYLMIWTD
CDREGEYIGWEIWQEAKRGNRLIQNDQVYRAVFSHLERQHILNAARNPSRLDMKSVHAVG
TRIEIDLRAGVTFTRLLTETLRNKLRNQATMTKDGAKHRGGNKNDSQVVSYGTCQFPTLG
FVVDRFERIRNFVPEEFWYIQLVVENKDNGGTTTFQWDRGHLFDRLSVLTFYETCIETAG
NVAQVVDLKSKPTTKYRPLPLTTVELQKNCARYLRLNAKQSLDAAEKLYQKGFISYPRTE
TDTFPHAMDLKSLVEKQAQLDQLAAGGRTAWASYAASLLQPENTSNNNKFKFPRSGSHDD
KAHPPIHPIVSLGPEANVSPVERRVYEYVARHFLACCSEDAKGQSMTLVLDWAVERFSAS
GLVVLERNFLDVYPWARWETTKQLPRLEMNALVDIAKAEMKAGTTAPPKPMTESELILLM
DTNGIGTDATIAEHIDKIQVRNYVRSEKVGKETYLQPTTLGVSLVHGFEAIGLEDSFAKP
FQRREMEQDLKKICEGHASKTDVVKDIVEKYRKYWHKTNACKNTLLQVYDRVKASM

CCAGTTCTCCGGGCAAGAACAGATAACATATAATAGTATACCCAAGAATGCAAATCTAA TTGATGGATCTACGAATTCATCGAAGAGGCCAATTGAAAAGTATGACAAGAGAATAGCCG ACCCAACAAAAAGCTATTTTCCACATAGCATATCAAGAACACCAAGGAGAAAATATACTT ACATTCTAGTCCTCACATCACTAAATGGAACTTTTGAGAGCAAACATGTGGTGATACCAT TTAAACCAGATGGTTTGAAATTGGGAAGGCCTGTTGCTAATAGTAATAGCAGCTCCAGTT CATCGCTCAGGGGCGGTAAAAGAGTGGATTCACACACTTTTTCCCAAGTAAGGTCCGATA ATGGTAATTTCGATTCAAGAGTACTCTCCAGGAATCATGCATTGTTAAGTTGCGACCCGC TCACGGGTAAGGTATATATACGAGACTTAAAATCCAGTAATGGTACGTTCATTAACGGTC AAAGAATTGGCTCAAATGACGTAGAAATCAAAGTTGGCGATGTGATAGACTTGGGAACAG ATATAGATACGAAAATTGAGCATCGAAAAATAAGTGCCACAGTTGAAGAACTATTTGTAC AACCTTTATTAGAATCACCGATTTTTGAAAATGAAGATAGTGATGATTGCCATACAATTA CAGAAAAAGAGGAGGCTGCCATAACAAGTCACATATATGGTGATTCCAACAACCTAG AATTGGAAGAGTTATCCTGGGCTCTGATACAGAAATACTGAGTGGAATTTTTATTAATA ATTGTATTGGTACGAGCCCGACTTTATCTAATATCATCAAAACCCTGGCAATGGAAATTC CGACACATCTAGAATACACGAACAAACTTTTAGTGGAAAAAAATGATCAGCAACTGGTAA AGCTGCAAAATGGATTAAGAAGGAAACTGTCGGGGAAATACGAAAAGATTATCGAACAAA ACAGAAATCAAGTAAAACAGTTGGAAAGGGACCATATGTTTTTCAAAAAGTCATTTGAAG TGAAGAAAAGAAGAAATAATGAAAAGCAAAAAAGCATGGAAAGGGAAATAGAAGACTTGA AAGAACAAGAACTCTCAACTGCATCTAAAAAAAAAGACTACCGAACATGACACTAGAGGCG TCCCGGGCATGAATCCTAAGGGTACTGACAAATTTAGCATCAAGAACACGCTATGTAATC ATTTCACACTATTAACATTTGGAACTATTTCCATCGGGATTATAGCTATTGTCTTCAAGA TCCTTTCCCCCAACTAG

YLR238W, 478 aa (SEQ ID NO 190)
MTGPGPEINKEEHPSSPGKKQITYNSIPKNANLIDGSTNSSKRPIEKYDKRIADPTKSYF
PHSISRTPRRKYTYILVLTSLNGTFESKHVVIPFKPDGLKLGRPVANSNSSSSSSLRGGK
RVDSHTFSQVRSDNGNFDSRVLSRNHALLSCDPLTGKVYIRDLKSSNGTFINGQRIGSND
VEIKVGDVIDLGTDIDTKIEHRKISATVEELFVQPLLESPIFENEDSDDCHTITEKEEAA
AITSHIYGDSNNLELEEVILGSDTEILSGIFINNCIGTSPTLSNIIKTLAMEIPFSKCDN
FKLQSMENFLINYTTHLEYTNKLLVEKNDQQLVKLQNGLRRKLSGKYEKIIEQNRNQVKQ
LERDHMFFKKSFEVKKRRNNEKQKSMEREIEDLKTRLEVERYKNSQMMKKNKQKEQELST
ASKKKTTEHDTRGVPGMNPKGTDKFSIKNTLCNHFTLLTFGTISIGIIAIVFKILSPN

YLR241W, 2849 bp, CDS: 501-2849 (SEQ ID NO 191) TTAATTTGAATATGTCCGAAGAAGATGCCACAGTGCATTTTCAGAATCTAATCAATGATA GTGTAAATGCTTTGCTGCCTATCGTGATTGATCATTACATAATCTGGCACAATACTGGC GGACCTGATTGGTTGATAATTGGTGCTTCAAAATTTAAATTTCGTCACTCTAATTATACT TAACATATAAATGGTACCTTCAATATATCTTCTTAGTAAAAAGTAGCATGATTTTGTGTT AATTTGCACTTTTTTTATTTAAAAATAAAATCACAGTTAATTTTTCATGATCTTGCAAA GACACGCCTCCCCTAATGTGGCATATATAACAATTGTGAATCAGAAAAACTCAACACTT TAACATAATGGCGGGCACGAAGGCTAAACAAACAAGATTAGCATTGAATGCCTTTTTTGG GTACAATAGAACAGTACTGAATGACATCATATATCGAAAGGCTCAAGTCGGCAGCATCGT ATCTTGATACAGTTCCAGATGAGCATCATGATTTCAGAAAACCCACCGCCAAGGTTGTAA TACTAAAAAAGTGGCCTAGATTATACGCAAGCAGACGATATAAAGATGACGGGAACCTTC GCTTACCGTCCTGGAATCAGTCAAGTTTATTCGGCTGGTTAACAGTGTTGTATAAGATAC GGGACGAACAGATTCTGGAATATGCAGGTTTAGATGCGTATGTGTTTTTTGAGTTTTTTCA TAAGATATCATTTTACTGGAAAAATTGATGACGGCAACGATGATGATGACAGTGAAAGTT CTTTAATACATCTGGTAAAAAGAATTGTGGAGGGAAGTGGCGATGGTGACAATCATTCAG CTCCCGAACGTACAAATGTGTACCTCTGGATGTATGTTCTCTTCACATATTTCTTCACCT TCATAGCAATTAAAATGGCAGTTGCGGAAACAAAGCACGTCGTAAGTACTAGGCAAGCTT ATCTTGGGAAGCAAAATACGATTACTGATAGAACGATAAGGCTCTCAGGCATCCCGATAG AGCTTCGTGATTCGGAAGCCTTAAAGACCAGAATTGAACAATTAAAAATCGGCACCGTTT CATCAATCACTATTTGTCGAGAGTGGGGTCCTTTGAACAAGCTATTTCATTGTCGGAAGA AAATACTCAAAAACCTGGAATTAAAATATTCAGAATGTCCAAGGGAGCTCCGTACTCGAC

AACCATATTCGGAGAACTATCATTTATTGGGAAACGAGCAATCAGGCGCAGTTACACATG GAGAAAATGTTCCATCAAGCAATAATAATGACGAGGATACTATACTATATTCTCAAATTT ATGCCATAGAGTACCTGGAGCAGCAATTAAAATTTATTGATGCTGAAATTATTGAAGCGA GGAAACAACACTACTCCGCAACACCTACGGCATTCGTTACGATGGATTCTGTTGCTAATG CGCAAATGGCAGCTCAGGCGGTATTAGATCCTAGAGTACATTACTTCATAACCAGATTGG CTCCTGCACCTCACGATATCAAGTGGGATCATGTTTGTCTTTCTAGAAAGGACCGGTTAA TATCATACTTAGCCACATTGCTAAATTTGAAAACACTTTCGAAATTCTGGCCAAGCGTAG GGCAGCTACTAAAAGATCACCAGTGGGCCGCTAACATTGTAACGGGGCTATTACCAACCT ATCTCTTCACATTGCTTAACTTTGGAATCCCCTATTTTTACGAGTATTTGACTTCTTATC AAGGATTGGTATCATACAGCGAAGAGGGAAATCTCACTTGTTTCAAAAAATTTCTTTTATA TTTTTGTCAACCTTTTCTTAGTTTTCACATTGGCAGGTACAGCATCTAATTACTGGGCGT ACCTCAGCGATACCACCAAAATTGCTTATCAACTTGCTACATCTGTGAAGGAGTTCTCCT TATTCTATGTCGATTTGATTATATTGCAAGGTATTGGTATGTTCCCGTTTAAGTTGTTAT TAGTTGGTAGTTTGATCGGCTTTCCTCTAGTGAAAATCAAGGCTAAGACACCTAGGCAAC GGAATGAACTTTACAATCCACCGATATTTAACTTTGGACTACAATTACCACAGCCAATTC TGATTTTGATTATAACGTTGATCTACAGTGTAATGAGCACGAAAATTTTGACTTCAGGGC TGGCGTACTTTATTATTGGGTTTTACGTCTATAAATATCAATTGATTTTTGCCACAGATC ATTTGCCCCATTCTACAGGAAAAGTATGGCCATTAATTTTTAGAAGAATCATCGTTGGAT TGCTATTGTTTCAATTAACAATGACAGGAACACTGGCAGGATTCGAAGGAGGATGGGTTT TGTCATCTTGCCTTTTCCCGCTTCCAGTAGTGACATTATGTTTCCTATATGATTTCGAGA AGAACTATTTGCCGTTGTCAAAATATATCGCATTGAGTTCAATTCGCGAGTACGAAAGAG ACAATTCTACGGTGAATTCTGCCAATGAGGAAGAGTCGTATGCATACCCTTACGCTGTGA GTGAATTAGAGGGTCCGATGTTGGATTGA

YLR241W, 782 aa (SEQ ID NO 192)
MTSYIERLKSAASYLDTVPDEHHDFRKPTAKVVTTQLTIATSLGIFALLSFSILLKKWPR
LYASRRYKDDGNLRLPSWNQSSLFGWLTVLYKIRDEQILEYAGLDAYVFLSFFKMCIKLL
SIFCFFSVCVISPVRYHFTGKIDDGNDDDDSESSLIHLVKRIVEGSGDGDNHSAPERTNV
YLWMYVLFTYFFTFIAIKMAVAETKHVVSTRQAYLGKQNTITDRTIRLSGIPIELRDSEA
LKTRIEQLKIGTVSSITICREWGPLNKLFHCRKKILKNLELKYSECPRELRTRQPYSENY
HLLGNEQSGAVTHGENVPSSNNNDEDTILYSQISLGERPKMKIGYRGIFGKEVDAIEYLE
QQLKFIDAEIIEARKQHYSATPTAFVTMDSVANAQMAAQAVLDPRVHYFITRLAPAPHDI
KWDHVCLSRKDRLTKVYSTTVFIGLSSLFLVIPVSYLATLLNLKTLSKFWPSVGQLLKDH
QWAANIVTGLLPTYLFTLLNFGIPYFYEYLTSYQGLVSYSEEEISLVSKNFFYIFVNLFL
VFTLAGTASNYWAYLSDTTKIAYQLATSVKEFSLFYVDLIILQGIGMFPFKLLLVGSLIG
FPLVKIKAKTPRQRNELYNPPIFNFGLQLPQPILILITLIYSVMSTKILTSGLAYFIIG
FYVYKYQLIFATDHLPHSTGKVWPLIFRRIIVGLLLFQLTMTGTLAGFEGGWVLSSCLFP
LPVVTLCFLYDFEKNYLPLSKYIALSSIREYERDNSTVNSANEEESYAYPYAVSEELEGPM
LD

YLR321C, 1781 bp, CDS: 501-1781 (SEQ ID NO 193) TTCAAGTGCACTCTTTGTAAGGAAGATTACAAGTCTCCAGTGGTCACAAACTGTGGCCAT TATTTTTGTGGATCGTGTTTTGCCAAAGATATGAAAAAGGGCACCAAATGCTTTATATGC AGGAAAAGTTGATGGAGAATGCCATATCACCCCAAAAATTACACGCACCCGATGCTAATG TACAGGAATTATAGAGCACATGACCCATAGATTTATCGAGCATTGTTGCAATTTCGAAAG ACTTAGAAAATACGACAAATAGAGATTATTGAATGAAGTACATTGAAAAAAAGAAGAAGA AAGGCACATAGCAGCACAATGTCGCACCAAAACCAGCTTATTCCACAAGCTTATATTT CTAACTTTCATAACAGATTGACAAACGAAGATGATGGTATCCCCATCTTTACAATGGCTC AACAAACAAGGCAGCATAAAAGGGCTAAAGTGGTCAACTATGCGGAATATGACAACGATC TCTTTGATGAATTCAATATGAACGGTTCTAATTTCAACAATGCTGATACACACTATAAAG ATAATGCAGTGTCTCATGAAAATACTCCGGCACTTACAAATGGTGTTACCATGGACGGTT CCGAATACAATGTCCTAGAGAACATGAATGGAGCTGATAGTATTATCTCTAACAACAAAT ACGATGCGGGTTCAAACATGGTTGTGGAATCTTTATCCGGTTTGAATAGCAATAACAACG CCAGCAATGGTCCGAGCAACAAGCGCAGGCACAGGATATTGGAAACGCCGTTCTACCGG ATCTGCAAGACCAACACCCCTTCAACATATTGAGATACCCTAAAATAAGAGATA

YLR321C, 426 aa (SEQ ID NO 194)
MSHQNQLIPQAYISNFHNRLTNEDDGIPIFTMAQQTRQHKRAKVVNYAEYDNDLFDEFNM
NGSNFNNADTHYKDNAVSHENTPALTNGVTMDGSEYNVLENMNGADSIISNNKYDAGSNM
VVESLSGLNSNNNASNGPSNKAQAQDIGNAVLPDLQDQHHNPFNILRYPKIRDTFINGKV
VSPYRLNTDQETKANANSGEAIMIPITLDIEHMGHTIKDQFLWNYNDDSISPEEFASIYC
KDLDMTSATLQTQIANIIKEQLKDLENIAATEIMSDLHVIINLTCNLQDRFFEDNFQWNL
NDKSLTPERFATSIVQDLGLTREFIPLISQSLHETILKIKKDWVDGHLIQDHVPNDAAFG
YLSGIRLDIDELGSNWCPRVEILTKEEIQKREIEKERNLRRLKRETDRLSRRGRRRLDDL

YLR322W, 104 aa (SEQ ID NO 196) MRHCIIFIVCISIVEIRTVHIEFIKEIVVIFRIVDHFSPFMLPCLLSHCKDGDTIIFVCQ SVMKVRNISLWNKLVLVRHCVLLCAFLLSFFNVLHSIISICRIF

YLR325C, 78 aa (SEQ ID NO 198)

MAREITDIKQFLELTRRADVKTATVKINKKLNKAGKPFRQTKFKVRGSSSLYTLVINDAG KAKKLIQSLPPTLKVNRL

YLR344W, 1331 bp, exon1: 501-519, intron1: 520-966, 967-1331 (SEQ ID NO 199) TAAGGGCTGTCAATTTTTCATTTCCCTCAAAGTTAATGCGCAAGAGTTAGGATGATCTTG ATTATTAGTTATTTGTTTCCATCAATTATGCCGACGTCCATGAATGCTATTGAAGTA TCGATTACTTATGCTATTCTATTGTATTTGAGCCGGCGGCTAGTAAACAAGACAGCATAC CTTTCCAACATCCGTACATATTGATTATTGTATCTATGATTTTCATGTAATGTATGGGTT AACTAATCCTTTCTCTTTTTTTTTTTTTTCTGAAAATCAGTAGCTAGAGGAACCTGTTC GTGAAAGATATGGAATATTCCGTCTAGGGAAGAGCCGAGAGCTGAGAGCAGTATCCATCG GATGGAATCTTGCCTGGATGCGTAACGACGACAGCTTGTCTAGAAGGCGAAGTACAAGAT ACTAAGAAGACTATAACAACAGAAGACAATTTTGTAGTGCGATTCTATATTATTGACGTA ACCAACAAAAAGTATCAGAATGGCTAAACAATCATTAGGTATGTGCACAAATGCTAAAT CACTGAAACCCTGTAGAGCTGGAATTGAAAATATAGTTTGTACCTTTTGCCTGAGGGCAG AATGACTCAATGTTATCTTAATTCGATTAGAAAAAGAAGGTGCGTTATCCAAGGTTGAAA CTTGTAAACTATTTAGGTGATGTCTCATAACTGCAACCACTGGAAAATGACGCAAATATC AAAATAATAGGGAGATAAAGTCTCACGACATGAAAAAATCATAGAATTATTGTTCAATTT ATCTAGCCGTATCTTACCTTATGGAAAAAGTGTGAATATGTTTTTCTAAATCGAGCTTCC CGGAAATTACACTATATTATGCATCCGTGATACATCTGAAATTCAATACTTTCTCCAAGG TCCTGCTTACTAAGAGGGTAAGATTTGTTGAAACTCGAAATACTAACATTATTTTCATTA TTTTAGACGTTTCCTCCGACAGAAGAAGGCTAGAAAGGCTTATTTCACCGCCCCATCCT CCCAACGTCGTGTTTTGCTATCTGCTCCATTATCTAAGGAGTTGAGAGCTCAATACGGTA TCAAGGCCTTGCCAATCAGAAGAGATGATGAAGTTTTGGTTGTTCGTGGTTCCAAGAAGG GTCAAGAAGGTAAGATTCATCTGTTTACAGATTGAAATTTGCCGTTCAAGTTGACAAGG TTACCAAGGAAAAGGTCAACGGTGCTTCCGTTCCAATTAACTTGCACCCATCCAAGCTTG AGTTGGAATAA

YLR344W, 127 aa (SEQ ID NO 200) MAKQSLDVSSDRRKARKAYFTAPSSQRRVLLSAPLSKELRAQYGIKALPIRRDDEVLVVR GSKKGQEGKISSVYRLKFAVQVDKVTKEKVNGASVPINLHPSKLVITKLHLDKDRKALIQ RKGGKLE

YLR367W. 1376 bp, exon1: 501-633 intron1: 634-1116, 1117-1376 (SEQ ID NO 201) ACTTTTTGTCTGCTGGTCGTTTGTCTTTCGTTTTAAAATTGCGCTAGACAAGTAAAC AGGGATTGCTTAAGAATCAAAGTAGCTTAACTCTAAAGTATTATTTTCCTCAGTTGTGGG CCCATGTGTTGGAGGGAAGGAATATATTGAAATGTAAATGTTCTTAAGTTCGGTTGAACT TGGATATTGTTACAAGAGTTCTAGTCTTTGATACCATTTTTACGCAATTACAACCGCATT ATTTACCTTTTCATCTTCAGTTTTACGGTTCAGTTTATTCTGTTACGAAAGAACTATGGT GATTCAAAGGCGAAGTGCGTAGGATTGTAACTCCTATATCTTTAGGATACTTACAATTTT GTACTGTTTCAAGACCACTGTAACCGATAATAAACCGGAGGACACATTTTAACCCACTA TTTTTTTCAGAAGATCAGATGCGAGAGCTCGAAGCATAAGTATAATACTAACGTTTCAAA ACATAGTAATTAGGTAAAAAATGACTCGCTCTTCCGTTTTAGCTGATGCTTTGAATGCCA TTAATAACGCCGAAAAGACCGGTAAACGTCAGGTTCTATTGAGACCTTCTTCCAAGGTTA TCATCAAGTTTTACAAGTTATGCAAAAGCATGGTATGTTCCAACTATTTTTCAATATTT TCACATGTGTTTCAATTTCTGCTTATTTTTAAATGTTACCACGAGGTTTGTCCAAGTTCA ATGTTGCGCAACTCTAACGAAGAAATAATTATTGCCATTGTTTTTTACTCCGGGCTGATA ACTAGATGGTGTGATCGGGCAGTATACTAATTTATACTGGACAAAGACTCGTAAAAGATG TTCTTTGTGCTTAGTCCCATACTGTTTTTTAAGTGTCCGGGATATTTAATCCCATGTGGA AATGCTTCTTACACGGTTATGGATTACACCTCATGTGTAGCTACTATATCCATTACCGTT TACTTTTCCTCAAAATCTCACTCTTAAAATTTTCAATGGCAAAATTCTTCCGCACAACTT AGACAACATTTTCTTGTTTTTTTATGAAGTAAGCAAAAATTTCGAATCAACAACGCTCCAT GAGATTCTTCAATACTAACATTTACTCCTTATTTAGGTTACATTGGCGAATTCGAATACA TTGACGACCACAGATCTGGTAAGATTGTCGTCCAACTGAACGGTAGATTGAACAAATGTG GTGTTATTTCCCCAAGATTTAACGTTAAGATTGGTGACATTGAAAAATGGACCGCCAACT TATTGCCAGCCAGACAATTCGGTTACGTTATTTTGACTACTTCTGCGGGTATTATGGACC ATGAGGAAGCTAGAAGAAAGCACGTTTCCGGTAAAATCTTGGGTTTTGTCTATTAA

YLR367W, 130 aa (SEQ ID NO 202) MTRSSVLADALNAINNAEKTGKRQVLLRPSSKVIIKFLQVMQKHGYIGEFEYIDDHRSGK IVVQLNGRLNKCGVISPRFNVKIGDIEKWTANLLPARQFGYVILTTSAGIMDHEEARRKH VSGKILGFVY

YLR393W, 1340 bp, CDS: 501-1340 (SEQ ID NO 203) CCCTCAACCCGCATTTTGCTGAGAATTTTCACCAAGGCCCTAGGTGATATTAGATTCCAC CTGACTAATTGCATTACAGCCGACCCAAGGCAATATCAGTTTAATAAAATATCATGTATC TCACCCTCTTCTTGGTATTAGTAAAGAGACGCCTGATCTTGTAACAGTGGTGAAGATTGT **ACTAGAGCAGAATCAAGAATTTAAAAAGTGTAAAGGCAAGGCAGAGGCGATGTACATAAA** ACTTCGAAGTAAGAAATATTTAATAGTTCTCGCCACATCACTATGCAGCTATATAAAAAAC TACTATAAACGTTTGTTTGTTCCTTACGCACAATATCCTTGCCTAGAAATCGTTTTTGA AATTTAAATTTTTATTACCATTTATTTGATTCGCCTTCAGAAAAATATGGAAGAGTGCAT ATTTAAAAAGGACTATTTCAGCATATAGTAAAAGTCAGGTTATTTGTTTATTTGCGATAT CAGAGTAACTAACTATGCAGGGCACTTTTAAAAGGTTTTACCATCCCACGCTTA CGCGGATGTCCTTCGGATAAATTCCTCAAGCCTATGATGGCAACGGCTTCCCCAAAGG AATACCAGATCAAACAACTGGTCAAGCCAATAGGCTTAACACAAGCACCAAGGAAAAGCA CCAAATACTCCCAGGGGAACTCTTTGAGGGATATGTTTGATTCGGAAAAGACAAACCACA GAGTTAAAGAGTTGGCCGTTGAATTCAGCAAATCTGGACTTTATGACGTGCAAGTCTTCC AAAAGACAAAGGGGAAATTGTTTATAGCTCCAGTTTCATATTGGAAAGAAGATAAAGCTT TGTTTTTCCTCATTTGATAGGAACGGCAATGGATGGTACGAAACAACAGAATATCGAGG ATATGTTAAGGGGTAAAACCAGTATAGTGAGGTTATTTAGTACAGCATCTGGCGATAAGT TGAGTAGTTCATACTTCCAAGGAATCGTAGACGATAACAAAAAAACTGACTACTTGACTG AAGCTGATGCGCGTTTAAGTTTAAATGACAGTAACGTCCAAATCATCGAGGTCAATCTTG TAGAAAACGCTGTGAAAAGTGCTCTAGTGAAAACGCTTGCTCGTTGGGCCAATCGCGTTC CATCCTGGCGCCAGCCATTTTATTTCGAATGTTCTAGAGGCCAATGGCCATTTTCCGTCA TAAAAATTAGGTGGGCAGCTTGCGGGGAGGCTACTCCATCTGAAAAGGAAGCATTGTGGA **AGTTTGCCAAACGTCTGTGA**

YLR393W, 279 aa (SEQ ID NO 204)
MQGTFKRFYHPTLTRMSFLDKFLKPMMATASPKEYQIKQLVKPIGLTQAPRKSTKYSQGN
SLRDMFDSEKTNHRVKELAVEFSKSGLYDVQVFQKTKGKLFIAPVSYWKEDKALFFPHLI
GTAMDGTKQQNIEDMLRGKTSIVRLFSTASGDKLSSSYFQGIVDDNKKTDYLTEADARLS
LNDSNVQIIEVNLVENAVKSALVKTLARWANRVPSWRQPFYFECSRGQWPFSVREELFCN
NVFSGYVFLVDQQLKIRWAACGEATPSEKEALWKFAKRL

YLR423C, 1754 bp, CDS: 501-1754 (SEQ ID NO 205) TTCTATTGGTGTAGTTATACCAGAACCATCCTTCCCAAGGCCTTTTCCCGCAACATATCC CATACTCGAAAGTAACTTCGCACCAATACCATATGTCTTCGTTAATTTTGAGATCGTTGG GGCATTGCCGCTACTAGTTTTCAAGGCATCATTAGTGTATGTCATGTCACTATTCATGCT GAACTTTTTATCTGTGTGGGGTCCGAATCCTCCATGTTTTGGCGTACTGAAGGCTTAAG TTCTTCGACCTCTCTCGGTTGTACTATTTCGAAATTTTGGATTTTTGTTATTGTTTTGAC ATAATGTAAATACTAGATGCGCGCTCTAAGGCCTCAGTATTAAAAATTGCAAGATATCCC TAACTTGATAATTATTTGAAAGTCGCATAACGTACGATAAATTCGATACTGCGAGGATAT TATCAACGTATTTAACACCTATGAACGAAGCAGATGTTACAAAATTTGTTAATAATGCCA GGAAAACGCTGACCGATGCTCAACTTTTATGTTCAAGTGCTAATTTAAGGATTGTAGATA TTAAGAAAAATTGTCATCTTGGCAGTTGAGTATTTCAAAACTCAATTTTCTAATAGTTG TAATCCAGAAACAATGGAATCAAGCTGTCTTAGTGGTCTTAGTTGATGAGATGAAGTACT GGCAATATGAAATCACTTCTAAAGTACAAAGGTTGGATGGTATAGTAAATGAATTGAGCA TATCAGAAAAAGATGATACCGATCCCTCTAAACTAGGAGATTACATCTCGAGAGACAACG TTAACTTATTGAATGACAAACTGAAAGAAGTGCCAGTAATTGAGCGTCAAATTGAAAACA TGACGGACGTAACTCAAAAATTCCAAAGTAAATTTGGTATAGATAACCTGATGGAAACAA ATGTTGCAGAGCAGTTTAGCAGGGAACTAACGGACCTTGAAAAAGATTTAGCAGAGATAA TGAATTCATTGACACAGCACTTTGATAAGACATTGCTGTTACAAGATAAAAAAATTGATA ACGATGAACGTGAGGAGCTGTTTAAGGTGGTACAAGGCGACGACAAAGAACTATACAACA TTTTCAAAACTCTGCATGAGGTAATTGATGACGTGGACAAAACAATTCTTAACTTGGGTC AATTTTTGCAGGCAAAAATAAAGGAAAAGACAGAACTACAGCGAAGTTTCTGAAATAA
TAAACGATTTCAATAGAAATTTGGAATATCTATTAATCTTTAAAGATATTTCCAATCTGA
TTGATAGCTTCAAAAAATTCCTGTACACAAGATATTCAAACAACTAAGGAACTTTGTGAAT
TTTATGATAATTTTGAAGAAAAGCTACGGTAACTTAGTTCTAGAAGCAAAGAGGAGAAAGG
ATGTGGCAAACAGAATGAAAACTATATTGAAAGATTGTGAAAAGCAGTTGCAGAATTTAG
ATGCTCAGGACCAGGAAGAACGTCAGAATTTTATAGCGGAAAATGGAACTTATCTTCCTG
AGACAATCTGGCCCGGTAAAATTGACGATTTTTTCTTCCCTGTACACTTTAAATTACAACG
TGAAGAATCCTTAG

YLR423C, 417 aa (SEQ ID NO 206)
MNEADVTKFVNNARKTLTDAQLLCSSANLRIVDIKKKLSSWQLSISKLNFLIVGLRQQGK
FLYTILKEGIGTKLIQKQWNQAVLVVLVDEMKYWQYEITSKVQRLDGIVNELSISEKDDT
DPSKLGDYISRDNVNLLNDKLKEVPVIERQIENIKLQYENMVRKVNKELIDTKLTDVTQK
FQSKFGIDNLMETNVAEQFSRELTDLEKDLAEIMNSLTQHFDKTLLLQDKKIDNDEREEL
FKVVQGDDKELYNIFKTLHEVIDDVDKTILNLGQFLQAKIKEKTELHSEVSEIINDFNRN
LEYLLIFKDISNLIDSFKNSCTQDIQTTKELCEFYDNFEESYGNLVLEAKRRKDVANRMK
TILKDCEKQLQNLDAQDQEERQNFIAENGTYLPETIWPGKIDDFSSLYTLNYNVKNP

YML026C, 1342 bp, exon1: 501-547, intron1: 548-948, exon2: 949-1342 (SEQ ID NO 207) ATCTGTAAATAATAAGCCCATGAAATATCAATCTCACAATGAAAGAATTGTATAATTCAG AATGATTTGACGTAAAAGCAAGTCTCATTCAAGAAACTGTAAAATCCGTACACACTACTG AATTTTACATCCATACATTTTTTTGAAATTTCATGTTTTTTTGAAAAATTGGAAAAGGGC TAAATTATCCGTCGGGGTGTCCTCCTAGCTCGGCTCAACCTAGGCAAATGCGTTTACTGG GGCCATCCAAGCTCATCCTTCCAGAGATTCGCCTTTCAGAGGCAAAGAACTCGTCTCCGC AGGCCTCTTGTTCCGGGAGGAGGAGAATTCTTGCGCGGAAACTGGTTGATGCCTGGGCTA TGGTAATTCTGACACCTTTGCTATCCTAACTGGAAAAGGTCCTTAGTAATAACAATATCA GGTACTTTAACATTGTTAAAGATATACTATTAGTGAAAAACCGATCTTACGAAAAGCCAA TTTTACGGTATGTTTTACGAGTACAGTGCAGATATGTTGAGAGAGTTTCACATTACATGG GATAATAGCTTAATATTGCGATTGAAAATATGTGAGTGCACTCCGATGGAATAATAAACG TCACGGGTTACCAAATACGAGGCCGAATTAACTCTACGCTACTATAAAAATTATCACTAG ATTTTAAAGTAATACACAGTTTATTGGAAAATACAATATATGACTCAATGCGAATTTAAA AATTTCAGTCAATACAGCTTGACAAATTCATATTTATCGTCCCTCCATGTTCGTACGCCA TTCCAAAATGATGCGCCATGTTGAAAATTTCTCGAAGAACCTAGCAGTGGTGTGAAATAA ATTACTAACAATAAGATGTACAATTTTTTGTGCGCCCATTACAATCAGTTTGTTGAACAC CAATGTCGATGGTAACATTAAAATTGTTTACGCTTTGACCACTATTAAGGGTGTTGGTCG TCGTTACTCCAACTTGGTCTGTAAGAAGGCTGATGTTGATTTGCACAAGAGAGCTGGTGA ATTGACCCAAGAAGAATTGGAAAGAATTGTCCAAATCATGCAAAACCCAACTCATTACAA GATCCCAGCCTGGTTCTTAAACCGTCAAAACGACATTACTGATGGTAAGGACTACCACAC TTTGGCTAACAACGTCGAATCCAAGTTGAGAGATGACTTGGAAAGATTAAAGAAGATCAG AGCCCACCGTGGTATTAGACACTTCTGGGGTTTACGTGTTAGAGGTCAACACACCAAGAC CACTGGTAGAAGAGAGCTTAA

YML026C, 146 aa (SEQ ID NO 208) MSLVVQEQGSFQHILRLLNTNVDGNIKIVYALTTIKGVGRRYSNLVCKKADVDLHKRAGE LTQEELERIVQIMQNPTHYKIPAWFLNRQNDITDGKDYHTLANNVESKLRDDLERLKKIR AHRGIRHFWGLRVRGQHTKTTGRRRA

YML063W, 255 aa (SEQ ID NO 210)
MAVGKNKRLSRGKKGLKKKVVDPFTRKEWFDIKAPSTFENRNVGKTLVNKSTGLKNASDA
LKGRVVEVCLADLQGSEDHSFRKVKLRVDEVQGKNLLTNFHGMDFTTDKLRSMVRKWQTL
IEANVTVKTSDDYVLRIFAIAFTRKQANQVKRHSYAQSSHIRAIRKVISEILTREVQNST
LAQLTSKLIPEVINKEIENATKDIFPLQNIHVRKVKLLKQPKFDVGALMALHGEGSGEEK
GKKVSGFKDEVLETV

YML128C, 2042 bp, CDS: 501-2042 (SEQ ID NO 211) TTAATAGGGTTAGCCACCATTGTCTCGAACATGTTCACAGGCTCGGAGCTTGTGGCGGGT GCCTCGCTTACTGGAGTACCATTTAGCGGTGTGTTTGAAGCTAACGAGTTCATCTTCAAT CTTTATTTCCACTTCTTTACAAGCTTTCTGCCTTTCTCTATGACGTCTTTCCCAAAACAC TACCTCTTGACACGACTTGTTGTTTTCGTTTTTCTCTAAGAATATCACTATTTTCACTTT TTTCACCTTTTCCACCATTACGTCGGTAAGCAACAGCATTACGCCGGCCTCACCTTAGAG GGGAAGAATAAGGGATCTTTGGAACTGAAGGAAAATAAGGGAGGAGGGAAACAAGGAG GCGGTGAAAGGGGATCGACAGGGTATTTAAAGCCACTCATGGAGTCGTATTCCTAGCATG ATTAGATTACCGGAGTTTAGAAGAGGATCTGCAATAGAAGAGGAGACAACTACAAAAGAA CTGTTAATTAAGAGAAGAAGATGAAGCAATTCAAGTTGGTTAATGCGGTTTCCGCATCAT TTGTGCTTATTGGCTTAGTGTTGGCCAATTCAGATTCAGTGTTCGACAAGTGGACGCAGG AAGACCTGGCCGATTATTTACGTGATAATAAGAAGAGCTTGGAAAAGTACGCTACAGACT CCATTGAGGACTTGAAAACGGAGGCATCGCAGGTATGGGACAAACACGCGCAGCCCAAAC CATGGTGGCAGGTGTGGTCTAGTGACAGCAGTAGCGTGAGCAACAGTAACCCCGGATGGT TTGGTTATACTGGTTCTTCGGATCACCCAGTTTCTGACTGGCTCTTTTGACACCTGGTCCA CAGACAGTCTACGTAACTTCTTGAAGAAAAACGGCGTGGATGTTGACGACGCTAAGGCTT CCAAGGACTCGCTGGAAGACTGCTAAGGAGAACTTCAACAAGATTTCCAAATCTTTGA AGTCGTCGGGATACTATCCTTCTAGCTCTTACTTTGATAGCTGGTCAACCAAAGATTTGC AAAACTGGTTGAATGACAATGGTATCGACTACGACAAGGCAGTTCAAAGCAAGGACGAGC TAGTTCAGAAAGTCAAGGAAAACATCTACCGAACTTCAGAAAAGGCAGAACAGCAGCGTC TGGGTTTGCTAGAAAGCTTGGATTTGGCTCACCAACAAATATTAGACACATCGGGACAAA ACAAGGTCAATATTGACAAGAACATGGCCAAGAAACACGACTATTTGGTTAGAATGGCCA AAGAAAATTCTGCCAATTTGAAAGATGATATCTACTGGTACCTGGACTATATGAAAAGAG AGTCTTCTCCATTTTTGACCAAGACCCCAGAATACGTTGGTTCCGTTTGGGACTCTTCTA AAAATTTCCTCACAAATTTGTACTCCAAGTTCAGAGGTAAGACTGACAATGTGATCAATG ATACTTTTTGGTTGGCCTAGACTCTTGGCCAAAGGACAAATTGAAAATGTTTTTAGATG CTCGTGGTATTAAGTACTCAATGCTGTCTACTGAACATCAATTGAGAGAATTAGTCAAAA AATCCAGAAACGAAAAACTCAAGATCCTGCCAAAAGACTACCAAAAATACTTTGACAACA GTAACTGGTCTTTGGATGACATAAAGGGTTGGTTTGCTGACAAAAAGGACGACTTCCAAG ATTCTCAGACTTACTCCACAATTATGCAGGATTTTGACAAGGTTTCCAAAAACACAAATG ATGCTAAGGACCAAATCGCTAAGACCTGGTCAAATACCTTTCAGAGCTGGTCTCAAGAAG ACCTATTGCAGTACCTAAAATCATTCGGTGTTCCGGTTAAACAGACTTCTACGAAGGACG ACTTAATCAACTTGGCCAAGCAGAATACGCAATGGTTGTTCGGCACTGTTAAGGAGCCTG CTTACAAGAGGTACCTACATAACGTTAAAAACTGGTCGAAAAGCATATTAGGGTTCAACT

YML128C, 513 aa (SEQ ID NO 212) MKQFKLVNAVSASFVLIGLVLANSDSVFDKWTQEDLADYLRDNKKSLEKYATDSIEDLKT EASQVWDKHAQPKPWWQVWSSDSSSVSNSNPGWFGYTGSSDHPVSDWLFDTWSTDSLRNF LKKNGVDVDDAKASKDSLVKTAKENFNKISKSLKSSGYYPSSSYFDSWSTKDLQNWLNDN GIDYDKAVQSKDELVQKVKENIYRTSEKAEQQRLGLLESLDLAHQQILDTSGQIKDTVFD KWSSDQLTNWLESHKVNIDKNMAKKHDYLVRMAKENSANLKDDIYWYLDYMKRESSPFLT KTPEYVGSVWDSSKNFLTNLYSKFRGKTDNVINDTFLVGLDSWPKDKLKMFLDARGIKYS MLSTEHQLRELVKKSRNEKLKILPKDYQKYFDNSNWSLDDIKGWFADKKDDFQDSQTYST IMQDFDKVSKNTNDAKDQIAKTWSNTFQSWSQEDLLQYLKSFGVPVKQTSTKDDLINLAK QNTQWLFGTVKEPAYKRYLHNVKNWSKSILGFN

YML130C, 2192 bp, CDS: 501-2192 (SEQ ID NO 213) ACGAGATCATTTTCTTATCTATCTATTGAGTAATGCTTACTTTTCATATTTTCAATGAAC AATAGGATATGTAGGAGAATTGATATATTCACTGCGTATCAGAGAAAAGGTCTACTGACA TTTTATGGCAAATGTATTCTACACAAATCGAGAATACCACAGACAATGGTACAAGACATA CACAAAGAGAAGACTGTTCTAATTAAACAAATAATATTGAGCTACCTGCTAAGTATGTCC TTTTCCCTTTGTCCTTTGGTTTCTCTTATAGAAGACCCTGGAAATTTTTCGCATTTTTCC GTACGTGTCATAAAAACTTGTTCAATCATCCTTGAAGCTAAGTATAAAGAGCTTGAAAAG GTTTACCACTTAAACTGGTTATACTATTTCAAGAGTGTAAACATTTTATTGCATATACCA CAGTAACGTGCAGGTAAAACATGAGATTAAGAACCGCCATTGCCACACTGTGCCTCACGG CTTTTACATCTGCAACTTCAAACAATAGCTACATCGCCACCGACCAAACACAAAATGCCT TTAATGACACTCACTTTTGTAAGGTCGACAGGAATGATCACGTTAGTCCCAGTTGTAACG TAACATTCAATGAATTAAATGCCATAAATGAAAACATTAGAGATGATCTTTCGGCGTTAT TAAAATCTGATTTCTTCAAATACTTTCGGCTGGATTTATACAAGCAATGTTCATTTTGGG ACGCCAACGATGGTCTGTGCTTAAACCGCGCTTGCTCTGTTGATGTCGTAGAGGACTGGG ATACACTGCCTGAGTACTGGCAGCCTGAGATCTTGGGTAGTTTCAATAATGATACAATGA AGGAAGCGGATGATGACGAATGTAAGTTCTTAGATCAACTATGTCAAACCAGTA AAAAACCTGTAGATATCGAAGACACCATCAACTACTGTGATGTAAATGACTTTAACGGTA AAAACGCCGTTCTGATTGATTTAACAGCAAATCCGGAACGATTTACAGGTTATGGTGGTA AGCAAGCTGGTCAAATTTGGTCTACTATCTACCAAGACAACTGTTTTACAATTGGCGAAA CTGGTGAATCATTGGCCAAAGATGCATTTTATAGACTTGTATCCGGTTTCCATGCCTCTA TCGGTACTCACTTATCAAAGGAATATTTGAACACGAAAACTGGTAAATGGGAGCCCAATC TGGATTTGTTTATGGCAAGAATCGGGAACTTTCCTGATAGAGTGACAAACATGTATTTCA ATTATGCTGTTGTAGCTAAGGCTCTCTGGAAAATTCAACCATATTTACCAGAATTTTCAT TCTGTGATCTAGTCAATAAAGAAATCAAAAACAAAATGGATAACGTTATTTCCCAGCTGG ACACAAAAATTTTTAACGAAGACTTAGTTTTTGCCAACGACCTAAGTTTGACTTTGAAGG ACGAATTCAGATCTCGCTTCAAGAATGTCACGAAGATTATGGATTGTGTGCAATGTGATA GATGTAGATTGTGGGGCAAAATTCAAACTACCGGTTACGCAACTGCCTTGAAAATTTTGT TTGAAATCAACGACGCTGATGAATTCACCAAACAACATATTGTTGGTAAGTTAACCAAAT ATGAGTTGATTGCACTATTACAGACTTTCGGTAGATTATCTGAATCTATTGAATCTGTTA ACATGTTCGAAAAATGTACGGGAAAAGGTTAAACGGTTCTGAAAACAGGTTAAGCTCAT TAGAGAACATCAATTCCACTAAAGAAGGAAAGAAAAAGACTAACAATTCTCAATCACATG TATTTGATGATTTAAAAATGCCCAAAGCAGAAATAGTTCCAAGGCCCTCTAACGGTACAG TAAATAAATGGAAGAAAGCTTGGAATACTGAAGTTAACAACGTTTTAGAAGCATTCAGAT TTATTTATAGAAGCTATTTGGATTTACCCAGGAACATCTGGGAATTATCTTTGATGAAGG TATACAAATTTTGGAATAAATTCATCGGTGTTGCTGATTACGTTAGTGAGGAGACACGAG AGCCTATTTCCTATAAGCTAGATATACAATAA

YML130C, 563 aa (SEQ ID NO 214)
MRLRTAIATLCLTAFTSATSNNSYIATDQTQNAFNDTHFCKVDRNDHVSPSCNVTFNELN
AINENIRDDLSALLKSDFFKYFRLDLYKQCSFWDANDGLCLNRACSVDVVEDWDTLPEYW
QPEILGSFNNDTMKEADDSDDECKFLDQLCQTSKKPVDIEDTINYCDVNDFNGKNAVLID
LTANPERFTGYGGKQAGQIWSTIYQDNCFTIGETGESLAKDAFYRLVSGFHASIGTHLSK
EYLNTKTGKWEPNLDLFMARIGNFPDRVTNMYFNYAVVAKALWKIQPYLPEFSFCDLVNK
EIKNKMDNVISQLDTKIFNEDLVFANDLSLTLKDEFRSRFKNVTKIMDCVQCDRCRLWGK
IQTTGYATALKILFEINDADEFTKQHIVGKLTKYELIALLQTFGRLSESIESVNMFEKMY
GKRLNGSENRLSSFFQNNFFNILKEAGKSIRYTIENINSTKEGKKKTNNSQSHVFDDLKM
PKAEIVPRPSNGTVNKWKKAWNTEVNNVLEAFRFIYRSYLDLPRNIWELSLMKVYKFWNK
FIGVADYVSEETREPISYKLDIQ

YMR022W, 998 bp, CDS: 501-998 (SEQ ID NO 215)

AACAGTATTGGCTGTTGATTCATTGCGCTGCAGCAGTCACCTTCAATTTGTGCACCATTT TCGTATTCTGTACTTTGCGATGTAGAGTCTACTAAAATAGCGTCTCTGATAGCCATGGGT GAAGGTCTTCCTCTAGTTCTCACCTTAATTAGCATTCGGTGAGAATGCCTGCATGTTGAA GAGCGATGCCCTCTGATGCACGATGCACGCATATTTGTTCCCATTAAATATTATCATC TCTGATAGAGCTTGAAGAACTTACCAGACTGTTTCAAGTTTAAAACAAGGCGCCTCATCG CATCTACCTCACGAAGATGCAGCAGCTTATTGTCTCGAGATCCTTCTTATAACTCCTTTT CGCCATTACCCGAAAACGAGATTACAGCCTCTAAACCAAGAGCTCGAAAAGCGCCAAAGT AAACTCTGGCGTTTAGCGTACGAAGGAGTTATCCTAAAAGGAACTTCCCTAGTAATAGT GTAATTTGGAAGGCATAGCATGTCGAAAACCGCTCAGAAACGTCTCCTCAAGGAGCTTC AACAGTTAATTAAAGATTCTCCACCTGGTATAGTGGCTGGTCCCAAATCGGAGAATAACA TATTCATTTGGGACTGCCTAATTCAAGGGCCTCCAGATACGCCATACGCTGATGGTGTTT CACCCAGCATACTACAATCCAAATATTTATCCAAATGGGGAAGTGTGCATATCCATTCTAC ACTCCCCTGGTGATGATCCTAACATGTACGAATTAGCGGAAGAAGATGGTCGCCAGTGC GTGGTGCCAACATTGATGCTTGCATCTTGTGGAGAGATAATAGACCTGAATTTGAGAGAC AGGTAAAGTTATCCATTTTGAAATCATTAGGATTCTGA

YMR022W, 165 aa (SEQ ID NO 216) MSKTAQKRLLKELQQLIKDSPPGIVAGPKSENNIFIWDCLIQGPPDTPYADGVFNAKLEF PKDYPLSPPKLTFTPSILHPNIYPNGEVCISILHSPGDDPNMYELAEERWSPVQSVEKIL LSVMSMLSEPNIESGANIDACILWRDNRPEFEROVKLSILKSLGF

YMR118C, 1091 bp, CDS: 501-1091 (SEQ ID NO 217) GTCCTTCCGCTTTATATGTTTCGTTATCCTATCACATTATCAAATGACTTTGTGCCACTG TGTTTTGACAAAATTACTGTAATATAATCAATAGTATTTACATGTTTGTACCAGAAGTAC TTGCATCGCATCCAGTTCTCATGCAATATAGTTGTATACCATGTCGTTGAAAGGAACCAG AGTAAACACTTCTACCAGTATTTCTTTACGGTTCGGATCAAAACCATCACTCATTCGGTC ATTCTTACCGTACGATAAACCAAATTACAAGGAAAAGTATCCCTAATTAGAGATCACTGC ATCCGTAATAGTTTTTTTTTTTTTGGACTTTTGTAAAAAAGGGATTAGGGATACGTTG CTCATAAAAAATTGACGAAGATTTTAGATAATGGCAAATAAAAATGAAATAGTATCAAT ATACCGAAAAATTAATCACACTCAATGCGACTGTGATAGCTGATAAGTGGAGCTCAGAAA TATTCAGAAGCGTAAGAATAATGAAAGCAACCATTCAAAGAGTAACATCTGTATTTGGAG TCTCTAATGGCAGAATGGACCTTTTTTCCAAAGAATTCCACAATGGCCGCGTATCCAAAT CTGATCTTTGGTCAAGCAACAAGGAAGAGGAGCTCTTAGTATCTCAAAGGAAAAAAAGAC CGATCTCTCCTCATTTAACTGTTTACGAACCTGAAATGAGCTGGTATCTTTCCTCTTTAC ATCGTATATCTGGCGTTTTACTGGCTCTTGGATTCTATGCTTTCACAATTACTTTGGGTG TGACGACAATAATGGGAATGGATACGACTTTTCAGGATCTAAACAAGTGGTATCACGAAA AGATGCCTAAGTGGTCCCAATGGGTGGCCAAAGGCTCTGCAGCATATCTGTTTGCATTCC ATTTTGGTAACGGTATAAGGCATCTCATCTGGGATATGGGCTACGAATTGACCAACCGTG GGGTTATAAAAACCGGATCAATCGTTTTAGCCGGCACACTCGTCTTAGGAACGTATTTAC TGGCTCAGTAA

YMR118C, 196 aa (SEQ ID NO 218) MKATIQRVTSVFGVPRASVFVPRISTPFILHNYISNGRMDLFSKEFHNGRVSKSDLWSSN KEEELLVSQRKKRPISPHLTVYEPEMSWYLSSLHRISGVLLALGFYAFTITLGVTTIMGM DTTFQDLNKWYHEKMPKWSQWVAKGSAAYLFAFHFGNGIRHLIWDMGYELTNRGVIKTGS IVLAGTLVLGTYLLAQ

TATCATATTCCTAAACAAAAATGTACAGCGAATATAAAGCCAGCGTCAGTGTCTTCCTGG
AAGGTTGCGCAACTAAAGAAGTTGAAATTAAAATGGCAAGCGCTACATTTTCATCCATTT
TCACTCATCAGATGTCCAAGATTTTCGAAAAATAAATATTCTCATTTTTCTCTCAATGAA
ATAATTGTTACTAACATTGAATTTCCTCGTAACTAATTGCATTACTTCTTTAGACTTTTG
GTAAGAAGAAATCAGCTACTGCTGTTGCCCATGTCAAGGCCGGTAAGGGTTTGATCAAGG
TTAATGGTTCTCCAATCACTTTGGTTGAACCAGAAATCTTAAGATTCAAGGTTTACGAAC
CATTATTGTTAGTTGGTTTGGACAAATTCTCCAACATCGATATTAGAGTTAGAGTTACTG
GTGGTGGTCATGTTTCCCAAGTTTACGCCATCAGACAAGCTATTGCTAAAAGGTTTAGTTG
CTTACCATCAAAAAATATGTCGATGAACAATCCAAGAACGAATTGAAGAAGGCTTTCACTT
CTTACGACAGAACCTTGTTGATTGCTGATTCTAGAAGACCAAAGAACCAAAGAAATTCGGTG
GTAAGGGTGCTCGTTCCAGATTCCAAAAAATCTTACCGTTAA

YMR143W, 143 aa (SEQ ID NO 220) MYSEYKASTFGKKKSATAVAHVKAGKGLIKVNGSPITLVEPEILRFKVYEPLLLVGLDKF SNIDIRVRVTGGGHVSQVYAIRQAIAKGLVAYHQKYVDEQSKNELKKAFTSYDRTLLIAD SRRPEPKKFGGKGARSRFOKSYR

YMR174C, 68 aa (SEQ ID NO 222) MNTDQQKVSEIFQSSKEKLQGDAKVVSDAFKKMASQDKDGKTTDADESEKHNYQEQYNKL KGAGHKKE

YMR191W, 1877 bp, CDS: 501-1877 (SEQ ID NO 223) GGTTCGATACAACACTTGTGCTGGCTGGTATATCAACCATGGGTACGTCAGCATATTGAT TCGATGTGGCAGTGTACGAGAGCCATTCTGTATCGTTCGACAAAGTTTGCATGACTTCAT GTTGTTTCGTAGCAGTATTCGTTGGTCCAGATGCAGGAATGCTGGTTATAAAGTTTGTTG TTCCTGGTCCACATTCATCTTTGGATGGCGTTGTTGGTGGCGAATTTGTCTTAGGCCTTT TGTTCGCGATGTGCTTTTGGATAGCCTGGAATACGAAATCTTTGTCTTCCTGTAAAGTCG CCGTTTCCTTTAACCATTTGTGCTCCCTTCTTAAGTTATGTGACGGCTTCGTCACCATTA CCGCCTTGTGTGTACGTGTATGATTTTTTAAATATATACAACAATAATCTGTATTTTTTC AAATCCGAAATGTATCACCAATGATCACCCAGCCTGCTAAGTGCCCTCTATTGATCCGTA TATCAGCTTTTAGATCAGGCTCGAGTTTCTTGTTATATGTGCATTGCAAAAGCATAAACA AATCCTGGCAGCCGAAGCCGGCAATCCACTTCGAAACGCACGGCTGAACTATATAAATA TAAAGGACATGTGGAGAGAAGCTTCTCTTCCTTCACATTTCGCATTTCATGATCTAAAGT GGTTCTTTCACAATAGAAGAGCACCAACACGAAATATGGCTGTCGGTGGTAATAACTGGA GCATGTGGCTGCGAATGTCACGGGTCCACCTCAGGCAGATCACGAAGTCTCTGGACCGAA CGCTGATCAGTTTGAGCCATGGGAATTTTTCCCACCAATATAATCGCAATATTTTTGTCA CTTGGTGGAAGAGCCTATTTGAGGCTTCTACAGCTTTTAGGAGGGCAAGTGGTTTAACGG TATCTCCTCTCACGAGGAGGAATCGCAAGGTTTGACCATTTCAGACCTGTTCCCAATG TCAGTAAATTTGCTTCTTTTCCCAGAGTGCCCAAAGGAGCCCCAAGGGGCCTTTTTACCA ACTGGAATATGACTACATCAAAGAGATTATTAGGGCAGAGAGCTTATTCGACTTCCAGTA TCAAATTTACCCAAGAAGCCGTGAATAACATGACTATATCTTTGAGGTGTTTTTTCAACT CACTAGGCGGATTAAATCAGTGCTCCCACTCTAATTCCTGCAAAGCTTATCAGAATGCGT CTAATGTTACCTCTAAACAGGATCACGTCCAACCAGTTGCCCTTAAGAAGTTATCTCAAA AGGATATCAATTTCATTCGTAATTTAGAACTATTTAAGATAATGAAGACCCAGAATGAAG TCGTTGATGAAACAAGCGCATATTACATGGAAAAACCAGGTTCCTATATTGAATTTACCA

TTTCAGAATTTAACGTTAATGGGACATTCTCCGCACCTTTGTCATTTTTAGATCCTTCTT
TGTTAGCGGATTTGGATGAAATGATTAGAAATTACAAATACGAATTAAAATCAATATACA
GTAGTGTTGACATGATCTTGCAGAATTATGGATCATTGCCGATAACTTTTCATCGAAATA
AGATTCGAATACATTTTCCAAACTCAACTGTGGTGGAAACAGAAAAACTAATTGCAGGTC
TGAATATTGCTACGGGTGTTATTTACGCAGATACGTCTCCCGATATCAGTCTAGAAGGTA
CAAATTTGAATGCTCTGGTTAATGTTGACAATTCAGGAAGCGTATGGTCTTTTTGTTAAGG
AGCCCTCGTTTCCCTCTAGGAGCGCTTTTTCACCTATTTTATCAGATGCATCCTATGATA
CTTATGAATTGGTCTAG

YMR191W, 458 aa (SEQ ID NO 224)
MITQPAKCPLLIRISAFRSGSSFLLYVHCKSINKSWQPKPGNPLRNARLNYINIKDMWRE
ASLPSHFAFHDLKWFFHNRRAPTRNMAVGGNNWSMWLRMSRVHLRQITKSLDRTLISLSH
GNFSHQYNRNIFVTWWKSLFEASTAFRRASGLTVSPLTRRGIARFDHFRPVPNVSKFASF
PRVPKGAPRGLFTNWNMTTSKRLLGQRAYSTSSIKFTQEAVNNMTISLRCFFNSLGGLNQ
CSHSNSCKAYQNASNVTSKQDHVQPVALKKLSQKDINFIRNLELFKIMKTQNEVVDETSA
YYMEKPGSYIEFTISEFNVNGTFSAPLSFLDPSLLADLDEMIRNYKYELKSIYSSVDMIL
QNYGSLPITFHRNKIRIHFPNSTVVETEKLIAGLNIATGVIYADTSPDISLEGTNLNALV
NVDNSGSVWSFVKEPSFPSRSAFSPILSDASYDTYELV

YMR230W, 1228 bp, exon1: 501-552, intron1: 553-962, exon2: 963-1228 (SEQ ID NO 225) ATCAAATATTGATCGAGTTCATATAAAGCTAAAGAGTAGGAAATATACCATCAATGGTGA TATAATTTGGCTACGTTGTCTTCCGGTGTTTTTCAATTGATTTAAGTTACAACACTCAAA TCTGGGTAATTTGATCTTTTTTAATAATTATTTTAGTGACATATAGTTCTTAGAGTTCGC AGATTTATTTTGTCATTTTTTGGATCGGCGTCTTATAAAATCAAGACATAATACATCCGC ACATCGCGCATGTGTGGGTGTATATGCCCTTTTCACGATTTTTAAGTTGCGTCTCAAAAT AGTTTCCGAGTTGGAAGCCTGAGTTTTTCAAAACAATATAGGAATTAAAGGTATACGTCT TTGGATACATGTTATTTGAAATGGGGTAGAACTAGCACAACTGAAACCAAGAAAACACAG ACTTGTTTCAAGGTATGTTTGCATTTTTTAGGTGAAATATGCAGTGATATGCTCCGAAAT GGATAGCAAAGATGATAAATGAAAATACAATTAAATTGAACTTGAATATCATTAAAAGTG GTAGAAAACCGATTGTTTCAAAAAGATCTTTGTGGACAAGTACGGCAGTGCATGAATCCG AAAGAAAAGTGCAACCTAAGCAGAATTCCATTATTTCACGCGTCCATTTTTATAATGTTT GAACTTTTGAGTCCTTATAGAAATGCTAATATTATGATCAAAGCGATTATATCATTTACT ATCGTAAGAAATATTATTACTAACAAGGAAGATCATTGAATTACGATCGCATATCGAAAT AGAAGGTGTTGTCGTCGCTAAGAAGGATTTCAACCAAGCTAAGCACGAAGAAATTGATAC CAAGAACTTGTATGTTATCAAGGCTTTGCAATCCTTGACTTCTAAGGGTTACGTTAAGAC TCAATTCTCATGGCAATACTACTATTACACTTTGACTGAAGAAGGTGTTGAATACTTGAG ATCCCAAAGACCTCAAAGAAGATACTAA

YMR230W, 105 aa (SEQ ID NO 226) MLMPKQERNKIHQYLFQEGVVVAKKDFNQAKHEEIDTKNLYVIKALQSLTSKGYVKTQFS WQYYYYTLTEEGVEYLREYLNLPEHIVPGTYIOERNPSORPORRY

YNL054W, 3998 bp, CDS: 501-3998 (SEQ ID NO 227)
CCCTTCGCTAAATCATTAAGAGGTCATTCATGAAGTTAATTCAGCACCAAAGTTGGACTG
TTAGACACGAGATACACATTGCAGTCCAAATGTGCAGATTTTTCAGATAATTGTCGTCGC
ACAAGACTGCCCCTCCCGTCCTCAGACAGACACAAAATTAGATTTTACGTTTACATAAAG
ATGTACATAACTTGAAAAAAACGTTAATCCCTCTTAAATTTAGACCTTGTAAGTCTTCCTG
GCCACTCTTTGTGATATATTGTAGTGCAATATATTGATTCGTTCTTCTTATTTCTTTGTT
CTTAGGCATTTCCGCTTTAGAAAATTCGTTGGGTGGTTTCTGCGACGGGTATCCCCTTCG
ATTTTGCATAATGATCTTCAATTCTACAACTAAAATCAAGTAGATACAGGAAAATATTCC
ATAAATTATAGTGTAAATCGCCCTGTATACACCTTATCGTTTCATCTCAGGCAAGTTAAA
GCATTTGGGAAACGTGCTAGATGACAGAAGAAGATAGAAGCTCACTGTAGAGACAGAAA
CAGTTGAGGCACCCGTGGCAAATAATCTTTTATTGTCGAATAACAGTAATGTAGTAGCAC
CTAATCCTTCTATTCCCTCTCCCCCCACACCTTTCCCCCTACACAGGGAAATAGTTG
ATGATTCTGTCGCTACTGCCTAACACCACCACCACCTTTTTACACCCTTACACACGGGAAATAGTTG
ATGATTCTGTCGCTACTGCCTAACACCACCACCACCTTTTTACACCACAACACATAATTTTGCCCACCA

TAGATAACAATTAATGGATTCCGATGCCACGTCACATAATCAAGATCATTGGCATTCAG ACATAAACAGGCCAGGAACATCAATGTCAACGAGTGATATCCCCAACAGATTTACATTTAG AACATATCGGCTCTGTTTCATCAACTAATAATAATAGTAACAATGCCCTAATCAACCACA ACCCTCTGTCATCTCATCTTTCCAATCCGTCATCTTCATTACGAAACAAGAAGAGCTCTT TGTTGGTAGCTTCTAACCCTGCGTTTGCTTCAGATGTTGAACTCTCGAAGAAGAAACCTG CCGTCATCTCCAATAATATGCCTACAAGTAACATTGCCCTTTATCAAACAGCGAGATCGG CGAATATTCATGGTCCATCATCAACTTCCGCATCTAAAGCGTTCAGAAAGGCTTCGGCCT TCTCCAATAACACGCACCCAGCACTAGTAATAACATCGGCTCGAATACACCTCCAGCTC CTCTTTTACCTCTACCTTCACTATCACAACAAAATAAGCCAAAAATAATAGAGAGGCCCA CAATGCACGTCACTAATTCAAGAGAAATACTTTTAGGTGAAAACCTGTTAGATGATACAA AGGCGAAGAATGCTCCCGCGAATTCAACCACACACGATAATGGTCCAGTAGCAAATGATG GGCTGCGTATACCGAATCACTCGAACGCAGATGATAATGAAAATAACAACAAAATGAAGA AGAATAAAACATTAATAGTGGGAAAAATGAACGTAATGATGACACCAGCAAAATATGCA CTACATCTACTAAAACAGCGCCTTCAACCGCACCTTTGGGCAGTACAGACAATACTCAGG CTCTCACTGCTAGTGTCTCCAGCAGTAATGCTGACAATCACAATAATAACAAGAAGAAAA CCAGCAGCAACAACGGCAATAACAGTAATAGTGCATCCAATAAAACCAATGCCGATA TCAAGAATTCTAACGCCGACTTGAGCGCTTCTACCTCTAACAATAATGCAATAAATGACG ACTCACATGAGAGTAATTCAGAAAAACCAACAAAGGCGGATTTTTTCGCTGCAAGGCTGG CTACAGCTGTAGGTGAAAATGAAATTAGTGATTCTGAGGAAACATTTGTTTATGAATCGG AACAGCAACCTCCAAAACAACAGCAACAGCAACAAAATCATGGAATAACCTCAAAGATAA GCGCCCCATTGCTAAACAATAACAAAAAATTATTAAGCCGACTGAAAAATTCAAGACATA TTAGCACTGGTGCCATATTGAATAACACAATCGCGACTATAAGCACAAATCCGAACTTGA ATTCTAATGTGATGCAGAACAATAACAATCTGATGTCGGGACACAATCACCTGGACGAGT TGAGCAGTATAAAACAGGAGCCACCGCATCAATTGCAGCAGCAGCAACCACCAATGGATG TACAATCGGTAGATTCGTATACCTCTGACAACCCAGACAGCAATGTTATTGCCAAGTCGC CTGATAAGAGGTCAAGCTTAGTATCCCTATCTAAAGTTTCTCCACACTTTACTTTCATCCA CATCAAGCAACGGTAACACAATATCGTGTCCCAATGTTGCCCACAAATTCGCAGGAATTGG AACCAAACAATGATATTTCAACGAAGAAATCTCTTTCCAATTCTACTTTGAGACATTCCT CTGCTAATAGAAATTCTAATTATGGTGACAACAAAAGGCCTCTTAGAACAACAGTGTCAA AGATATTTGATTCAAACCCTAATGGAGCTCCTTTACGGAGATACTCTGGGGTACCGGATC ACGTTAATCTAGAAGATTACATCGAACAGCCGCATAATTATCCAACAATGCAAAATAGTG TGAAAAAGGATGAATTTTATAACAGCAGGAACAATAAGTTTCCCCCATGGTTTAAACTTTT ATGGTGATAACAATGTTATTGAAGAGGAAAATAATGGTGACTCGTCTAATGTAAATCGAC CGCAACACACTAACCTTCAGCATGAGTTTATTCCAGAAGATAACGAAAGTGATGAAAACG ATATTCACTCCATGTTTTATTATAATCATAAGAACGATTTAGAAACAAAACCGCTAATAT CCGATTATGGTGAAGATGAAGACGTAGATGATTATGATCGCCCAAATGCTACTTTCAACA GTTACTATGGCTCAGCATCCAACACGCACGAACTTCCATTACATGGAAGGATGCCTTCAA GATCAAATAATGATTACTACGATTTTATGGTTGGCAACAATACTGGCAATAACAACCAAT ATAGCATAATGAATGGTAGCATCCATATGAATGGTAACGATGACGTTACCCATTCCAATA TCAATAATAACGATATTGTTGGTTACTCACCGCACAACTTTTACTCAAGGAAGTCCCCAT TTGTGAAAGTAAAGAATTTTCTTTATCTTGCATTTGTTATATCATCACTATTGATGACAG GATTCATTCTGGGATTTTTATTGGCCACTAATAAAGAACTACAAGATGTAGACGTGGTAG TGATGGATAATGTGATTTCAAGTTCGGACGAGTTGATCTTCGACATCACAGTAAGTGCTT TTAATCCAGGATTCTTCAGTATAAGCGTTTCCCAAGTCGATTTTGGACATTTTTGCAAAAA GTTCTTACCTGAAGTGCGATTCTAATGGTGACTGTACAGTAATGGAACAGGAACGGAAAA TTTTACAAATAACGACAAATCTTTCGTTAGTTGAAGAGAGTGCTAATAATGATATTAGTG GTGGGAACATAGAGACGGTATTACTAGGAACCGCTAAAAAACTAGAGACACCATTAAAGT TCCAGGGCGCGCATTTAATAGGAACTACGATGTGTCAGTCTCGAGTGTCAAGCTTTTAA GTCCTGGGTCTCGTGAAGCCAAGCACGAAAACGACGATGATGACGATGATGATGGCGACG ATGGTGACGATGAAAACAATACTAATGAAAGACAATACAAAAGCAAACCAAATGCTAGAG ATGACAAGGAGGTGATACTAAAAAATGGAAGCTACTAATCAAGCATGATTACGAATTGA TAGTCCGTGGAAGCATGAAGTATGAGGTGCCCTTTTTCAATACGCAAAAATCTACGGCTA TTCAAAAGGATTCCATGGTCCATCCTGGTAAGAAGTGA

YNL054W, 1165 aa (SEQ ID NO 228) MTEEDRKLTVETETVEAPVANNLLLSNNSNVVAPNPSIPSASTSTSPLHREIVDDSVATA NTTSNVVQHNLPTIDNNLMDSDATSHNQDHWHSDINRAGTSMSTSDIPTDLHLEHIGSVS STNNNSNNALINHNPLSSHLSNPSSSLRNKKSSLLVASNPAFASDVELSKKKPAVISNNM

PTSNIALYQTARSANIHGPSSTSASKAFRKASAFSNNTAPSTSNNIGSNTPPAPLLPLPS LSQQNKPKIIERPTMHVTNSREILLGENLLDDTKAKNAPANSTTHDNGPVANDGLRIPNH SNADDNENNNKMKKNKNINSGKNERNDDTSKICTTSTKTAPSTAPLGSTDNTOALTASVS SSNADNHNNNKKKTSSNNNGNNSNSASNKTNADIKNSNADLSASTSNNNAINDDSHESNS EKPTKADFFAARLATAVGENEISDSEETFVYESAANSTKNLIFPDSSSQQQQQQQQPPKQ QQQQQNHGITSKISAPLLNNNKKLLSRLKNSRHISTGAILNNTIATISTNPNLNSNVMQN NNNLMSGHNHLDELSSIKOEPPHOLOOOOPPMDVOSVDSYTSDNPDSNVIAKSPDKRSSL VSLSKVSPHLLSSTSSNGNTISCPNVATNSQELEPNNDISTKKSLSNSTLRHSSANRNSN YGDNKRPLRTTVSKIFDSNPNGAPLRRYSGVPDHVNLEDYIEQPHNYPTMQNSVKKDEFY NSRNNKFPHGLNFYGDNNVIEEENNGDSSNVNRPQHTNLQHEFIPEDNESDENDIHSMFY YNHKNDLETKPLISDYGEDEDVDDYDRPNATFNSYYGSASNTHELPLHGRMPSRSNNDYY DFMVGNNTGNNNQLNEYTPLRMKRGQRHLSRTNNSIMNGSIHMNGNDDVTHSNINNNDIV GYSPHNFYSRKSPFVKVKNFLYLAFVISSLLMTGFILGFLLATNKELQDVDVVVMDNVIS SSDELIFDITVSAFNPGFFSISVSQVDLDIFAKSSYLKCDSNGDCTVMEQERKILQITTN LSLVEESANNDISGGNIETVLLGTAKKLETPLKFQGGAFNRNYDVSVSSVKLLSPGSREA YEVPFFNTQKSTAIQKDSMVHPGKK

YNL067W, 1076 bp, CDS: 501-1076 (SEQ ID NO 229) GACGACTATTGATGCCAGGCAAATTTTGGATTTACTGCTCCTCTTTTAAGAAGACAAGTG TATTTTCATGTTTAGCATTGCCATTTCTTCTGTGTCACACGTTGTGCTTGCCAGGAACTA TAGGAGAGACGTATACAAGCATCAATGTTACGAATGTACGATCCCGTTTGCATCTGATGT GTAAACTCATGTGGTGCACTGGTGTTGTTTCCAAGACTGCACTATTAACTGGGAATTTTT TTTTTTCTTCTAGTGAATTTTTTTTAAAGCGACGCACAGGAAAAGTGAAAATTATTTAA ACGGACGGCAAACATGAAAAAAAAAATTACCAACCATATTTCTATTTCCTTTCCCTTTAC CTATTCTCTTTTTGAAATAGTTCATTTTCTCTCTCTGAAACGACAATAAACCAAACTCTA GCCTCCAATAGTCACTAAAGATGAAGTACATTCAAACCGAACAACAAATTGAAATCCCAG AAGGTGTTACTGTCAGCATTAAGTCCAGAATCGTCAAGGTTGTCGGTCCAAGAGGTACTT. TGACCAAGAACTTGAAGCATATTGATGTTACCTTCACCAAGGTCAACAACCAATTGATCA AGGTTGCTGTTCACAACGGTGACAGAAAGCACGTTGCCGCTTTGAGAACCGTTAAATCTT TGGTTGACAACATGATCACTGGTGTCACCAAGGGTTACAAGTACAAGATGAGATACGTCT ACGCGCATTTCCCAATCAACGTCAACATTGTTGAAAAGGATGGTGCTAAATTCATTGAAG TCAGAAACTTTTTGGGTGACAAGAAGATCAGAAACGTCCCAGTTAGAGATGGTGTTACTA TCGAATTCTCTACTAACGTAAAGGACGAAATCGTCTTATCTGGTAACTCTGTTGAAGACG TTTCCCAAAATGCCGCTGACTTGCAACAAATCTGTCGTGTTAGAAACAAGGATATCCGTA AGTTTTTGGATGGTATCTACGTTTCCCACAAGGGTTTCATTGTCGAAGACATGTAA

YNL067W, 191 aa (SEQ ID NO 230) MKYIQTEQQIEIPEGVTVSIKSRIVKVVGPRGTLTKNLKHIDVTFTKVNNQLIKVAVHNG DRKHVAALRTVKSLVDNMITGVTKGYKYKMRYVYAHFPINVNIVEKDGAKFIEVRNFLGD KKIRNVPVRDGVTIEFSTNVKDEIVLSGNSVEDVSQNAADLQQICRVRNKDIRKFLDGIY VSHKGFIVEDM

YNL075W, 1373 bp, CDS: 501-1373 (SEQ ID NO 231) TCGATGGATATCCCATCCAAGAACAGGAATACTGGGTTTTTGAAGACCAGAATGGAGATC TCTGAGGAAGAAAGATGGTACGTACAATATCACGGCTTGACAATACGAGTATTGCAAAC AGTAATGGAAATGGTAATGATGACACCTCTAATCAGAGAACGGAAGCACTGGGGCGTAAG TTCTTTCAAAAAAAGATAATGTCATATATTTTACTATCTACGCAGTGAAAGAGTTCCTTC TAATGACACACTATTCACTTCGGGTAACGGATATTGTGTACTGAAAAATATAAAAAATTT GTTGGACTTGAAAGGGCATATATACTCGGTTTTATCATTGATTCAAGTGTTCCCATAAAT AATAAAACAGTTAAATCGAAATGCTAAGAAGACAAGCCCGTGAAAGGAGAGAATATCTAT ACAGAAAAGCGCAAGAATTACAAGATTCTCAACTGCAACAAAAACGTCAAATAATTAAAC AAGCGCTAGCTCAGGGGAAGCCATTGCCAAAGGAACTAGCAGAAGATGAGAGTTTACAAA AGGATTTCAGATATGACCAAAGTTTAAAGGAGAGCGAAGAAGCAGATGATCTACAGGTTG ATGATGAATATGCTGCCACAAGTGGTATAATGGATCCAAGAATCATCGTCACAACATCTC GTGACCCAAGCACTCGTCTCTCGCAATTTGCCAAAGAAATTAAACTGCTATTTCCAAATG CTGTCAGGCTGAACAGAGGTAATTATGTGATGCCAAATCTAGTGGATGCTTGTAAAAAAT

CCGGTACTACAGATTTGGTGGTATTACATGAACATAGAGGTGTTCCAACTTCTTTGACCA
TATCACATTTTCCACATGGACCCACTGCACAGTTTAGTTTACACAATGTTGTTATGAGAC
ATGATATTATAAATGCTGGTAACCAAAGCGAAGTGAATCCACATCTAATATTTGATAACT
TTACTACCGCTTTAGGGAAAAGAGTAGTCTGTATTTTAAAGCACTTGTTCAATGCGGGGC
CCAAAAAAGATTCCGAAAGAGTAATCACTTTTGCGAATAGGGGTGATTTCATTAGCGTTA
GACAGCATGTATATGTGAGAACAAGAGAGGGGAGTAGAGATTGCCGAAGTTGGTCCTAGAT
TTGAGATGAGGTTGTTTGAACTGAGGTTGGGAACTTTAGAAAATAAGGACGCTGATGTTG
AGTGGCAGTTGAGAAGATTCATAAGGACTGCCAATAAAAAAAGACTATTTGTGA

YNL075W, 290 aa (SEQ ID NO 232)
MLRRQARERREYLYRKAQELQDSQLQQKRQIIKQALAQGKPLPKELAEDESLQKDFRYDQ
SLKESEEADDLQVDDEYAATSGIMDPRIIVTTSRDPSTRLSQFAKEIKLLFPNAVRLNRG
NYVMPNLVDACKKSGTTDLVVLHEHRGVPTSLTISHFPHGPTAQFSLHNVVMRHDIINAG
NQSEVNPHLIFDNFTTALGKRVVCILKHLFNAGPKKDSERVITFANRGDFISVRQHVYVR
TREGVEIAEVGPRFEMRLFELRLGTLENKDADVEWQLRRFIRTANKKDYL

YNL096C, 1418 bp, exon1: 501-644, intron1: 645-989, exon2: 990-1418 (SEQ ID NO 233) AAACACCTACTTATAGACACGACCAAACTTTCCACAACCTTTCATCAGAGAGAAATGTTG ATCAAGTTGAATGCGTGAAAGTAGCAATTCGAAACAACAACTACCTGTCATTCTGCATAG CTCCATCCGTACCTCTTTAAATCCGTACATTATTGTTTTGCTTAATTTCAATATTTCGGA AAAAGCGAGCGCCCTGGTAAAATGTGGTTCAAGCCTGCGAGCCTTTGCTTGGTAACTCAC CAAATGCAATTCAGTCACGTTCCACACAGTTTGGGTTTCCAGCCTGGCTTTAGGGAAGAA TGGGCTCACTAGGCGTTCATAATACGCGGAGGGGAAATACCAAATGCTATTGATTATGG ACTAGACACATAACTGACCAATGTCCTCTGTCCAATCCAAGATCTTATCCCAAGCTCCAA GTGAGTTGGAATTACAAGTCGCCAAGACCTTCATCGATCTAGAAAGCTCCTCTCCAGAAC TAAAGGCTGACTTGAGACCATTGCAAATCAAATCTATCAGAGAAGTATGTTAAAAGTTAT ATAATTTGGAAGCAGCAACATTGTGATTTCTTCTAAAGGGGTTCTTTGCAGTAATTTTTT CAAAAAAGAGTGATTTTGAGCAGTATCTGTATGAAATTTTCATGTGTTCGAGAAAAATAG TAATTCCGAGAGCTGTCAATACCATGAACGTTGCGATGAGCCTTTGAACTATAAAGGCCT CCTTGGTCAGTACCAATATCGATGAATAAAATAGAAGCACGCGAAAAAGACCTTACCCCA AGGAGAAGAATCACAAACCCTTTTTTGTTATGAATGAACCAATTCAGTTACTAACTTTAT TTCAACGCTGCTTGATTCTTATTGTTTAGATTGATGTCACCGGTGGTAAGAAAGCACTAG TCCTTTTTGTCCCAGTTCCAGCTTTGTCTGCATACCATAAGGTCCAAACCAAATTGACCC GTGAATTGGAAAAGAAATTCCCTGACCGTCATGTTATTTTCTTGGCTGAAAGAAGAATCT TGCCAAAACCATCTAGAACATCTAGACAAGTCCAAAAGAGACCAAGATCCAGAACTTTGA CTGCTGTTCACGACAAGGTTTTGGAAGACATGGTTTTCCCAACTGAAATTGTCGGTAAAA GAGTTAGATATTTGGTTGGTGGTAACAAGATCCAAAAGGTTTTGTTAGACTCCAAGGATG TTCAACAAATCGACTACAAGTTGGAATCTTTCCAAGCTGTCTACAACAAGTTGACTGGCA AACAAATTGTTTTTGAAATTCCAAGCCAGACCAACTAA

YNL096C, 190 aa (SEQ ID NO 234)
MSSVQSKILSQAPSELELQVAKTFIDLESSSPELKADLRPLQIKSIREIDVTGGKKALVL
FVPVPALSAYHKVQTKLTRELEKKFPDRHVIFLAERRILPKPSRTSRQVQKRPRSRTLTA
VHDKVLEDMVFPTEIVGKRVRYLVGGNKIQKVLLDSKDVQQIDYKLESFQAVYNKLTGKQ
IVFEIPSQTN

YNL162W, 116 aa (SEQ ID NO 236) MVRCLIYFFYLVNVPKTRKTYCKGKTCRKHTQHKVTQYKAGKASLFAQGKRRYDRKQSGF GGQTKPVFHKKAKTTKKVVLRLECVKCKTRAQLTLKRCKHFELGGEKKQKGQALQF

YNL178W, 1223 bp, CDS: 501-1223 (SEQ ID NO 237) GGTCCACGTCAGTTCCACACAATAACATTTACGTAGTGTTCACGCGAAGCAGTTACATCT CAACTAACATAATTGCTGGTGAGCCTACAACACTGCATGCGTAAACGTCAACGGGATTAC CATGTTCCTTTGGAATAATCTAATTCCTCATGATTAAATGAGACTGTTTTTTGTTTCCGT AACATTTTCTTTGAGATGAGGCGCCGCGAGCCTTTCTCCCCATGGGCAGTGGTAAAT TTTCCAAATCAATGCAGCTCTTTGAAATACAACAGCATTTTTCATACATTTTAAGCAATT TCTAGTTTGTAGATATTGTTAGATTAGTTTTTGAACATTGTTTTGATAACTGAAAATAAA ACGGTGTCTTCTACGCTGAATTGAACGAATTCTTCACCAGAGAATTAGCTGAAGAAGGTT ACTCCGGTGTTGAAGTCCGTGTCACTCCAACCAAGACCGAAGTTATCATCAGAGCTACCA GAACTCAAGATGTTTTGGGTGAAAACGGTAGAAGAATCAACGAATTAACTTTGTTGGTTC AAAAGAGATTCAAGTACGCTCCAGGTACTATTGTCTTATATGCTGAAAGAGTTCAAGACC GTGGTTTGTCCGCTGTCGCTCAAGCTGAATCTATGAAATTCAAATTGTTGAACGGTTTTGG CTATCAGAAGAGCTGCTTACGGTGTCGTCAGATACGTTATGGAATCTGGTGCTAAGGGTT GTGAAGTTGTTTCCGGTAAACTAAGAGCTGCCAGAGCTAAGGCTATGAAATTTGCTG ACGGTTTCTTGATTCACTCTGGTCAACCAGTCAACGACTTCATTGACACTGCTACTAGAC ACGTCTTGATGAGACAAGGTGTTTTGGGTATCAAGGTTAAGATTATGAGAGACCCAGCTA AGAGCAGAACTGGTCCAAAGGCTTTGCCAGATGCTGTCACCATCATTGAACCAAAAGAAG AAGAACCAATTCTTGCTCCATCTGTCAAGGACTACAGACCAGCTGAAGAAACTGAAGCTC **AAGCTGAACCAGTTGAAGCTTAG**

YNL178W, 240 aa (SEQ ID NO 238) MVALISKKRKLVADGVFYAELNEFFTRELAEEGYSGVEVRVTPTKTEVIIRATRTQDVLG ENGRRINELTLLVQKRFKYAPGTIVLYAERVQDRGLSAVAQAESMKFKLLNGLAIRRAAY GVVRYVMESGAKGCEVVVSGKLRAARAKAMKFADGFLIHSGQPVNDFIDTATRHVLMRQG VLGIKVKIMRDPAKSRTGPKALPDAVTIIEPKEEEPILAPSVKDYRPAEETEAQAEPVEA

TAATCAATGTCTACAATCTGTCAGGTTCTTTCAAAAGAGAATCTGTTGAACAGCGCTTAC CATTACCTGAAATCCTAAAATGTCTGGAAGTAGTTGAAAATGATGGTGTGCAGTATGATA GAATTCAAGGTGTCAATCATAATTTACCAGACTTCAATCTTCCGTACCTTTTACTTGGCT CCACCGAATCGGGTAAATTGTACATATGGGAGTTAAATTCAGGGATTTTATTGAACGTGA AGCCTATGGCTCATTACCAAAGTATCACCAAGATTAAGTCCATTTTAAACGGCAAGTATA TTATTACTTCTGGTAACGATTCGAGAGTTATTATATGGCAAACTGTTGACTTGGTATCAG CGTCCAATGATCCTAAGCCTTTATGTATCCTTCACGATCATACTCTACCCGTGACAG ATTTCCAAGTTTCTTCTAGTCAAGGAAAATTTTTATCATGTACTGATACGAAACTCTTCA CAGTATCTCAAGATGCTACCATTAGATGCTATGATTTGAGTTTAATAGGCAGCAAAAAGA TTACAACTCCTTATTCTATCAAATCCATTGTACTGGATCCTGCTGACAGAGCATGCTATA TTGGTACTGCGGAAGGTTGTTTTTCATTGAATTTATTATAAACTAAAGGGTAATGCTA TCGTTAATCTGCTACAGTCCGCCGGAGTAAACACAGTTCAAAAAGGTAGGGTTTTTTCCC TAGTGCAACGTAACTCACTAACTGGCGGCGAAAATGAAGATTTGGATGCACTATATGCAA TGGGCCAACTTGTCTGTGAGAATGTCCTAAATTCAAATGTGTCATGCCTAGAAATATCAA TGGATGGTACATTATTGATCGGTGATACGGAGGGGAAAGTTTCTATTGCGGAAATTT **ACTCAAAACAAATCATTAGAACTATCCAAACTTTAACTACATCACAGGATTCAGTTGGAG** AAGTGACCAATCTCTTAACCAACCCTTACAGACTCGAACGTGGAAATTTACTTTTTGAAG GAGAATCCAAAGGCAAACAACCTAGTAATAATAATGGTCACAATTTTATGAAGATACCAA **ACTTACAAAGAGTTATCTTTGATGGTAAAAACAAAGGCCATTTACACGATATTTGGTATC** AGATAGGAGAACCAGAAGCAGACAGATCCTAACCTCGCATTACCACTTAACGACTTTA ATGCCTATTTGGAGCAGGTCAAAACGCAAGAATCGATATTTTCACATATCGGTAAGGTGT CAAGCAATGTAAAAGTGATTGACAATAAAATCGACGCCACTTCATCTTTAGACAGCAATG CCGCTAAAGATGAGGAAATTACAGAACTTAAGACCAACATAGAAGCATTAACTCATGCCT ACAAGGAGTTACGTGACATGCACGAAAAGCTGTACGAGGAACACCAACAGATGCTTGACA AGCAATAA

YNL182C, 555 aa (SEQ ID NO 240)
MDEQVIFTTNTSGTIASVHSFEQINLRQCSTQSRNSCVQVGNKYLFIAQAQKALINVYNL
SGSFKRESVEQRLPLPEILKCLEVVENDGVQYDRIQGVNHNLPDFNLPYLLLGSTESGKL
YIWELNSGILLNVKPMAHYQSITKIKSILNGKYIITSGNDSRVIIWQTVDLVSASNDDPK
PLCILHDHTLPVTDFQVSSSQGKFLSCTDTKLFTVSQDATIRCYDLSLIGSKKKQKANEN
DVSIGKTPVLLATFTTPYSIKSIVLDPADRACYIGTAEGCFSLNLFYKLKGNAIVNLLQS
AGVNTVQKGRVFSLVQRNSLTGGENEDLDALYAMGQLVCENVLNSNVSCLEISMDGTLLL
IGDTEGKVSIAEIYSKQIIRTIQTLTTSQDSVGEVTNLLTNPYRLERGNLLFEGESKGKQ
PSNNNGHNFMKIPNLQRVIFDGKNKGHLHDIWYQIGEPEAETDPNLALPLNDFNAYLEQV
KTQESIFSHIGKVSSNVKVIDNKIDATSSLDSNAAKDEEITELKTNIEALTHAYKELRDM
HEKLYEEHQQMLDKQ

YNL190W, 1115 bp, CDS: 501-1115 (SEQ ID NO 241) AATGCGCTCCCGTACGTCAGTGGCTGTTGCTGAAACGAGACAATTTCTCAATTCGTTTGT TTGTGTACTGTATTTGTTATCTTTACTATATATGTTGTTAAGTTTCTTTTACCAATTA GTGCTCACTTCTCGTCTTTTATTAGGTGTGTGTGTGTGCGTAATTTTCGTTTCGCTG **ATTACTTTATATAGTGTAGTTTGTTCTTGAATGTAATAAAGACTTCTGTTTTATTTTGTT** TTGTTATTTAGAAACAGTCTATCTGGTTTAACTTAAACGAGTGAGCTTAAGATAATCTGA CTTCTAACTCACACACTTTTGGAAGAACATTTATTTTTTCGACCTTCTTTCCCAAATACC CAGCGCTTTATAATTGAAATATGAAGTTCTCTTCTGTTACTGCTATTACTCTAGCCACCG TTGCCACCGTTGCCACTGCTAAGAAGGGTGAACATGATTTCACTACCACTTTAACTTTGT CATCGGACGGTAGTTTAACTACTACCACCTCTACTCATACCACTCACAAGTATGGTAAGT TCAACAAGACTTCCAAGTCCAAGACCCCAAACCACACTGGTACTCACAAGTACGGTAAGT TCAACAAGACCTCCAAGTCTAAGACCCCAAACCATACCGGTACTCACAAGTATGGTAAGT TCAACAAGACTTCCAAGTCCAAGACTCCAAACCATACCGGTACTCACAAGTACGGTAAGT TCAACAAGACCTCCAAATCCAAGACTCCAAACCACACTGGTACTCACAAGTACGGTAAGT TCAACAAGACCTCCAAGTCTAAGACCCCAAACCATACCGGTACTCACAAGTATGGTAAGT TCAACAAAACCAAACATGACACTACCACTTATGGTCCTGGTGAAAAGGCCCCGTAAGAACA ATGCCGCCCTGGTCCATCTAATTTCAACTCCATAAAATTGTTTGGTGTTACCGCTGGTA GTGCTGCCGTAGCCGGTGCCTTATTACTATTATAA

YNL190W, 204 aa (SEQ ID NO 242) MKFSSVTAITLATVATVATAKKGEHDFTTTLTLSSDGSLTTTTSTHTTHKYGKFNKTSKS KTPNHTGTHKYGKFNKTSKSKTPNHTGTHKYGKFNKTSKSKTPNHTGTHKYGKFNKTSKS KTPNHTGTHKYGKFNKTSKSKTPNHTGTHKYGKFNKTKHDTTTYGPGEKARKNNAAPGPS NFNSIKLFGVTAGSAAVAGALLLL

YNL208W, 1115 bp, CDS: 501-1115 (SEQ ID NO 243) GGTTATACACATATATATTTTTCATTTTTAATGTCTTAGCTTTTGTATCTTAGATGAA GTTTTAGTTCTGTATATCACGATCAAGATATCATACAATCATAAATTCAATTATTCTTCT GTTTCCCCTCTTGAGGCATCAAACGAGTGTTTGACTGATACACACCAACATACTAAGGCA ACTTTTCTGGCTGCCCAAAGCTGTGGCACGTATGAAACTGCTTTTCGGCTGCATAAAACA ACCATGTGGAGTTTTTACTGTATTCGCATTTCGCCCCGCTAGCATTCTTCGTTCATGCTA AAAATGAGGCGTGGGCTAATATTCAGTATTAATAATTCCGGCACCCGCACAGCCCATACC GGAAAAGGGGCTGGCTGTTGGGCTTGGCAAAAAACTCAATCTGAGCAGTCATTTATAAAG AAAGACTTTAATTTGTCTTGCTAAACACTTGTAAGCCTTCCAAATATAGATCACTTAAGA CAATCTAACAAGTGTCCAAAATGTCTGCAAACGAATTCTACTCAAGTGGCCAACAAGGTC AATATAACCAGCAAAACAACCAAGAAAGAACTGGTGCTCCAAACAACGGTCAATATGGTG CCGACAATGGTAACCCCAACGGTGAACGTGGTTTATTTTCCACTATTGTAGGTGGCAGTG CCGGTGCGTACGCTGGATCTAAGGTGTCGAACAACCATTCTAAGTTGAGTGGTGCTGG GCGCCATAGGTGGTGCATTCCTTGCCAACAAGATATCTGATGAGCGTAAAGAGCATAAGC AACAAGAGCAATACGGCAACTCAAACTTCGGAGGTGCTCCTCAAGGTGGACACAACAACC ATCACCGTCAGACAATAACAATAACGGTGGATTTGGCGGTCCAGGCGGCCCTGGCGG TCAAGGTTTCGGAAGACAAGGCCCACAAGGATTTGGAGGTCCTGGTCCACAAGAGTTTGG TGGTCCAGGTGGCCAAGGATTCGGTGGTCCAAATCCTCAAGAATTCGGCGGCCAGGTGGC CAAGGATTCGGTGGTCCAAACCCTCAGGAATTCGGGGGCCAAGGTCGTCAAGGATTCAAT GGCGGTTCACGTTGGTGAATGGCTCAACAGAGTGA

YNL208W, 204 aa (SEQ ID NO 244)
MSANEFYSSGQQGQYNQQNNQERTGAPNNGQYGADNGNPNGERGLFSTIVGGSAGAYAGS
KVSNNHSKLSGVLGAIGGAFLANKISDERKEHKQQEQYGNSNFGGAPQGGHNNHHRQTIT
TITVDLAVQAALAVKVSEDKAHKDLEVLVHKSLVVQVAKDSVVQILKNSAARWPRIRWSK
PSGIRGPRSSRIQWRFTLVNGSTE

YNL210W, 1313 bp, CDS: 501-1313 (SEQ ID NO 245) TCATAACGGGTTCTTTCAAAAAACCGTAAAAATTTGAGGTCACACCAACTAAATACAAA TTGTTTCATCACGGTGACTATATCAAGAACTTCGTAAGGAAACATTTAGAAAACTCAATA TAGTAAAGTTTCATCAGCAATCTTATCTGAGTAATATTATCTACGATCTAAATATAGGAT GATCTGCCGATTTAGGAATCGTACTGTAGATTGCTCTTGGCGACAGATATAGTGAAATAC CTTTTACAAAGTGGATACAGGTTGCCTATCACTACCGCCATTTCACTAGCAAGTAGAGTA CTATCCGCTAAACGGGACGATCGCATTTTAGCCGCCGACAGTGTTAATATAAGTAATGAA CTTGGGTTAATTTGATTACGCGTCACAGCTACTAATAAAATAAGACCGAGAGTTTTAATC CCAAATTGGTGAAACTATTAGAAGAGCTCCAGGAGGGAAAGCAATTCAACAATAAAAACA ATTTACTAGAGTTTTGCGTCCACCTTGACAAGATAAAAGGAGTCATTAGACCAAACTATG ACACTATATATTTTGTGCCTGTTGGAGGTGGATCTCCTCAATCTGGTATTTACCGACA ATATATTGGAAATATGTTTGCCCAGGTTTGTTTCAAGGGAGGACTTGAGGGTTTTTAATA ATACTTTTTACACATATCACGATAACCGCCTACGTATTCTCCAAGAAGACTTTTCTCAAT TGTTCAAAAAATCAAAACTAAGGCTTCTGTACTATGTTTTACAGTTGAGGAAATTTTTC TGACAAACCAAGAAATTTTACCTCAAAACTCAACAGTGGCAGAACTGCAAAAGAGCACTA ATAAAGTACAGACAAATGGGCCGCAACGGCACGATTTCATAGTCACTCTAGAAATAAAAC TGAACAAAACACAAATCACTTTCCTCATTGGAGCTAAAGGAACGAGAATTGAAAGCTTGA GGGAAAAATCAGGCGCCAGCATAAAAATAATACCTATTAGTGATAAAATGACTGCACATG AAAGGAACCACCTGAATCTGTTCAACAAACAATACTAATTTCGGGTGACTTATACTCAA TTGCATTAGCCGTCACCAGTATAGAGTCTGCATTAATTACTTTGGATTTATAG

YNL210W, 270 aa (SEQ ID NO 246) MSNQHSPQPFCLDTKLVKLLEELQEGKQFNNKNIFPEKALYLKLALDYSFFRKNLLEFCV HLDKIKGVIRPNYDTIYILCLLEVDLLNLVFTDNILEICLPRFVSREDLRVFNNTFYTYH DNRLRILQEDFSQLFKKIKTKASVLCFTVEEIFLTNQEILPQNSTVAELQKSTNKVQTNG PQRHDFIVTLEIKLNKTQITFLIGAKGTRIESLREKSGASIKIIPISDKMTAHERNHPES VQQTILISGDLYSIALAVTSIESALITLDL

YOL031C, 1766 bp, CDS: 501-1766 (SEQ ID NO 247) AGTTTTTTTTCTCGAGAAATTGTGAACAAAAGAAAGCAAAGACACAGAAGATGATAAGAG AGAGAAACAACGAAGAAAGAACAACAATGTTGGGGTTCACCCGAGAGATATTGACATACT GACCTTAGAAAAGGCATTACTGAGGCTACTGACTAAAGCGCGTTACATAAATGCATAGTA TATTTCTTGTTGTATACGCAGCGGCCAACTAGTGGCAGCAAGAATGTAATGAACGATTCA TCTGCAGGTTTGGAGGCCGCAACTAGATCAAAACGTAAATAGCGGGTGAAGTGTTCTGGA CGTTAGAAGTAACGTCCGCAGATCGAAGCTAAACACGGATTAGATTTCGGGTAACGGAA TTGTGATAATTAAGAAAGACCAGACTATGTGAAAAGGCCACGTAAATGATAGAGCACACA TTAGCAACTATAATAGACTAGTTTTCGCATCGCTGGAAGTTCTCGATATTGAATATCACT TCCAAGAACGCAAACTTAGAATGGTCCGGATTCTTCCCATAATTTTGAGCGCCCTATCTT CGAAATTAGTGGCGAGTACAATATTGCATTCATCCATACACTCAGTGCCATCTGGAGGCG AAATCATATCTGCAGAAGATCTTAAAGAACTTGAAATTTCAGGGAATTCGATCTGCGTTG ATAATCGTTGCTATCCTAAGATATTTGAACCAAGACACGATTGGCAGCCCATACTGCCAG GTCAAGAACTCCCCGGTGGTTTGGACATTAGAATAAACATGGACACAGGTTTAAAAGAGG CAAAACTAAATGATGAGAAGAATGTCGGTGATAATGGTAGCCATGAGTTAATTGTATCTT CAGAAGACATGAAAGCATCGCCTGGTGACTATGAATTTTCCAGTGATTTCAAAGAAATGA GAAACATCATAGATTCTAACCCGACTTTATCTTCACAGGACATTGCCAGATTGGAGGATA GTTTTGATAGAATAATGGAATTTGCGCATGATTACAAGCACGGCTACAAAATTATTACCC ATGAATTCGCCCTCTTGGCCAACCTTAGTCTCAATGAAAATTTGCCGTTAACATTGAGAG AGCTCAGTACTAGAGTCATTACCAGCTGCTTGAGAAACAATCCTCCTGTAGTCGAGTTCA TTAATGAAAGTTTTCCAAATTTTAAAAGCAAAATCATGGCCGCTCTGTCAAATTTGAATG ATTCTAACCACAGATCCTCTAATATCCTAATAAAAAGATACTTGTCCATTTTAAACGAAT TACCTGTCACATCCGAAGATCTTCCTATATACTCTACGGTTGTTTTACAAAATGTATATG AAAGAAACAACAAGGACAAACAGTTACAAATAAAAGTCCTGGAGTTGATCAGCAAAATTT TGAAGGCCGACATGTACGAAAATGACGATACAAATCTAATTTTGTTCAAAAGAAATGCTG AGAATTGGTCGTCAAATCTGCAAGAGTGGGCAAACGAGTTCCAAGAGATGGTCCAGAACA AAAGTATAGATGAACTACATACAAGAACGTTTTTTTGACACCCTTTACAACTTGAAGAAAA TTTTCAAAAGTGACATCACGATCAACAAAGGGTTTTTGAATTGGTTAGCGCAACAATGTA TTGATAAGAAACTTATCGACAGCAGACACTTGATCTTTGGCAACCCCATGGCTCATAGAA TAAAAAATTTCAGAGATGAACTCTGA

YOL031C, 421 aa (SEQ ID NO 248)
MVRILPIILSALSSKLVASTILHSSIHSVPSGGEIISAEDLKELEISGNSICVDNRCYPK
IFEPRHDWQPILPGQELPGGLDIRINMDTGLKEAKLNDEKNVGDNGSHELIVSSEDMKAS
PGDYEFSSDFKEMRNIIDSNPTLSSQDIARLEDSFDRIMEFAHDYKHGYKIITHEFALLA
NLSLNENLPLTLRELSTRVITSCLRNNPPVVEFINESFPNFKSKIMAALSNLNDSNHRSS
NILIKRYLSILNELPVTSEDLPIYSTVVLQNVYERNNKDKQLQIKVLELISKILKADMYE
NDDTNLILFKRNAENWSSNLQEWANEFQEMVQNKSIDELHTRTFFDTLYNLKKIFKSDIT
INKGFLNWLAQQCKARQSNLDNGLQERDTEQDSFDKKLIDSRHLIFGNPMAHRIKNFRDE
L

GGTGTACTTCGCTACTAAAGGGTGAAAGAAGAAGAAGAATGA

YOL048C, 106 aa (SEQ ID NO 250) MFFKVSNFTSLTLLSLIPIVGPILANQLMAPKRTFTYLQRYFLLKGFSKKQAKDFQYEHY ASFICFGMSAGLLELIPFFTIVTISSNTVGAAKWCTSLLKGERKKE

YOR010C, 1256 bp, CDS: 501-1256 (SEQ ID NO 251) ACATTTCCCAAAAAAGACATTTCTGTCCAAAAGTAGAAGGCAAGAAAACCCTGGAGGAAT CATAGGCAAAGAAAGAAGAAGAAGTTCATCTTTAAAACTACCTTTCAAGCCTTTATTC GTTCCTCGTAAAGGACACACGAAAAAAATAAACAGTACCTTGCAGAAGGAGTGCAGAGTT AGGTCGCAGGGAATCCTTGAAAGCCAAGAGTTTTTTTTTCCGTAATGATCTCCCAAAGCAA CCATCAACATTGTGGTGCAAAGTTTAGTGTAAGATGTTCTACTGAACTATCTTAATAGCT GAGCATCATGTGAGTAAACGAGTAAGCAAGAAAACAACAAGTAATGTTCAACTTTCGTA ACTACGGAAAATAATATATAAGTAGTTAACGAAATTCGAACAATGAGAGCTCTCACATAT CATCTTCTTTTCCAGTTTAGCCATTATCAGCACAATAATACAAAACACACTCGTACACTC GCTTCAACTATAACAAAAAAATGGCTTACATCAAGATCGCTTTATTAGCTGCTATCGCTG CTTTGGCTTCTGCCCAAACTCAGGAAGAAATTGACGAATTGAACGTTATTTTGAATGACG TTAAGTCCAACTTGCAAGAATATATTAGTTTGGCTGAAGATTCTTCATCTGGATTTTCCT TAAGCAGTCTGCCATCTGGTGTTTTAGACATCGGTTTAGCTTTGGCTTCCGCCACTGATG ACTCCTACACTACTTTGTACTCTGAGGTTGACTTTGCTGCTGTTAGCAAGATGTTGACCA TGGTTCCATGGTATTCTTCCAGGCTTCTACCAGAATTGGAATCCTTGTTAGGAACTTCTA CCACCGCTGCCTCTTCTACTGAAGCTTCTTCTGCTGCTACTTCTTCCGCTGTTGCTTCCT CCAGTGAAACTACTTCTTCTGCCGTCGCTTCCTCCAGTGAAGCTACTTCTTCTGCCGTCG CTTCTTCCAGTGAAGCTTCTTCTTCTGCTGCTACTTCTTCTGCTGTCGCTTCTTCCAGTG AGGCTACCTCTTCCACCGTCGCTTCCTCTACCAAGGCTGCCTCTTCCACTAAGGCTTCTT CCTCTGCTGTTTCTTCAGCTGTTGCTTCTTCCACCAAAGCCTCCGCCATTTCTCAAATCA GTGATGGTCAAGTTCAAGCCACTAGCACTGTTTCCGAACAAACTGAAAACGGTGCTGCCA AGGCTGTCATCGGTATGGGTGCTGGTGTCATGGCCGCCTGCCGCCATGTTATTATAA

YOR010C, 251 aa (SEQ ID NO 252)
MAYIKIALLAAIAALASAQTQEEIDELNVILNDVKSNLQEYISLAEDSSSGFSLSSLPSG
VLDIGLALASATDDSYTTLYSEVDFAAVSKMLTMVPWYSSRLLPELESLLGTSTTAASST
EASSAATSSAVASSSETTSSAVASSSEATSSAVASSSEATSSAVASSSEATSSTV
ASSTKAASSTKASSSAVSSAVASSTKASAISQISDGQVQATSTVSEQTENGAAKAVIGMG
AGVMAAAAMLL

YOR019W, 2693 bp, CDS: 501-2693 (SEQ ID NO 253) CATTGATCTCGAGCACAGCTGCTCTTTTCTCTCAATGAATTACGTTATATGTTAATCACA CAAGCATCAGTTTTTCATCGCAAAAGAAAATATTTAGAGTTCTTGCAATTCAGATGTACC TCAATTAATAACTCAATCACCTCCTATGTTCTTGCTGGTAGTACTGCTTTTGTCTTAATT ACTGCTGAATCAGCCTTCTAGAAGACCGTTCTGTTTCAGCCGCTCGCCCCTTTTCAAAGC TTGCGCGGCTGAGTTTTATGAGGGGCGCCTTTTTTGTGAATGGCAATCTACCATTATTAG TAGCAATATGATTTGCAGATAGATACATATATATCCTTCTGGGTTCATGTCTCGTTACCA TCCACACTAATGCATAGGACCAGAAAGAAAGGACATCGAATCCAACACGTATTAAAATAA GGACTCCTCATTAAAAAGGCTTTTAATATTCAACTTGCTATAGATCACGCACCCTTTTGG CAAGTCAACCTTAAATTATTATGATTTCTGTTTGCCCACAAAATGACTTGCAAAAATGCT ACAGAAGCCTCACATTCGATGTTCCAGGACAACAATTCGAAGAGAGAAATGAACAAAACC TTAAAAAACGGGCCAAAAAGAAAGGCAGTTTCCAACCATCTGTTGCCTTTGACACAGTGC CTTCCACCGCTGGTTATTCTTCTATAGACGACAGCAGGGAAGGATTCAAAGGTGTACCTG TTCCCAACTATTACACGATGGAAGAGTGCTATGACGATGAAACAGACTCTTTTTCGCCAA ATTTGCAATATTATTTGAGAGATACATTCCAATCATCACCTTTTCTGAATACTAGAAAAG AGAACAAATCTGAATCCAGTAGTTTTCCAATGAGATCCTCAAAGTTGTTGGAAAAGAATT CTGACATCAAAAAATATTTCTTGGTATCCAAGAATGGAAAAATAGTGAGGAGAGACTATC CAAGCACGCCAGTAATTGTCAACGAAACGTTGATGATAAACAGGTTTGAAAAGAACTGGA GGTTTACTTACCCAGAACTTATCTTCTCTGAAGAGCGTATTAAACCGTTATATAGAGGAG ATGATAGTGCACCATGTACAAAAGAACAAAAAAGAAAGCATAAAATACTTCAACAAAAGG TCGGATATCCCAATAACCCTAAGACAATAGTTTGTCACATTAACGGAAAAAAACATACGT GGGTTGCCCTAGACTGGACAGTCTACAAGTTTGCACGAAATCTTGATCACATTGTTGTCA TAACTACACTGCCAAAAATGATTTCTAACAGGAAAAAAACTGCAAAAGATGATACAGAAT

GGGCACCGGGATATCAAAAAGAAGTAATAGATCAAAAATTAAACGACATTTTTGATTATA TTTTACAGCTAGTAAAAGTGGTCAAAATATCCGTCAAAATTACTTTAGAAATAATTGTAG GCAAAATTAAAAAAGTCTGGTAGATGTCATTAATGTCCATACTCCAGATTTCTTAGTTC TTGCTACTTTAAAGCACGAGCGAAATGAGAATCTTATTACATATAAATCCAAAAAGCTGA CAGATGTCTTTCCTGTTAGTTATCCGATTCCCACATTTGTTGTTCCCTCGAAACGAATGT ATTCGTTCGAACTGAATCTACAAAGAGAAGTAAATGAACATTATGTCTCAAAAAATCATA TATCAGATATTTCTTCACATATTTCCGTAGATTCGTACGCCGAAGATTTCAAAAGGCAAG GCTACATCAAAAAGCAGTTCAACACCTCTAATGATTCCATTCCAAGAAAATTGACCGGTC TCGCCCAGCATTCAAGAAGGAAGATCACGGGTGATATAGAAAAATTACAAGACGATGAGA AAGATAGAGAATGTACTAAGGAAAAACTTTTGTTGAAGAAAATTGATATCATAATTAGAG AGTCATTGAAGTCTTCTTTAGCGATAGAGACGTTGCCTGGTAAAAATGTATCGCAGTCCA GTCACGGTGACCAAATTTCCAGCTTTAAGAATGCTTTGATAGGCAATGGGTCGAAAAACA CAAAGTTTAGAAAATCTTTAATACCATATTCTTCCTCAGAGGAACAAAATACCACAACAA CTATTAAACTCAGTAGCTCGCCTACGTCCCAAATCAAGTTTGCAACCTCTGTAAAACACA AAGATGGAAGAGCCGCCCTTGGCAAAGCCAGAAATCTGCCTGATATAAGGCACAGTATTT CCTTCGACAAAGAAAATTCCTTTGATCCATCTGATAAAAGCAGTAGTGTTGATAATAGCA TTCCTTTGAGGAAAGTTAAAAGTGCCGGTGCGTTAAGAAAAGTCAAAACTAATGACTCCT CAAGTAGTGCAGGGTCAAAGAAAGCTCGTCTAGTTTTAGTACTGTGAACACCTTCACTG CCAGTAGAAGGAATAGTAGCAGTGGCGATGTTTTTGAAAGTGATGATCGTAACGACAAGA AAAAGAAGAAGAAAAAAAGAAGAAATCATTGTTCTTATTCGGCAAAATATGA

YOR019W, 730 aa (SEQ ID NO 254)
MISVCPQNDLQKCYRSLTFDVPGQQFEERNEQNLKKRAKKGSFQPSVAFDTVPSTAGYS
SIDDSREGFKGVPVPNYYTMEECYDDETDSFSPNLQYYLRDTFQSSPFLNTRKENKSESS
SFPMRSSKLLEKNSDIKKYFLVSKNGKIVRRDYPSTPVIVNETLMINRFEKNWIKLWRQR
KLQINERLNDKKKWFTYPELIFSEERIKPLYRGDDSAPCTKEQKRKHKILQQKVGYPNNP
KTIVCHINGKKHTWVALDWTVYKFARNLDHIVVITTLPKMISNRKKTAKDDTEWAPGYQK
EVIDQKLNDIFDYILQLVKVVKISVKITLEIIVGKIKKSLVDVINVHTPDFLVLATLKHE
RNENLITYKSKKLTDVFPVSYPIPTFVVPSKRMYSFELNLQREVNEHYVSKNHMKHEHTD
VESMSSSMFKKNTISDISSHISVDSYAEDFKRQGYIKKQFNTSNDSIPRKLTGLAQHSRR
KITGDIEKLQDDEKDRECTKEKLLLKKIDIIIRESLKSSLAIETLPGKNVSQSSHGDQIS
SFKNALIGNGSKNTKFRKSLIPYSSSEEQNTTTTIKLSSSPTSQIKFATSVKHKDGRAAL
GKARNLPDIRHSISFDKENSFDPSDKSSSVDNSIPLRKVKSAGALRKVKTNDSSSSAGSK
KSSSSFSTVNTFTGGGVGIFKVFKSGSSSGNKSSSRRNSSSGDVFESDDRNDKKKKKKKK

YOR027W, 2270 bp, CDS: 501-2270 (SEQ ID NO 255) AATTTTCCCCCCGTCATAAGTTCCTATACACGGCTGGCTCTGATGGCATAATTTCATGCT GGAACCTACAAACCCGCAAGAAAATAAAAAATTTCGCCAAATTTAACGAAGACAGCGTGG TTAAAATTGCTTGTTCGGACAATATTCTATGTCTGGCAACTTCTGATGATACTTTCAAGA CAAACGCCGCAATTGACCAAACTATTGAACTAAACGCAAGTTCAATATACATAATATTTG ACTATGAGAACTGATATCTTCGTGAAGATTCGTGTAGTATGATAGAACATTCCAGAAAAA AAATTCAGATTCATCGCTCTCTTCGCTTCTCCTCCTTTAAGGAATAAAGAAAAATCA TTAAGGTATCTTGTTTAAGCCCAAAAGTCTGCTCCCAAATTCCTCACTGTAGCTACTAAA CTGCATTTACCGCTAAGGATTACGATAAAGCGATAGAGCTCTTCACTAAAGCTATTGAAG TTTCTGAAACTCCAAACCATGTTTTATATTCTAACAGGTCCGCCTGTTATACTTCTTTAA CTAAGGGTTATAATAGACTCGGTGCCGCCCACTTAGGTCTTGGCGATCTCGACGAAGCTG AAAGCAACTACAAAAAAGCCTTGGAGTTGGATGCCAGTAACAAGGCCGCCAAAGAAGGAT TGGATCAGGTTCATCGTACCCAACAGGCAAGACAGGCACAGCCTGATTTAGGGTTGACAC AGTTGTTTGCTGACCCAAATTTAATTGAAAATTTAAAGAAGAACCCAAAAACTAGCGAAA TTGGCCAAGATCTGTTTACTGATCCAAGATTAATGACCATCATGGCTACATTGATGGGGG TTGATTTAAACATGGATGATATAAACCAATCAAACTCCATGCCAAAGGAACCGGAAACCA GTAAAAGCACTGAACAAAAGAAAGATGCTGAACCACAAAGCGATTCCACTACGAGCAAGG AAAATTCCTCTAAAGCACCACAGAAAGAAGAAGTAAGGAATCCGAGCCAATGGAAGTTG

ATGAAGATGACTCTAAAATTGAGGCCGACAAGGAAAAGGCCGAAGGTAACAAGTTTTACA AGGCACGTCAATTCGATGAAGCTATAGAGCACTACAACAAGGCGTGGGAACTGCATAAAG ATATTACCTATTTAAACAACCGTGCTGCTGCTGAATACGAAAAAGGCGAATACGAGACAG CTATTTCTACCTTGAATGATGCTGTTGAGCAAGGTAGAGAAATGAGAGCGGATTACAAGG TCATTTCCAAATCATTTGCGCGTATTGGTAATGCCTATCACAAATTGGGTGACTTGAAGA AAACTATAGAATACTACCAAAAATCATTGACCGAACATCGTACTGCTGACATTTTGACCA AGTTAAGGAATGCTGAAAAAGAATTGAAGAAAGCTGAGGCGGAGGCGTATGTTAACCCTG AAAAGGCGGAGGAAGCCCGTCTTGAAGGTAAGGAATATTTTACCAAGAGTGATTGGCCGA ATGCTGTTAAGGCTTACACTGAAATGATCAAAAGGGCACCTGAAGATGCTAGAGGATATT CTAATAGAGCTGCTGCACTAGCGAAGTTAATGTCTTTCCCTGAAGCTATCGCAGATTGTA ACAAAGCCATTGAAAAAGATCCAAATTTCGTGAGAGCTTATATCAGAAAGGCCACCGCAC AAATTGCTGTTAAAGAATATGCTTCCGCTTTGGAAACACTAGATGCGGCCAGAACCAAAG ATGCTGAAGTGAATAATGGTTCTAGTGCAAGGGAAATTGATCAACTGTACTACAAGGCAA GCCAACAAAGATTCCAACCTGGTACCAGTAACGAAACCCCAGAAGAAACCTATCAAAGGG CCATGAAAGATCCTGAAGTGGCTGCGATCATGCAAGATCCTGTTATGCAAAGTATTTTGC AGCAGGCCCAACAGAATCCCGCTGCTTTACAAGAACACATGAAAAATCCAGAAGTATTCA AAAAGATTCAGACGTTGATCGCTGCTGGTATCATCCGGACTGGCCGCTAA

YOR027W, 589 aa (SEQ ID NO 256)
MSLTADEYKQQGNAAFTAKDYDKAIELFTKAIEVSETPNHVLYSNRSACYTSLKKFSDAL
NDANECVKINPSWSKGYNRLGAAHLGLGDLDEAESNYKKALELDASNKAAKEGLDQVHRT
QQARQAQPDLGLTQLFADPNLIENLKKNPKTSEMMKDPQLVAKLIGYKQNPQAIGQDLFT
DPRLMTIMATLMGVDLNMDDINQSNSMPKEPETSKSTEQKKDAEPQSDSTTSKENSSKAP
QKEESKESEPMEVDEDDSKIEADKEKAEGNKFYKARQFDEAIEHYNKAWELHKDITYLNN
RAAAEYEKGEYETAISTLNDAVEQGREMRADYKVISKSFARIGNAYHKLGDLKKTIEYYQ
KSLTEHRTADILTKLRNAEKELKKAEAEAYVNPEKAEEARLEGKEYFTKSDWPNAVKAYT
EMIKRAPEDARGYSNRAAALAKLMSFPEAIADCNKAIEKDPNFVRAYIRKATAQIAVKEY
ASALETLDAARTKDAEVNNGSSAREIDQLYYKASQQRFQPGTSNETPEETYQRAMKDPEV
AAIMQDPVMQSILQQAQQNPAALQEHMKNPEVFKKIQTLIAAGIIRTGR

YOR031W, 69 aa (SEQ ID NO 258) MTVKICDCEGECCKDSCHCGSTCLPSCSGGEKCKCDHSTGSPQCKSCGEKCKCETTCTCE KSKCNCEKC

YOR096W, 190 aa (SEQ ID NO 260)
MSAPQAKILSQAPTELELQVAQAFVELENSSPELKAELRPLQFKSIREIDVAGGKKALAI
FVPVPSLAGFHKVQTKLTRELEKKFQDRHVIFLAERRILPKPSRTSRQVQKRPRSRTLTA
VHDKILEDLVFPTEIVGKRVRYLVGGNKIQKVLLDSKDVQQIDYKLESFQAVYNKLTGKQ
IVFEIPSETH

YOR248W, 100 aa (SEQ ID NO 262) MTPLLCLHHLLQQVSVTKIQTTKMQRSSPLNRLQLPMVASQSQSLSLSPMSPLPSTLQSP QIRLHNTLLSPVHLLLPLQVTYNGTTPLRLLIRPVGEL

YOR293W, 1255 bp, exon1: 501-552, intron1: 553-989, exon2: 990-1255 (SEQ ID NO 263) AACTTTCGAAATATATACTCTGAGTTCTTGCTCCCCGTTTTGTACGATGTTCCTAATGCA AACACACGTCCTTTAAAGATCCCCTGATAGGTTTCATTAAAGGCAACTTCCATACACGTT GAAGTGCCAATTTTTTCCCTACATCCAAGCATTCTGGGTTTTGTATGGGTGTTACACCGGT TTTTCTTTTTTATTTCCAGAGAAGTACAATTTTAGGCGGGTTTCAAATTTCCCCTGTGTG CGAGAAACGCTCCGGTACGCCTAGGCTCACTCCGGTCCTTCTCCCCATTTCTATCAGCGC GATAGGCATACTGTGGGAGAGCGGCACTAGGGAGACCGGTGGGAAGCACCGTATCTAGTA ACGCACGCTCTTTTGCAAAAATATCCATTAATTGCATGTAACTTAGATTAACACTGGTAT TAAGATTTCGCAATTTTGGGCTGGATTATTAAGGTCGAGTAGCAAAGTTTAGCAAGAACA GTACGAACTAAGTAGCCAAGATGTTGATGCCAAAGGAAGACAGAAACAAGATCCACCAAT ACTTATTCCAAGGTATGTTTTAGAATAACTTTCAGAAAGCATGAAGATACACGGAAAGTC AAGCGAGGGAAGTTATGCGTATACACAGTAGCGGTAGTGTGCATTCACATACACGATGTT TCAAACACACAGATGGATACCATGCATATGAGGTTAAAGGATTTCTTATGAATATATTAG TGGATTACATAGAAGTAATTACAAGGAACCGTGTGACGACATTTTCGAAAGGACAGCACA AGGCCATCGACCCTGGAGACGTATGAAATATGGTATACGTCCTATATTTGGGCAAGAAA

YOR293W, 105 aa (SEQ ID NO 264) MLMPKEDRNKIHQYLFQEGVVVAKKDFNQAKHEEIDTKNLYVIKALQSLTSKGYVKTQFS WQYYYYTLTEEGVEYLREYLNLPEHIVPGTYIQERNPTQRPQRRY

YOR312C, 1432 bp, exon1: 501-507, intron1: 508-914, exon2: 915-1432 (SEQ ID NO 265) TATTTACAAGCTAGATAAAAAAAAAAATCAAATAGCAAGCTATTCTGTCATATCTTAAGGT CGGGACTGTTCACCCGTACATTTTACGTTTCCGACGGCGCGATGCTATCTTTGAATTTTT ATCTCTTTCAGGTAACCCCATGACCAGTAGGGCGGCTTACTACCGAAGAGAAAAATGTCC GCGGCCTAGACAGTTACTTCCCAGGCCAGGCCAGGCCACACGGACAGAGGCAGATTCCA AGTTGTTCCGCATAGTCTGTCTAGCTCTTTCTCAATTTTCCGCCAGATTCTGTCTAATTT TTTGAGGGCATTATTTTTGCAGAAGATAATAGAAGAGAACCGTAACAAAGGAATCAAGCA TTTATATGGTGAGCTCAAATTGAATGAACATATCGTGGAAATTTAAAATACTGAAGAATA CCCAATAAGTCAATGCAACCTGTGAATGTTTTTCCTGAAATACGCCGAATACTGAATACG ATTATTACCATAAATTGCTTCTAGAAGGAAGGCGGTGTACCATTTAATACTGATGATATG GTTAATATCATTTGAGAAGTCTTCACATGAGGACTATAGAACTACCATCCAGGAATTATA AATAAAGCAATATTTTTGAAATATGCAAGTTTACTAACAAGAATAAATTCTTTTTTGATT TTTATCTTTAACAGTGGCTCATTTCAAAGAATACCAAGTCATTGGTCGTCGTTTACCAAC TGAATCCGTTCCAGAACCAAAGTTGTTCAGAATGAGAATTTTTTGCTTCAAATGAAGTCAT CGCCAAGTCTCGTTACTGGTATTTCTTGCAAAAATTGCACAAGGTTAAGAAGGCTTCTGG TGTTTGGGTTAGATACGATTCCAGATCTGGTACTCACAACATGTACAAGGAAATCAGAGA CGTATCCAGAGTTGCTGCCGTCGAAACCTTATACCAAGACATGGCTGCTAGACACAGAGC TAGATTTAGATCTATTCACATCTTGAAGGTTGCTGAAATTGAAAAGACTGCTGATGTCAA GAGACAATACGTCAAGCAATTCTTGACCAAGGATTTAAAATTCCCATTACCTCACAGAGT CCAAAAATCTACCAAGACTTTCTCTTACAAGAGACCATCAACCTTCTACTAA

YOR312C, 174 aa (SEQ ID NO 266) MYLAHFKEYQVIGRRLPTESVPEPKLFRMRIFASNEVIAKSRYWYFLQKLHKVKKASGEI VSINQINEAHPTKVKNFGVWVRYDSRSGTHNMYKEIRDVSRVAAVETLYQDMAARHRARF RSIHILKVAEIEKTADVKRQYVKQFLTKDLKFPLPHRVOKSTKTFSYKRPSTFY

YOR369C, 932 bp, CDS: 501-932 (SEQ ID NO 267) CGCACCTCGTTATTGAGGTATTGCGAATGTAGCAGTTGAATAAGCAAAGACGAGGTTTGT ACATCTTGGCATATTAAATGGTTATTTCGGGGTTTTGTTTCGGCTCAACGGTGATATAAAA AGAAATCCAGTACTGTTTACCATTGTGCATCCGTACATTTGATTTGTTTACAACATCTTC CAAGCAAACTTACAATTTGCAAAATTTCATCGAATTCTCCGCAGGACATATTATAAAAGT TATGTCATCTCTTATCACAACAGGTCTATAAGTGTTCCTTGTTCAATTGTTTTTCCCAAT TCAAAACTCTTCACGGAGCAGTTTAATTATCTTACTGTCGAAGAAGTCAAAAACTAGACT ATATATTATTGAGAAGAAAATGTCTGACGTTGAAGAAGTCGTTGAAGTTCAAGAAGAAA CTGTTGTTGAACAAACTGCCGAAGTTACTATCGAAGATGCTTTGAAGGTTGTTTTGAGAA CCGCTTTGGTTCACGATGGTCTAGCTAGAGGTTTGAGAGAATCTACCAAGGCTTTAACCA GAGGTGAAGCTTTATTGGTTGTTTTGGTCAGCTCTGTTACTGAAGCTAACATTATCAAGT TGGTTGAAGGTTTGGCTAACGACCCAGAAAACAAGGTTCCATTGATCAAGGTTGCTGATG CTAAGCAATTAGGTGAATGGGCTGGTTTGGGTAAGATCGACCGTGAAGGTAACGCCAGAA AGGTTGTCGGTGCCTCCGTTGTTGTTGTCAAGAACTGGGGTGCTGAAACTGATGAATTGT

CCATGATCATGGAACACTTCTCCCAACAATAA

YOR369C, 143 aa (SEQ ID NO 268) MSDVEEVVEVQEETVVEQTAEVTIEDALKVVLRTALVHDGLARGLRESTKALTRGEALLV VLVSSVTEANIIKLVEGLANDPENKVPLIKVADAKQLGEWAGLGKIDREGNARKVVGASV VVVKNWGAETDELSMIMEHFSQQ

YPL047W, 99 aa (SEQ ID NO 270) MTEETITIDSISNGILNNLLTTLIQDIVARETTQQQLLKTRYPDLRSYYFDPNGSLDING LQKQQESSQYIHCENCGRDVSANRLAAHLQRCLSRGARR

YPL090C, 1605 bp, exon1: 501-506, intron1: 507-900, exon2: 901-1605 (SEQ ID NO 271) GTAAGCAGAAGCCGGAAGAAGACAAGAGGTTCATTCAGAGAAAACATCCGTACATTCGAG TTCTCATTGAACCCATACATTTCAACTATTTTTACATAGTTCGTTTTTCATGTGTAAAAT TGTCATCGACGCGCCGGAGCATCGGAAAGTTGGAACGTGCGCGATTGCACCAATCCCACT GGGGCCGTGCATTCTGTAGGCAGGAAGCCACTGGACACTCTGCCCGTTCCCACTTGGAAG ATTGGCGTAATTCCACGCTCCTCTATCGATTCTAGCGGGAAAGTTATCTCTCCTGGTAAG TAGGAACATCATGATGCTGCAGTTTCTTTGAAATTTCATATACAGTGTTACCAAGGATAA AGTGGTTAATGCTTATTCGTCATTGAATTTTTATATTTTGCTTAAGAGAAGTGACAAAAGA GTGAAGACAGACTATACATCATGAAGGTATGATTATGATACTATTATTGAGGGGCAACA ACCAGACGTCGTAAAGATTTTAGAAATTTTTTATGGAAAGAAGAGCAGGAAGACTACCATAT ACTAATTGATGCGTTTGTGGCGTTATTTTTAAACAAACAGAGCGGGTTTACATATACTGT TACTACAAACCGTGAAATTGAAGCAGTTCATATACTTGGAGTATAGTCAATAAAAGACAA GCTTTTTCATCTTCCACTTAATAATTTCTCTAGAGTAATAAACTTCACCCTATTCAAACA TTAATTTTGCAATAGTATACTAACAAATTTTCTTAATAACCTGTTGAAAATTTAAAATAG TTGAACATTTCTTACCCAGTTAACGGGTCTCAAAAGACCTTCGAAATTGATGATGAACAC CGTATTCGTGTTTTCTTCGACAAGAGAATCGGTCAAGAAGTCGATGGTGAAGCCCGTTGGT ATGAAGCAAGGTGTTTTGTTGCCAACTAGAATCAAGTTGTTGTTGACCAAGAACGTTTCT TGTTACAGACCAAGACGTGATGGTGAAAGAAAGAGAAAGTCCGTCAGAGGTGCCATTGTT GGTCCAGATTTGGCTGTCTTGGCTTTGGTCATTGTCAAGAAGGGTGAGCAAGAATTGGAA GGTCTAACTGACACTACTGTTCCAAAGAGATTGGGTCCAAAGAGAGCTAACAACATCAGA AAGTTCTTCGGTTTGTCCAAGGAAGATGACGTTCGTGATTTCGTCATCAGAAGAGAAGTC ACCAAGGGTGAAAAGACTTACACCAAGGCTCCAAAGATCCAAAGATTGGTTACTCCTCAA AGATTGCAAAGAAAGAGACACCAAAGAGCTTTGAAGGTCAGAAACGCTCAAAGA AAGGCTGAAATCAGAAAGAGAAGAGCTTCTTCTTTGAAGGCTTAA

YPL090C, 236 aa (SEQ ID NO 272) MKLNISYPVNGSQKTFEIDDEHRIRVFFDKRIGQEVDGEAVGDEFKGYVFKISGGNDKQG FPMKQGVLLPTRIKLLLTKNVSCYRPRRDGERKRKSVRGAIVGPDLAVLALVIVKKGEQE LEGLTDTTVPKRLGPKRANNIRKFFGLSKEDDVRDFVIRREVTKGEKTYTKAPKIQRLVT PQRLQRKRHQRALKVRNAQAQREAAAEYAQLLAKRLSERKAEKAEIRKRRASSLKA

YPL137C, 4331 bp, CDS: 501-4331 (SEO ID NO 273) ACGCCATACTCCAAACAATAACAATATTAGACCTAGCCAATTGATACCCATGAGCGTGCA GTCATTGCCATGGATTATTCATCTCTTTTCGCTGTTCTCTTTTCTAAGTTTGTCATC ATCATGCCTTCACTTTTGCCTTTCCATCTTTCTTTTTGCTGCAAAATAAAGGGAAGAGGG GAGCGTGTTTTGGGAAATAACACCACAGCATAAAGCTAAAATTCAGTTTATATAATCTAT GTGGAGATAGCATCTAGGTTATGATAACTAACACCGAGTTCGATGTGCCCGTAGATTGGT TGTATAAAGGTAAGAGTAGACGGAAGACAAATACGAAGCCATCGAGGCCTTCTACGTCGC CAGCCTCCTCTTCATCTACGTCCTCTTCGAAAAACGGAGACAATAGCACGAGTGGTAACA GGTCTAGCAATGATAAGCCTCGTGCGAGGTCGTCATCTGTATCCAATGCAGCACTTTGTA ATACTGAGAAACCAGATTTGAAGAGGAACGATGGTAATACCTCTGCATCAGACACTGATA ACATACCGCTACTTACTCCTATTAATAGCGGTAACCGGAGCGATTCCGCTGACATTGATA ATCCGGCTACCGTAGACGCCATAGACCTTATAGATAATGATGACAACGGCTCAAGTACTC AATTTGTAAGGAAAAAACGTTCCACTTCTATATCCAATGCTGTGGTCTCGTCCAAACCAA GACTGGCCAGTTCTGCCATAAACGCCACCGCATCTTCTTCTGTTGGCAAGGGAAAGCACC CGCCAATTTCTTCACCATCTAATGCTACTCTCAAGAGAAGCAACTCGACTAGTGGAGAAA AGACTAAAAGGTCGATTTTTGGATCTTTGTTTAGCAAACGGTCTACCTCTTCTTCAGCTT CCACTGCCAAGAAACCATTACCTGTTGTTAATACTAGCACGACTGAGAATGAGTCTGGTG GCATTAAAGCAGTTGCGACTCCTGATCCACGGGTGAAGGAGATATCATCACCAATGAGAG GAGTGGCACCAACAGCTAGCAAGCCACAGACACCTATACTCCCCTCCCCTGCACTTGCAG TAAAAGACCTATCTACAGTTTCATTGAAAAGGGTCTCGTTTGCCGTCGATAAATTCGAAT CCGATCCTCCCAACAACTTCCTTCAAGAACCCCAAAAAAGGGAAACATCCTTATCCCTG ATGACATGATAAGCGAGGTTCCTTCTATTTCCGTGGGTATTTCCAGTAGCAACCAATCGG CCAAGTCAACCAATTCCAACATTAAGGGACCGTTGTACACTAAGAAGTCTAAAGAATATA TACTCGCCCTGGAAAATCAAAAGTTGGCTTTAAGGGAGGCTGCTAAGCATCAGCAAGAAG CTCATTTTGCTGCTAATAGAATAGCCTTTGAAGTAGCCAATTTTAAGACTGCTTCGGATG TGTCACCTCCAAATGTTGAAGCTGATCGGGAGCTTGAGAATAATAAACTTGCAGAAAACC TCTCAAAAGCCGGCATTGATAAGCCCATTCATATGCATGAGCACTATTTCAAGGAACCTG ATCAAGATAAGTACCAAGACGGTCATTCTATTGAAAATAACGAAGTTACGCTGGATGTTA TTTACACAAGATGCTGCCATTTAAGGGAAATTTTACCCATTCCGTCTACCCTAAGACAAG TAAAGGACAAGACAGCTCCCTTGCAAATATTGAAGTTTTTGAACCCTAAGCCTACCTTGA TCGATATTCTTTCCTTTTGTGATTTCATCACCATTGCTCCCATTCACACGATTGTTTTCG ACAATGTAGCTTTAAACCAGGATATGTTCAGAATAATTATTTCTGCTTTGGTAAACTCCA TATGTAAGTTCCTTTTGCTAAACAAATCACTGAACAAGCTCGACATTTCCCAAACGAAAA TCAAATCTGACCTTGCTGAATCACTATATCGCCATAACATGGATTGGAACTTGTTTACTG ACGTCTTGTCTCAGAGATCTCACAAACCTATAGAAGAATTGTTATTCAATGGTATTCAAT TTAGCAAAATTCCTTACTCATGCTTTGCACGTTTACTGACATCCTTTGCTACCCAAAAA ACTTTCCAGAATCGGGCATCAGGCTTGGTTTAGCAGGTGCCACTACTTCCAATATCTCTC AGGATTGTCTGAAATTTATCTTCAATTGGATGTCTCAATATAACGTCCAGGGTGTGGATC CATATGATAACTTAAGATATTTCATTTTGAACAGCACTAATATTTCGACTTCTTATGATT TAGCTTTGCTCTTGAAATATCTTTCTAAGTTGCCTAACTTGATTTTTTTGGATTTGAGTA ATTTGTCGCAATGCTTTCCTGACATTTTACCCTACATGTACAAGTATTTACCAAGATTTC CGAACCTGAAGAGGATACATTTGGATAGCAATAATTTGACATTAAAGGAACTAGCTGTCG TTTGTAATATTTGATTAAGTGCAAATCGCTCTCGCATGTGTCAATGACTAATCAAAACG TTGAAAACTTCTATCTAATGAACGGCACAGATTCTCCCGTTCAACAAACTAACACAGACG GCGACTTGGATAGTTCGAGCACATTGGACGTTAAGGGCCAATTTGCTAAAAATAGTTTTT CATCCACACTTTACGCATTTGCTAGAGACTCTCCAAACTTGATTGGTTTAGATTTTGACT ATGATTTGATATCAGAAGAGTTCAATCAAGAATAGCACTGTGCTTGATGAGAAATATGA AACGGACCATGGATTCGACTTTCCAGTTAGATGAATTGGATTCGCAAGATGATTTGCTAT TCGATGGCTCTTTAGTAACTATGACCGCTGAAAGTGTTTTAGAAAAACTGAACTTGTTAA GCGATAAGAGTACAAAAGGTCAAAAAAGACACCACGAAGAGATATTTGCTGAAAAAATATA

TTGAAAAGTTCCATATCTTGCACCATAATGTTCAGCATACAATAGATACTATGTTCGAAA AAAGGAAATCAGGTGAATTGCCATTGCAAGAAAAAGAAAACCTTGTAAGATTACTCCTTT TGGAACAAAACTTATGCAATATACTAGAATTGTTTTCGCATAATCCGAATCTGAATGATG TCCTTGGATCCAGCAGGATGATTCGAAGGAAAGTGTTGACTCCAGCGAAGATTCAAAAT TACCAGCATTGAAGCACGTTGAATCCGGATACCATGTTCCCGAAGAAAAAATACAACCTG AGAATGATGTAATTACAGCAAGACCACATTTAATGGCCACCGATTCTGGTAAAACTATTG ACGTTTTCACAGGCAAACCATTGGTGTTCAAGCATACATCATCTAGTACTTCTGTAGGTT GTAAAAAGCAGGAAGAAGAAGAAGGTGAACTACATAAATGGGGTTTCTTCGTTCAGCAGC AGAGGTCTTTATACCCTGAAAATGAATCAACAAGGCAGACACCTTTTGCATCAGGTGATA CGCCTATCAACACAGAAACAGCTGGTAAGTCAACTTCATCTCCTTCAGTTTCAACTTCTA ACAATGAAACTGCTACCACTAGTTTATTTAGCCCAGCTAATCCTAAGATTTTACCAAAAA TTCCATCCGGTGCTGTCTTAAGATCGGCAATCATGAAGGCTAAAGGTATTGATTCTATCG ATGATTTGATTCAGAACGTTAACTCCAACAACATAGAATTGGAGAACATTTATGGTGAAT CCATTCAGAATAGCGCTTCGACATTTACACCAGGCGTGGATTCTGATGTATCTGCGCCCA ATACCGATAAAGGATCCGTAGAAACATTGCCTGCAGTCTCAACTGACGACCCAAATTGTG AAGTCAAAGTCACTGCTACCTATGACAAACTATTAAATAATTTGTCGATGGAGAGGTCAA TCAGACTTTGA

YPL137C, 1276 aa (SEQ ID NO 274) MITNTEFDVPVDWLYKGKSRRKTNTKPSRPSTSPASSSSTSSSKNGDNSTSGNRSSNDKP RARSSSVSNAALCNTEKPDLKRNDGNTSASDTDNIPLLTPINSGNRSDSADIDNPATVDA IDLIDNDDNGSSTQFVRKKRSTSISNAVVSSKPRLASSAINATASSSVGKGKHPPISSPS NATLKRSNSTSGEKTKRSIFGSLFSKRSTSSSASTAKKPLPVVNTSTTENESGGIKAVAT PDPRVKEISSPMRGVAPTASKPQTPILPSPALAVKDLSTVSLKRVSFAVDKFESDPPOOL PSRTPKKGNILIPDDMISEVPSISVGISSSNQSAKSTNSNIKGPLYTKKSKEYILALENQ KLALREAAKHQQEAHFAANRIAFEVANFKTASDAGGKLTEKSSEGTITKQREEVSPPNVE ADRELENNKLAENLSKAGIDKPIHMHEHYFKEPDQDKYQDGHSIENNEVTLDVIYTRCCH LREILPIPSTLRQVKDKTAPLQILKFLNPKPTLIDILSFCDFITIAPIHTIVFDNVALNO DMFRIIISALVNSTVLDKLSLRNVRIDQDGWKLLCKFLLLNKSLNKLDISOTKIKSDLAE SLYRHNMDWNLFTDVLSQRSHKPIEELLFNGIQFSKIPYSCFARLLTSFATQKNFPESGI RLGLAGATTSNISQDCLKFIFNWMSQYNVQGVDLAFNDLSTMIKPMVGKLSALSYDNLRY FILNSTNISTSYDLALLLKYLSKLPNLIFLDLSNLSQCFPDILPYMYKYLPRFPNLKRIH LDSNNLTLKELAVVCNILIKCKSLSHVSMTNQNVENFYLMNGTDSPVQQTNTDGDLDSSS TLDVKGQFAKNSFSSTLYAFARDSPNLIGLDFDYDLISEEIQSRIALCLMRNMKRTMDST FQLDELDSQDDLLFDGSLVTMTAESVLEKLNLLSDKSTKVKKDTTKRYLLKKYIEKFHIL HHNVQHTIDTMFEKRKSGELPLQEKENLVRLLLLEQNLCNILELFSHNPNLNDVLGSSRD DSKESVDSSEDSKLPALKHVESGYHVPEEKIQPENDVITARPHLMATDSGKTIDVFTGKP LVFKHTSSSTSVGCKKQEEEEGELHKWGFFVQQQRSLYPENESTRQTPFASGDTPINTET AGKSTSSPSVSTSNNETATTSLFSPANPKILPKIPSGAVLRSAIMKAKGIDSIDDLIQNV NSNNIELENIYGESIQNSASTFTPGVDSDVSAPNTDKGSVETLPAVSTDDPNCEVKVTAT YDKLLNNLSMERSIRL

YPL159C, 1262 bp, CDS: 501-1262 (SEQ ID NO 275) AAACAAAGCGATTTGAGTATTACGTTAAGATCTCCATTTGCTATGCTAAATCCTGCCTAC TCAAACAGCATTATATCGCTACCAACAGGTGTGGTCAAGAGGTCATTGACTCTTCCTGTC TCAACGTATCAACCATAAGAACCATAATCATAATAATTGTTTACCTTAATGGCGATATCG CCTTTTATCACCATCGACGATAACAAACGCCTATTCTGTCTACCGTTTCTTTTTTCGCT CGCAATATCAGAATCGTTTATCCCAAAGGGTAGTTATAGCAACTATTTAAATAACTTAGA TGTTTCTTTAACTTATTCCGTCATACGTACACAAACACCCGCTAGATATAGCACTCCTTG CTGTCGAACATTATAAAGGTGCTTTTAAAACTACTAATCGTATATTCAGCAGGTCAGAAC GCAAAGTCGGACGATAAACTATGTTGAAGCTAGCTCGTCCATTTATTCCGCCTTTATCAA GGAACAATGCCATTTCTTCAGGAATAGTTCTCACTTCTAGAAGATTTCAGTCTTCCTTTA CGTTCTTAAGTAACCAGTCTTTACTATCTAAAAATCAAATGAAATCCAAAAGAAAAAAGG GCAGTAAAAAGGCAGCGTACCATCGTCAACCCCCGGAACACGAACATACTGCACCACTTA TAAAGCAAAACAAGACAATCACAAAGAAAGAACATAGCGATGTGAGAGGTTCTCATTTAA AAAAGAAAAGAAGCGATTTTTCGTGGCTACCAAGAGTACCATCCACCTCACATTTAAAGC AGAGTGACATGACCACAAATGTACTCTATTCTGGATATAGACCCTTATTCATCAATCCCA ATGACCCGAAGCTAAAGGAAGACACCGGAAGTACGTTATACGAATTTGCGATGAAGCTTG AAGATTTAAATGAACCTCTATCACCATGGATTTCCTCTGCCACTGGACTTGAATTCTTTT CAGAGTGGGAGAATATACCTAGTGAACTACTGAAAAATTTGAAGCCTTTTCATCCACCTA AGGAAAAATCAATGAACACAAATGAGCTTATTCATGTAAGTGCTAAGAGAAATACATTAG TTGACAATAAAACAAGTGAGACGCTTCAGCGGAAAATGGATGAATTTTCAAAGAGAAGAG GAAAGGGGAGAAAAAAGTCAGTAGTGACGTTGCTCCAAATGAAGAAAAAACTTGAGGGAT GA

YPL159C, 253 aa (SEQ ID NO 276)
MLKLARPFIPPLSRNNAISSGIVLTSRRFQSSFTFLSNQSLLSKNQMKSKRKKGSKKAAY
HRQPPEHEHTAPLIKQNKTITKKEHSDVRGSHLKKKRSDFSWLPRVPSTSHLKQSDMTTN
VLYSGYRPLFINPNDPKLKEDTGSTLYEFAMKLEDLNEPLSPWISSATGLEFFSEWENIP
SELLKNLKPFHPPKEKSMNTNELIHVSAKRNTLVDNKTSETLQRKMDEFSKRRGKGRKKS
VVTLLQMKKKLEG

YPL175W, 1940 bp, exon1: 501-514, intron1: 515-568, exon2: 569-1940 (SEQ ID NO 277) ACGTTATTTTCAAAACACATACGAAATCGCTGGACTTTCTCACTAAAGGCTTCCGGAGCC TGCGGTTCTTCCATCCCCATCTTCCACATATACCGGGGGTTCTGATGGCATTCCTATA GCTTGCTCAAAGTCCTGCGAGTTTAGCTCATCTTGTGAGTTATTTGCTGGTTCTTCAACA TTCGGAAGAGTAGTGTAGCCCCTAGTATTCACCATATCCTTTGTATACTCATATGCGAAC TTGTCTAATACAATGTATACCAAAAATAACAGCTTGAAAAAAATCTCAGGGTCTTTTCAT TGAATAATCTCATTCTGCTATTTTAAGTTTTTCGTTTGCAACCCGAGACTGTCGAGCTAG AAAATTTCATTGATACGATTTAAAAATAATCGATGCCAGTAATAGCCTCAAAAAACTTAT GCAAAAATACGAGATACTATAAACTACAGCTTAGCTAACTCTAACATTATTATATAAAAC AATGGGCTTCAATATAGCGTATGTCTAGCTCACAGCATGTGTTCCAAATACATTAAAGAA GATCTCTTTTGTTGATACTAACCAGTAAAGTTGAGAGTTATAACAATGAAAATAGGA CGCAGAAACTAATCGATTTGGGCCATTCTGTCGTCATTATAACTCACGCTTACAAAGATC GAGTCGGCGTACGACATCTTACCAACGGTCTAAAGGTCTATCACGTACCATTTTTTGTGA TTTTCAGAGAAACCACTTTCCCCACTGTTTTTTCAACATTTCCAATAATAAGGAATATTC TTCTCAGAGAGCAGATCCAAATTGTTCATTCTCATGGTAGCGCTTCCACGTTCGCTCACG AGGGAATTCTTCATGCTAATACTATGGGATTGAGAACTGTGTTCACGGACCATTCACTCT ACGGTTTTAATAACTTAACGTCGATTTGGGTGAATAAGTTGCTAACATTTACCTTGACAA ACATAGATCGGGTTATATGTGTTTCTAATACATGCAAAGAAATATGATTGTTAGAACAG AATTAAGTCCTGATATAATCTCAGTAATTCCCAACGCAGTGGTGAGCGAAGATTTCAAAC CAAGGGATCCTACTGGTGGCACCAAGAGAAAACAAAGTAGGGATAAGATAGTGATCGTGG TTTGTTCCTCACATGAAGATGTCGAATTTATAGTAGCGGGCGATGGTCCAAAGTTCATAG ATTTTCAACAAATGATTGAAAGTCATAGACTACAAAAACGTGTGCAACTCTTAGGCTCTG TTCCACATGAGAAAGTCAGGGATGTATTATGTCAAGGTGACATATATTTACACGCTAGTT TAACAGAAGCATTTGGTACAATTCTAGTTGAGGCCGCATCTTGTAATTTGCTAATTGTAA CGACACAAGTCGGAGGAATTCCCGAAGTGTTACCAAATGAGATGACTGTTTATGCAGAAC AGACATCCGTTTCTGACCTTGTTCAAGCAACAAATAAAGCTATCAATATCATAAGAAGTA TAGCCAAAAGGACAGTAGAGATATATACTAATATATCTTCTACTTCTTCCGCTGATGATA AAGATTGGATGAAAATGGTAGCAAATCTTTACAAAAGAGATGGAATCTGGGCTAAACATC TTTATCTGTTATGTGGAATTGTAGAGTACATGCTTTTTTTCCTCTTAGAGTGGCTATACC CCAGGGATGAAATCGATCTAGCTCCAAAATGGCCCAAGAAAACAGTGTCTAACGAGACGA AGGAAGCAAGAGAAACTTAA

YPL175W, 461 aa (SEQ ID NO 278)
MSSSHKVESYNNENRMLCDFFYPQLGGVEFHIYHLSQKLIDLGHSVVIITHAYKDRVGVR
HLTNGLKVYHVPFFVIFRETTFPTVFSTFPIIRNILLREQIQIVHSHGSASTFAHEGILH
ANTMGLRTVFTDHSLYGFNNLTSIWVNKLLTFTLTNIDRVICVSNTCKENMIVRTELSPD
IISVIPNAVVSEDFKPRDPTGGTKRKQSRDKIVIVVIGRLFPNKGSDLLTRIIPKVCSSH
EDVEFIVAGDGPKFIDFQQMIESHRLQKRVQLLGSVPHEKVRDVLCQGDIYLHASLTEAF
GTILVEAASCNLLIVTTQVGGIPEVLPNEMTVYAEQTSVSDLVQATNKAINIIRSKALDT
SSFHDSVSKMYDWMDVAKRTVEIYTNISSTSSADDKDWMKMVANLYKRDGIWAKHLYLLC
GIVEYMLFFLLEWLYPRDEIDLAPKWPKKTVSNETKEARET

YPL180W, 2900 bp, CDS: 501-2900 (SEQ ID NO 279)

CTCAATGGGAATTGAGTGAAGATCAGTCTGATCGAGAGGAATTTGTACGATTCGTGGAAA ACCAGCATTTCGTAGAAAAAGTTGATACGATTTACAACGGTTATAATGAAAGTCTATCAA TGATGGACGACCTGACTAGAGAGTTACTACTATGGGAGAAAAAATATTCAAATAACACTA ATGCCATTCAATAAACGCAAAACACTGCAATATTATTCTCAACCAAAGTATAACTGTAAT GAGGCGAACAAACACATCTATACATATATATACATCTATATGGATATAAAAACGACTAAT TCAACGTTGTTTTTATCAACCGAGCTTACTCTTGTACGGGTAACCGCAAGGATAGCTAGT TGCGGATGGTATAGCGATTTGGCTGGCACGATGATTAAGGAATCCAAACATCTAATGGAC TAGCACATTCTATCGATTTACGGGTCAGGTAAACATAGATATTGGGATATATCATATATC CTTACTGAGTAACTATAATTATGGTTCATCGAGGAAGGACTTTGAAGTCAGACACTGATG TAACATCTCTTAATGCGTCAACAGTATCACACCAGTCAAAGCCATTTAGACAGTTTTCGA CTAGGTCGAGAGCAAAGAGTAACGCAAGCTTCAAAGGTTTGCGTAGAGTTTTAACACATG ATGGCACCCTGGATAATGATTATTTAATAAGCACAACGTTTCTCAGAAATGCAAGAGTT CTGATGCACTTTTCAGAAAGCGAACGATTAGTGGGTTGAATATGACAGCTTTAACAAGAG TAAAGTCCAATCAAGGAAAAAGATCAGCATCCTTTCATAGTCCGGTGCATAATACGCTGC TCAGTCCAAAGAACAGCAGTCATTCTAATACTGGAACTGCTGGTTTCGGCCTGAAACCAC GAAGAAGTAAAAGTACCCAATCTGTTCTGAGTCTTCGAGATGCGCAAGAATCTAAAAAGA GTGAATCTACTACTGACGAGGGGGGGAATGTTTTTCGGAAGACAACATTGAAGATGGAA AGCAATTAAATCAGAATGAATTACAATCCCCGGATTCAATAGATGAACAAGAAGAAGATA AATCAGGTACTGATGGAAAGGAAAATCATAGAGCTGTATCCTTACCATTACCTCATTTAT CTTCCAATAACTATTTCGGAGAATCAAGCCATTCTATAGAACATCAGAAAGATGGAGAAA CATCTCCAAGCTCAATTGAAACAAAACTGAATGCAACAAGTGTAATCAATGAAGAGGGGC AATCAAAGGTGACGAAGGAAGCTGATATTGATGACTTGTCCAGCCATTCTCAAAATTTGA GGGCCTCATTGGTTAAAGCGGGCGATAATATATCAGAAGCACCATATGATAAAGAAAAA AAATTCTTGATGTTGGTAATACCTTAGCTGCACATAAAAGTAATCAAAAACCAAGTCATT CAGATGAACAGTTTGATCAGGAAGATCACATTGATGCCCCCTAGGAGTAATTCATCAAGAA AAAGCGACTCGAGCTTTATGTCTCTTAGGAGACAAAGTTCTAAACAACACAAATTATTAA ACGAAGAAGAAGATCTAATCAAGCCTGATGATATTTCTTCCGCTGGTACCAAGGATATTG AAGGGCATAGCTTACTGGAAAATTATGCGCCTAATATGATTCTCTCCCAGTCGACTGGAG TTGAACGTAGATTTGAAAATTCATCATCCATCCAAAATTCGCTTGGGAATGAAATTCATG ACTCGGGTGAGCATATGGCTTCAGGTGATACTTTTAATGAACTGGATGATGGCAAATTGC GCAAGAGCAAGAAAATGGTGGAAGATCTCAACTTGGCCAAAATATACCGAACTCTCAGT CTACTTTCCCCACCATTGCTAACATCGGTAGTAAAGATAATAATGTACCACAGCACAACT TTTCGACCTCCATATCGAGTTTAACCAATAATTTGAGGAGAGCTGCTCCTGAAAGCTTCC ATGGTTCAAGAATGAATAATATTTTCACAAGAAAGGTAATCAGAATCTACTTCTGAGAT CCAACGATCTCAACAAAAATTCTGCAGCCCCGGCCTCTCCATTGTCCAACGAACATATTA CATCTAGTACGAACTCCGGTAGCGATGCAAACAGACAATCCAACTCAGGTGCCAAATTTA ATAGCTTCGCCCAGTTCCTTAAATCAGATGGGATTGATGCAGAATCAAGAACACAAAGAA **AATTATGGTTGCAGAGGGAGAATTCTATTATGGACTTAAGTTCACAAAATGACGGTAGTG** ACTCTATCTTTATGGCAGGAAACATTGATGCGAAAAGGGAGTTTGAGAGAATATCCCATG AATACTCTAATGTAAAAAGATTTTACAACCCATTAGATGAAGCATTGTTGAGAGTACAAC CTATAATAACGGGAAATGCAAATAATATCAGGAAAAAAAGCCATAACGATGCTCAGTCAA TCGCACATTCTAGCAGTGATACAGATCATAAGGATGAGGACGATTTGCTCTTTACTAACT ATGACAAAAATTTGATGATCTTTATCCACATCTTGCAAGTGCAAAGATTCAGGCAGTGT TGTCCGGTATATGGAAAAGCGAAAGTTACTTATTTAACAAGGATGTTAATCCAATCAACA AGAATAGGACAACGAGTACAAACCACAGCGTTGGCCACACTGCTTCACAGAATGCACGTA ACTTGCTGAGGGCCCGATGGGTTCCAGCACGACTTTGCACCACCAACGCGTCATTAACT CTCTGCAGCCGACTACGAGGCAGTGAATCGCAGGATGGAAAATGTGGGCTACATGCATA CACAGCCACAACAAAGGTGA

YPL180W, 799 aa (SEQ ID NO 280)

MVHRGRTLKSDTDVTSLNASTVSHQSKPFRQFSTRSRAKSNASFKGLRRVLTHDGTLDND
YFNKHNVSQKCKSSDALFRKRTISGLNMTALTRVKSNQGKRSASFHSPVHNTLLSPKNSS
HSNTGTAGFGLKPRRSKSTQSVLSLRDAQESKKSESTTDEEVECFSEDNIEDGKVNNDKV
IAEHVMPEEKKNVQQLNQNELQSPDSIDEQEEDKSGTDGKENHRAVSLPLPHLSSNNYFG
ESSHSIEHQKDGETSPSSIETKLNATSVINEEGQSKVTKEADIDDLSSHSQNLRASLVKA
GDNISEAPYDKEKKILDVGNTLAAHKSNQKPSHSDEQFDQEDHIDAPRSNSSRKSDSSFM
SLRRQSSKQHKLLNEEEDLIKPDDISSAGTKDIEGHSLLENYAPNMILSQSTGVERRFEN
SSSIQNSLGNEIHDSGEHMASGDTFNELDDGKLRKSKKNGGRSQLGQNIPNSQSTFPTIA
NIGSKDNNVPQHNFSTSISSLTNNLRRAAPESFHGSRMNNIFHKKGNQNLLLRSNDLNKN

SAAPASPLSNEHITSSTNSGSDANRQSNSGAKFNSFAQFLKSDGIDAESRTQRKLWLQRE NSIMDLSSQNDGSDSIFMAGNIDAKREFERISHEYSNVKRFYNPLDEALLRVQPIITGNA NNIRKKSHNDAQSIAHSSSDTDHKDEDDLLFTNYDKKFDDLYPHLASAKIQAVLSGIWKS ESYLFNKDVNPINKNRTTSTNHSVGHTASQNARNLLRGPMGSSTTLHHQRVINSLQPTTR AVNRRMENVGYMHTQPQOR

YPL218W, 1212 bp, exon1: 501-528, intron1: 529-667. 668-1212 (SEO ID NO 281) TGATACAAGACAGGCATTAGGAAACACATGAGTTTTGCATATGTATTATGCAGGTTCATT GGATTTTATTTATTTCTTTTTTAATGCTAAGAAAGTAATTCCGCATAATTAAACGTGTG CTGGCCTCGATAGGTACCTATAGTATACAGAAGCTTACGAAAAGCTCCTGCAGGATGGCA CTTCTAAAATTCGCGCTCAACATGGCCGTATTGTACATTATATCGTTCTATCATTATATC GTATACGCCCGCATTACCCGACAACTCCGTCTGCAACGCGTTGACCAGAAAACTCGAACA AGAGATCGCATAAAAAACCAAAAGGAAACGAATTACTTGTCAAATAGTTATTGTAATGGA TCCTCTAGAAAGGCAAACAGTAGATTTATTTCCTTCTTTTCTAGAAACATCATTATAACT CCTGTTCACGTTTTTCGGATACTTAGTTTTATTCAATGTGGTAAACATTGAATGTTTTCA GCTTAAGATCTATTTTTTTTTTTTTTTAGAAGAAATTGCGTCCTTTACTAACTTTATTTTAC TTCTTGGGTTTGGATAATGCCGGTAAGACCACATTGCTACATATGTTAAAGAACGATAGA TTGGCAACCTTACAACCAACATGGCATCCAACTTCTGAAGAACTGGCTATTGGTAACATT AAGTTTACAACTTTCGATTTGGGTGGTCATATTCAAGCTCGTCGTTTATGGAAGGATTAT TTCCCAGAAGTTAATGGTATCGTCTTTTTAGTCGATGCTGCTGACCCTGAAAGATTTGAT GAAGCACGTGTCGAATTAGATGCTTTATTCAACATTGCCGAATTGAAGGACGTTCCTTTT GTAATTCTTGGTAACAAGATCGATGCTCCAAACGCCGTTTCTGAAGCGGAGCTACGTTCT GCTTTAGGATTATTGAATACCACTGGCTCTCAAAGAATTGAAGGTCAAAGACCAGTTGAA GTTTTCATGTGTTCCGTTGTTATGAGAAATGGTTATTTAGAGGCGTTCCAATGGTTATCT CAATATATTTAA

YPL218W, 190 aa (SEQ ID NO 282) MAGWDIFGWFRDVLASLGLWNKHGKLLFLGLDNAGKTTLLHMLKNDRLATLQPTWHPTSE ELAIGNIKFTTFDLGGHIQARRLWKDYFPEVNGIVFLVDAADPERFDEARVELDALFNIA ELKDVPFVILGNKIDAPNAVSEAELRSALGLLNTTGSQRIEGQRPVEVFMCSVVMRNGYL EAFQWLSQYI

YPR102C, 1025 bp, CDS: 501-1025 (SEQ ID NO 283) TTCTTTACAATTCACCTTGCATTATTGAAGGAGTGCTATTCTTCGTTTTTGCCACCCTTTT GCTGTTTTCCCTCATATCACATAATACCCGGAGAGGCTCTTTCCTGCGACAGCGCAACAT CCAACCATCCTAAAGGTATGGGTGTACTGACGATGCGATTATTTCATTAAGTTCTGTCTT TTTTGTATAAATGAAAAAGAACGGTGAAATCCATAGAAATACAGAGAGCGACGCAAACA GCGCGCAGACTCTACGGGTAATAGACTCACATCCACGTGACCAGTTTCCAATCGAACTTT TTCACTTTGCAGGGAATTATTGTTTCACTAGCAAAGGTAGCCCACTTACCACTCAGCTAT ATTTTATTGTATTTCAACTAATATTATTTTTTTTTCAGTGGAAGGGAAGGTGAACCAAGA ACATACAAACATAGCCAAAGATGTCTGCCAAAGCTCAAAACCCTATGCGTGATTTGAAGA TCGAAAAGTTGGTCTTAAACATTTCTGTTGGTGAATCTGGTGACAGATTGACCAGAGCCT CCAAGGTTTTAGAGCAATTATCTGGTCAAACTCCAGTTCAATCCAAGGCCAGATACACTG TCAGAACTTTCGGTATCAGAAGAAACGAAAAAATTGCTGTTCACGTTACCGTCAGAGGTC CAAAGGCTGAAGAATTTTGGAAAGAGGTTTGAAGGTCAAGGAATACCAATTGAGAGACA GAAACTTCTCTGCTACCGGTAACTTCGGTTTCGGTATTGACGAACACATTGACTTGGGTA TCAAGTATGACCCATCCATCGGTATTTTCGGTATGGATTTCTATGTCGTCATGAACAGAC CAGGTGCTAGAGTCACTAGAAGAAGAGATGTAAGGGTACCGTTGGTAACTCCCACAAGA CAACTAAGGAAGACACCGTCTCTTGGTTCAAGCAAAAGTACGATGCTGATGTTTTGGACA AATAA

YPR102C, 174 aa (SEQ ID NO 284) MSAKAQNPMRDLKIEKLVLNISVGESGDRLTRASKVLEQLSGQTPVQSKARYTVRTFGIR RNEKIAVHVTVRGPKAEEILERGLKVKEYQLRDRNFSATGNFGFGIDEHIDLGIKYDPSI GIFGMDFYVVMNRPGARVTRRKRCKGTVGNSHKTTKEDTVSWFKQKYDADVLDK

YBL003C, 899 bp, CDS: 501-899 (SEQ ID NO 457) CGCGATTTTACCAGAACTAGATGGCGCTCGTGATCCTGAAAACGGGGAGAAATTTTGAGAAC ACCGCTTTATTAGGCGAAGCGGTGGGCACAGCTCACGCGTAAGGTGTTCCCATTATTTCTCA AAGTGATGCGAATTTCAGAGAACACATTAACCTGGGGGCCATAAACGCGACGTGCTACCATT TTCGTTACGTATACTTAGGCCAGAGATTACAACATGACTACTAATATCAAACATAACTCTAT ATATAAGGGATGAAGATGTATGCTTTCTTAGAATTTCAAACATGTTCCGTTAAAGTTTTACT TCATAAATTCTTGTCTTTTTACATAAGAATTAGGAAAGTACAGAACAAGAGCAAATTTAATA TATAATGTCCGGTGGTAAAGGTGGTAAAGCTGGTTCAGCTGCTAAAGCTTCTCAATCTAGAT CTGCTAAAGCTGGTTTAACATTCCCAGTTGGTAGAGTGCACAGATTGCTAAGAAGAGGTAAC TACGCCCAGAGAATTGGTTCTGGTGCTCCAGTCTATCTAACTGCTGTCTTAGAATATTTGGC TGCTGAAATTTTAGAATTGGCTGGTAATGCTGCTAGAGATAACAAAAAAACCAGAATTATTC CAAGACATTTACAATTGGCCATCAGAAATGATGATGAATTGAACAAGCTATTGGGTAATGTT ACCATCGCCCAAGGTGGTGTTTTGCCAAACATTCACCAAAACTTGTTGCCAAAGAAGTCTGC CAAGACTGCCAAAGCTTCTCAAGAACTGTAA

YBL003C, 132 aa (SEQ ID NO 458) MSGGKGGKAGSAAKASQSRSAKAGLTFPVGRVHRLLRRGNYAQRIGSGAPVYLTAVLEYLAA EILELAGNAARDNKKTRIIPRHLQLAIRNDDELNKLLGNVTIAQGGVLPNIHQNLLPKKSAK TAKASOEL

YDR442W, 893 bp, CDS: 501-893 (SEQ ID NO 459) CTTGTTATTTTTGTAAATTGAGCTATGCAACATAAGATTCCTGCGATGTAAGAACTACTTGC TAATCAAGAGAACTTCAACAATTTTCCATCGCAGAGACGAAAAAACTGGAAAAAAATAAAAA GAAAAAATTGAAAAAGAATCGCGACTTCCGATTACATAACCTTATACGGAGTATGATACCAT TCTTGACATCAACACCACCGCGCAGACCCACGTGGCCGCTTCGTGTGCCTTGAAAATAC AGCCTTAAACGCAATCTCATTCGCGTTCTGTGGAAATTGTCTCGGACTACACGCTGGGCGTG CATCACCAGTGAAAATGCCGTACCGCCCCGCTTCCGGTTTTGTTTTTATAAATCCGACTGGA GAAATAGACTTCTGGGTTTACACCCCGGAATAATACTAAAACCAAAACTGGTAAATAGGGCT AAGTAGCGGTATGCACAGTAGCGGCGGAAGTATTAGCAATTTTTACTCTGGTGTGCACAAGA GTGTTCATCATTTTTTCACGGCTAGGATATGCCATGGAATATGGCCATCTTCGCCATCAGA GAGACCGTACCACACGTTTAGAGCAGCCAGGTTGCGAAACTCTTCTAAGATGGTTTCCAGCA ATTGTGTACTATCAGAATGTGGACAGTTTAAAAGGTTGACTGCGAATTTGTCCCAAACCGTA TCACCGTCGCATTTTTTGAATTTGATCAAAGCACCACTCCTAATAGCACAGCGATGCTGTGA GTGTGCCAGTGGGAACGGGTGCTGA

YDR442W, 130 aa (SEQ ID NO 460) MSRKTLPEKVYLSERIIDEEVAVCTVAAEVLAIFTLVCTRVFIIFFTARICHGIWPSSPSER PYHTFRAARLRNSSKMVSSNCVLSECGQFKRLTANLSQTVSPSHFLNLIKAPLLIAQRCCEC ASGNGC

WO 01/02550 PCT/BE00/00077

CTGTTGCCATACATATTAGAAGCTGAAGCTGCAGCTAAGGAGAAGGACGAGTTAGACAACAT AGAGGTCTCCAAATGA

YDR529C, 127 aa (SEQ ID NO 462) MPQSFTSIARIGDYILKSPVLSKLCVPVANQFINLAGYKKLGLKFDDLIAEENPIMQTALRR LPEDESYARAYRIIRAHQTELTHHLLPRNEWIKAQEDVPYLLPYILEAEAAAKEKDELDNIE VSK

YGR085C, 1025 bp, CDS: 501-1025 (SEQ ID NO 463) TCCTTACTTTAGTCTATTATCAATATCTCTTCCCCCTCCTAAATATGTACTCTTTTATTTTT TTTAATTGTGAAGGAACAATTCAAGTTAGAACTCTTTTGATAGGAAACATTATTTCCTGTGT TAGACATCTATATATAACAAGCACAGAACCGTCTAATTGGTATTTTTCAGGACATTTTAAAC ATCCGTACAACGAGAACCCATACATTACTTTTTTAATATTCTTTTTTCACCGCCTTC TTTTTATTTTATCCGAAGATCTTTTGGAACCCGCTCTGCGAATAGCGAAGCTAGGATACCA GTGTATTATAACGTTTAGCATCAGTTACCCTTGAAAGCCCCAACATATACAAAAATACGCGTC CAAGATGTCTACTAAAGCCCAAAACCCTATGCGTGATTTGAAGATCGAGAAATTGGTCTTGA ACATCTCCGTTGGTGAATCTGGTGACAGATTAACCAGAGCCTCCAAGGTTTTAGAACAATTA TCTGGTCAAACTCCAGTTCAATCCAAGGCCAGATACACTGTCAGAACTTTCGGTATCAGAAG AAACGAAAAATTGCTGTTCACGTTACCGTCAGAGGTCCAAAGGCTGAAGAAATTTTGGAAA GAGGTTTGAAGGTCAAGGAATACCAATTGAGAGACAGAAACTTCTCTGCTACCGGTAACTTC GTAAGGGTACTGTTGGTAACTCCCACAAGACAACTAAGGAAGACACCGTCTCTTGGTTCAAG CAAAAGTACGACGCTGATGTGCTCGATAAATAA

YGR085C, 174 aa (SEQ ID NO 464) MSTKAQNPMRDLKIEKLVLNISVGESGDRLTRASKVLEQLSGQTPVQSKARYTVRTFGIRRN EKIAVHVTVRGPKAEEILERGLKVKEYQLRDRNFSATGNFGFGIDEHIDLGIKYDPSIGIFG MDFYVVMNRPGARVTRRKRCKGTVGNSHKTTKEDTVSWFKQKYDADVLDK

YGR106C, 1298 bp, CDS: 501-1298 (SEQ ID NO 465) GCAACATTACCACTTTGTACGGAGCGTCAGAAAGAACGCACCTCATCATTATTATGAGAACA GTACGATAACTTCTGTCTGAGATACGCTTCGTTGTTATAATACAAGTGAAACCGCCACGGAT AATTAGCAGCAATTGAACACAAGGGATATCATTTGTGTGACCTTTGTTCCTCCTCATAGTTGC TGTGAACCCTTTAGTAACTATTAATGTTTATTTCATGAGACTAGTCAAAACATTCAATAACA ACACTGACTATGCTGCAGTTTCCGCAATAGCAAAATTGTGTCACATTACACGAAAGAAGAA AGAACGCTATTTCTTATAAGAGCAAACTGTTGATAAGTTTATAGCAAGAATAAAAAGGGTAA AAAGTCATTGATAATAACCACTGCTGTGACTATATATAATAAGAATCGAACTGTAAAGTTAA AGCAATGGTGTTCGGTCAGCTGTATGCCCTTTTCATCTTCACGTTATCATGTTGTATTTCCA **AACTGGGATACCATCAGCACTATATCTTCAACGGCAGATGTTATATCATCCGTTGACAGTGC** TATCGCTGTTTTTGAATTTGACAATTTCTCATTATTGGACAACTTGATGATTGACGAAGAAT ACCCATTCTTCAATAGATTCTTTGCCAATGATGTCAGTTTAACTGTTCATGACGATTCGCCT TTGAACATCTCTCAATCATTATCTCCCATTATGGAACAATTTACTGTGGATGAATTACCTGA AAGTGCCTCTGACTTACTATATGAATACTCCTTAGATGATAAAAGCATCGTTTTGTTCAAGT TTACCTCGGATGCCTACGATTTGAAAAAATTAGATGAATTTATTGATTCTTGCTTATCGTTT AGATGAAGATGGTGACGATGAATATGCAACAGAAGAGACTTTGAGCCATCATGATAACAACA AGGGTAAAGAAGGCGACGATGATATTTTAAGCTCCATCTGGACTGAAGGACTACTAATGTGT TTAATAGTTTCTGCGTTGCTATTGTTCATTTTGATTGTTGCACTTTCTTGGATATCTAATTT

YGR106C, 265 aa (SEQ ID NO 466) MVFGQLYALFIFTLSCCISKTVQADSSKESSSFISFDKESNWDTISTISSTADVISSVDSAI AVFEFDNFSLLDNLMIDEEYPFFNRFFANDVSLTVHDDSPLNISQSLSPIMEQFTVDELPES ASDLLYEYSLDDKSIVLFKFTSDAYDLKKLDEFIDSCLSFLEDKSGDNLTVVINSLGWAFED EDGDDEYATEETLSHHDNNKGKEGDDDILSSIWTEGLLMCLIVSALLLFILIVALSWISNLDITYGALEKSTNPIKKNN

YGR182C, 117 aa (SEQ ID NO 468) MSRQSAFKFQNGNRHERACLSDVHKILIIILYSTKGKRELGKRITHFMYIHIFCTYLYQASI VQYCSSTLLNVIAFSWYPLNLIYKYEYILRSKLILMVCLDFARSGGVLDSGDVSL

YGR183C, 914 bp, exon1: 501-503, intron1: 504-716, exon2: 717-914 (SEQ ID NO 469) AAATACAAATCCAAGAAACCTCGATGAGGATGACTCTGATGATGATGACTCTGATGAGC GAGAGATTTGGTAGATTCAAGCCCTCTACTATGTTTTATAGTTGACATATTTGTATAAAA ATACCAACCTAATTACAAATACTTCGAAGTGACTATCATAAGTTTCCTTATCTAGCGAAGGC AACTTTTGAACTCCCCAGTTGTTAATATGTATCATTATACACGACCCAATCAAACGCGGGGA AGTCAATGCCGAAAGAATTCTAGGACCTAAAAGCTGCTCAATCCTTGGGCCTTTCCCTAATG ACATCCCCTCTCAAACTTTAGCTTAGCAGTTGTATTTAATGTCCTGTCACGGATAGTCAATA ATCGTTGAAGGTTGATTTTCATATCCTTCGCAATTTCGTAAAGCAACAATAGCAATACGGAC TAAAATGGTATGTTGTGTGTGTGTGCTGCTTCACATTTCAGGCTAAAAATGTTATCCGT GGAATCTTCCTTAGCCAAGTATCATGGGCTTTGGAAATTAGTTTCCCACCGATGAGCGCAAC GACTTAGCGAAGCTTATGAAATTGGTGACAGCAGCTCTATGAATATGTTCCATGCGTTTCCA TTCAGGTTACTAACAATGCATAAATTATGAGTAGTCTTTTTCATCACTATATAAAACCTTTT TCAAACGAAACGCTGTTTTTGTTGGTACTATCTTTGCAGGTGCCTTTGTTTTCCAAACTGTA TTTGATACTGCTATTACTTCATGGTACGAGAATCACAACAAAGGAAAATTATGGAAAGATGT CAAGGCTCGAATAGCTGCAGGCGATGAGGACGACGATGATGAGTAA

YGR183C, 66 aa (SEQ ID NO 470) MSFSSLYKTFFKRNAVFVGTIFAGAFVFQTVFDTAITSWYENHNKGKLWKDVKARIAAGDGD DDDE

YKR040C, 167 aa (SEQ ID NO 472) MTSFQAVSFALGCNTLVACYAFTVLEKRSLMTSCTNALSFLFFLLTLRRIHRHWYKPYGAFL LIFVLTLRWFRGPIAWVVVDVVFASCNVVFFSPALSDENWPYVSFFGVVVVIAVHIIVVTHI GAFTACCLLKRVSLKSSEEKKKKKKKKKKKKKKKKKKK

1343 bp, exon1: 501-513, intron1: 514-927, exon2: 928-1343 (SEQ ID NO 473) TCTTATCTTGTATGCCCGATATAGCAACCTTGTTGGTACCAATCTAACGGTTTCCGTACTTT GCAATGAAGAGATGAGGAGGCATGGGTCACTTATTTAATATGTACGGGTGTTTACATGGAGT GTCCACGCTCTGGAGTTAGGCTCTCCCATTACGGAGAGAGCATTTCCTCAGCCTGGGAGCC GCACAAGGGGATTTTCTTCTACCTTCGGCTTGCCTCACTGCGTTGGGGCTTCCCAATGCAA CTTCGTTCGTATGCATACAATCTTTTAGATATTATCTTTTAAAAATTATTTTAAAACAATTTT AAATGTATCTCATATGCTTTTCTTCTGCTGTTGAAAAGGCTAAACAAAGAAGATCAATAAGA TAAAATGGCTCCATCTGGTATGTGAACTGCAATATTAATAGCACGAGAAAATTGAGAGGAAG CCGACGACAAGAATAGTGCATTAAGGACTTGATTAAGATATGGTGAGCAACGTAATTATCGG GCTCAACAGTTTATTAGCAATCGTTTTGATAGAAGCGTTGATGCTGTGGAAGTTGTTCTTTT GAAAATTATTCCATCCTCATTATACTTTTTTCTTCTATTTCGTGCTCCACGTCGAGGTATCA AGGAACATAGTTTACTAACATTAACGAATTCATCTCCTATGAATTTACTTTTTGTATAGCTA AGGCTACTGCCGCTAAGAAGCTGTCGTTAAGGGTACTAATGGTAAGAAGGCTTTGAAGGTC AGAACTTCTGCTACCTTCAGACTACCAAAGACCTTGAAGTTGGCTAGAGCTCCAAAATATGC TTCCAAGGCTGTTCCACATTACAACAGATTGGACTCATACAAGGTCATTGAGCAACCAATCA CTTCTGAAACCGCTATGAAGAAGGTTGAAGATGGTAACATTTTGGTTTTCCAAGTTTCCATG AAAGCTAACAAATACCAAATCAAGAAGGCCGTCAAGGAATTATACGAAGTTGACGTATTGAA GGTTAACACTTTGGTTAGACCAAACGGTACCAAGAAGGCTTACGTTAGATTGACTGCTGACT ACGATGCTTTGGACATTGCTAACAGAATCGGTTACATTTAA

YOL127W, 142 aa (SEQ ID NO 474) MAPSAKATAAKKAVVKGTNGKKALKVRTSATFRLPKTLKLARAPKYASKAVPHYNRLDSYKV IEQPITSETAMKKVEDGNILVFQVSMKANKYQIKKAVKELYEVDVLKVNTLVRPNGTKKAYV RLTADYDALDIANRIGYI

FIG. 2:

YBL051C_homolog_1 1229bp PathoSeq: 1..1229; CDS: <1..>1229 (SEQ ID NO 285)

AGAGAACGTATTGAAGAGGGAGAAAAGGGGAGAAAAGAGGTCAATTGGAAGAACAACATCGTTCTGCA TCAAATGCTTCTATGGCTTCTTTATTGTCAGCTGCTTCAACTACAGCAGCAACTAAAAATTTGAGT GTGGCTGGCACAAATCCTTCTCATACCACTGAAAGAATGTTTTTAAATTTACCTTTTAACAATTCC CTGTTCAATGCCCCACCAGTAGAAATTAATTTTAATGATCTTGAAGTTTTGGAATTGTACACTCAA TTAGTATTATACCGAGATGATATTACCAAATCTACTTTTGAATTAGCTATATCACCAGCAAATTTG AATATTTCTCAACGGAAAATCATATCAATTTTATGTAATTATTTGAATTTATTAGAATTGTTTGAT AATGGGTTGATAATAATTAGAAGAAAACCAGGATACATTGCTCAGTGTATAACTCAACAATCTATT ATTCCTAATTCTCAACAGGTGTCTGGGCCAACTCACCCGCAACAACATCAACAGAATCAACTTCAA CAATTGGGTGGTACATTAGCTGTTCCAGCGCACCCTGAATTATTAAGATCCCAATCGCAATCAGCA TTACCGTTGCCAAGATTGAGACAGCAAACCTCTACACCAATTCAACAAAATCAACAAGTTCAGCAC CAAAATCAACCACCACAACAACAACAGCAACAGCATGTTCAACCACAATATAATTATTACAATCAG CAATCTATTCAAAGCCAACCACATTCTGCGAGACCTTATTCTCAATCATATAATATTTTATCAACAA CAACAGCAACAACAACAAGCTCAACAAGCTCAACAACAACAACAACAACAACAATTACAA TATCAACAGGGACACCAGTCACAAGTTTCAACACCTACATTGAATTCTTCTAGTGCTGCTGCATTA CTTAGATCAAGTAGCAGTAGATCATTTGTTGATGTGAGATCCACACCTCCCACAAGTAGTTTTGCT CAACAGCAACAACAACAACAACAACAGCAACAGCCGCCACTAACTTCATCAATCCATGATTCT CCAACACCACATCATCATTACCACTTCAACAGCAGCCACCACAACCAAATCATTACCTATCCAAT TACCATCAGGGGGTTGGATCTCAACCAAAAACTCCATTGGC

YBL051C_homolog_1 409aa (SEQ ID NO 286)
RERIEEEKREKRGQLEEQHRSASNASMASLLSAASTTAATKNLSVAGTNPSHTTERMFLNLPFNNS
SFNAPPVEINFNDLEVLELYTQLVLYRDDITKSTFELAISPANLNISQRKIISILCNYLNLLELFD
NGLIIIRRKPGYIAQCITQQSIIPNSQQVSGPTHPQQHQQNQLQQQQQQQHQHQHPSHSSSMMNLH
QLGGTLAVPAHPELLRSQSQSALPLPRLRQQTSTPIQQNQQVQHQNQPPQQQQQHVQPQYNYYNQ
QSIQSQPHSARPYSQSYNIYQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQVSTPTLNSSSAAAL
LRSSSSRSFVDVRSTPPTSSFAQQQQQQQQQQQQQQQQQQQQPPLTSSIHDSPTPHHHLPLQQQPPQPNHYLSN
YHQGVGSQPKTPL

YBL051C_homolog_2 2153bp public: 1..2153; CDS: 501..2150 (SEQ ID NO 287)

CTGGAAAATCAAAATTGAACTCCAACCAGCAGCGGCGGCGGCGACAGAAAATATATTAACAGAAT ATTTGATTTGGGAAAAAACAAATTTTATATTTGGAGAATTGAATTTCAATCATTTTAACAAATTCA ATTCATATTACATTGACTTTTGACAAGAGGTATATATAATGGATTTTAGAAATTTATCAACTACAC CGAATCAAATGGGCACTGTAATGCAACGTCGTCCCTCTCTATCATCATTATCGTCAGCCTCGGGCT ATTCTTCTTCCAATTATGGTGGAAATCCTACACCCAATCCCAACAATTCCAATACCAATACAATA GTAGTGGCAATAGTAATAACAACACTCATGGCAATAACACTCCCAAATTATCAACTCAAAGATTGA CTTGGGTGGAACAGCAACAACAACCCTTGATCTGTTGGAAAATAATACTAAAACAGACTCCA GTAATGATGCTTCTGCTACTAATAATAATAATGTTAATGTTAATGTTAATGCCAATGCCAATGTTA ATGCCAATGCCAATATCCATGCCCAAACCCATGTCAACACAAATGTTAATGCAAACACAACAGCAA CTAGTATTAATGCTTCCACGATTTTAAATACTACACCAAGTATTAATGACACTAATGATAATGCCA AAAAAATTAATGTTTCCATGATTAGTAATAACAATAACAATAACAGTAACAATAATAACAACAACA ACGAGTTAATTCCTACTGCGATTGTGATTAAAAATATTCCATTTGCCATTAAAAAGGAACAATTGT TAGATGTGATGACAAAATTAAACTTGCCATTACCATATGCCTTTAATTATCATTTTGATAATGGTG

YBL051C_homolog_2 550aa (SEQ ID NO 288)
MDFRNLSTTPNQMGTVMQRRPSLSSLSSASGYSSSNYGGNPTPNPNNSNTNNNSSGNSNNNTHGNN
TPKLSTQRLTNNRNLQSLWINQPSIAPSNVVPWVEQQQQQTLDSLENNTKTDSSNDASATNNNNVN
VNVNANANVNANANIHAQTHVNTNVNANTTATSINASTILNTTPSINDTNDNAKKINVSMISNNNN
NNSNNNNNNTNNSSTGSSNIANMLPSVSNATTMNNSNSINSTTNNTTINEADDDELIPTAIVIKNI
PFAIKKEQLLDVMTKLNLPLPYAFNYHFDNGVFRGLAFANFTSTDETSAVVNQLNGREIGGRKLRV
EYKKMLPAQERERIEREKREKRGQLEEQHRSASNASLASLLSAASTTAATKNLSVAGTNPSHTTER
MFLNLPFNNSSFNAPPVEINFNDLEVLELYTQLVLYRDDITKSTFELAISPSIFEYFSTENHINLC
NYLNLLELFDNGLLLIRKKPGSIAQCITQKSIIPNSQQVSGPTHPHHHQKNQLHQQQQQHTSTSTS
LTFIIDDEPSSIGWYISCSSAP

YBL066C_homolog 3254bp PathoSeq: 1..94/2146..3254, public: 95..2145; CDS: 501..3251 (SEO ID NO 289)

ATAAAAAAGGAAATACAATTAAAAAAATTTTCCTTCTGTGAAAAGGCAATTTCGGGTCTAGTAGTA AACAAAGCTTAATAATTTCTCCCATTCAAATTTACAACGGACGATGCAGAAAGTAGTTTTCAAATT AATATTCTTTTTAACTTATTTTTCAATCAAGAAGGTACTGAAGATATCAATTAACTCTCAGTTAAA TAATATAAAATTATCACCAAAGCTGCCATCAACGTGTGTCGACAACCAATCGACTCCTCCCTTAAC TAGAACCATAGAACCTCAACATTTGTTTCTATAGAAAAATGAAGTTTTGAAAAAAGGTAAAGTGAGAA TTTTGCCTAAACCATCCCCTACACCAACCAACCCACAAACCCCATTGCCATTACTTCCAGCTCAAA CTAAACCTGTAAACTCAAAAAGAAAATCAGCAGCCAGTACACCTGGAAATGAATCAAAGAAATCAA GAAAATCAAATTCTACAGCTTCAACACCCAACAGTGCTACACCAACATCAGTCGGAACACCTCCAC AGAAAACTTCCAAACCAACAGGTCATAGGCCAGTGACTTCATGTACTTTTTGTCGTCAACATAAAA TCAAATGTAATGCTTCAGATAATTATCCAAACCCATGTGAAAGATGTAAAAAAATGGGTTTGAAAT GTGAAATTGACCCCGAATTTAGACCTCGCAAAGGGTCACAAATCCAATCATTGAAACTGGATGTTG ATGAATTGAAGGCCAAGATTGAAATGTTGACTAAAAATGAATCTTTGCTCACACAAGCTTTGAATC AACACAATTTGAACCACGCTTCGCAACAGCAACAACTGTCTGGATCGCAATCTCAACAACAACATC CTCCAAATCCACAACGTGCATTGTCATATACGTCTGCAAACTCATCACCACAAGTTGCATTTAGCA ATGCATCGCCAATTCCTTCTGACAAGTATTCAACAAAATGCACCGTTGACTCACGAAAATTCCG ACAATTCTCCATACGCTTTAAATACACCAGAAAACATTGAAGAATTACAACCAATCTCAGAATTTA TTTTGGGTGACGTTACTTTGCCATTAAACAGGGCCAATGAGTTACACGACAAGTTTATGACCACAC ATTTACCATTTTTGCCAATAATAATATCTCGATCTGCCACCGAATTGTATCATAAATCTCAATTGC TTTTCTGGGCCGTGATTCTTACCGCAAGCTTATCAGAACCAGAACCCAAACTTTATATGTCGTTGG CATCCTTAATTAAACAATTAGCAATTGAAACATGTTGGATTAAAACACCAAGATCAACTCATGTTA TCCAAGCCTTGATCATACTTTCAATATGGCCGTTACCTAATGAAAAAGTTTTGGATGATTGCTCTT ATAGATTTGTTGGATTGGCAAAGAACTTGTCATTACAATTAGGTCTACATCGTGGTGGAGAATTCA TTCAAGAATTTAGTCGGAATCAAGTAAGTCTAGGACCTGATGCAGAAAGGTGGAGGACTCGTTCAT GGTTAGCAGTTTTCTTTTGTGAACAGTTTTGGTCATCATTGTTGGGGGTTGCCACCTTCAATAAACA CTACTGATTATTATTAGAGAATGCTCGTGTTGATAAATCGTTGCCTAAAAATTTCCGTTGTTTGA

TTTCGCTATCTATTTTCCAATGCAAATTAGTTAATATTATGGGTATTAGCGTTACTAGACCAGACG GTTTATTGGAGCCTCTGAATCGTGCTGGTTCACTTAGTTTATTGGATAGAGAATTGGAAAGATTAA GATTTAAACTTCAATTTGAAGAAGGGGGCCCAATTGAAGTATATTATTTGTATATTAAATTGATGA TCTGCTGCTTTTGCCTTTTTACCAGGTACACCTATCGAGGATCAAGTCAAGTATGTCAGTTTTGCAT TGCCAATATATATCAGACAAGCAGTGACATATAGTGTTTTCATGTTGTTCAAATTACATTTGTCAA GAAACACGTTGAGTTCCTGGAAAGATTTGCAAAACGATATTTCTCGAACAGCCAAAGTTCTAGAAA ATTTGAACATGGTGTTGTATAATTATCCTGAAATATTTTTAAATGATCTGGAAAATGAGGATTCAA GTATTATCACCAGAATGAGGTCACATTTGACAGCATCTTTATTCTATGATTTGGTTTGGTGTGTAC ATGAGGCAAGAAGACGATCAGTACTTGATAAGGGGAAAAGACAGGCTCAGCCTAACAAGAAAATCT TGCCCTTGCCATTTTACAACCAAATCACTAAGGATGATTTCAAGACAATTACCACGACATCACCTA ATGGAACTACTATTACTACATTAGTTCCAACTGATCAAGCTATGAATCAAGCAAAACTGAAATCTT TTGATTCCAGCAAACCACTTGAAATAAATGGTATTCCCTTACCTATGCTTGAAGCTACTGGTTCAA CAAGAGAAGTTTTAGATTCTTTACCCTCGCAATCTTTACCATCACAAGCACCAACTCTTCAGCAGT ATCCAATGCAGCAAGATCAACAACAGCAAGAACCATCACAACAACAACAACAAAGCACCTGCAGC AACTGCAGCAATACCAACAGCAGCAATCGAATCAACAGCAACCACATCTTCAACATCAAAGAC AGTTTCAACAATCACCACCACCGCAATTTTCAATGATTTCTTCAACGCCGCCCCTTCAGCAACCAC CACCAGAAGTAAAACAAGAAAACTCTGTTGCTCCATTTGCATCTCAAATCACCAACTTTTTTTGATC ATATGATGCAAGAGAAATAA

YBL066C_homolog 917aa (SEQ ID NO 290)

MKFEKGKVRILPKPSPTPTNPQTPLPLLPAQTKPVNSKRKSAASTPGNESKKSRKSNSTASTPNSA
TPTSVGTPPQKTSKPTGHRPVTSCTFCRQHKIKCNASDNYPNPCERCKKMGLKCEIDPEFRPRKGS
QIQSLKSDVDELKAKIEMLTKNESLLTQALNQHNLNHASQQQQSSGSQSQQQHPPNPQRALSYTSA
NSSPQVAFSNASPIPSVTSIQQNAPLTHENSDNSPYALNTPENIEELQPISEFILGDVTLPLNRAN
ELHDKFMTTHLPFLPIIISRSATELYHKSQLLFWAVILTASLSEPEPKLYMSLASLIKQLAIETCW
IKTPRSTHVIQALIILSIWPLPNEKVLDDCSYRFVGLAKNLSLQLGLHRGGEFIQEFSRNQVSLGP
DAERWRTRSWLAVFFCEQFWSSLLGLPPSINTTDYLLENARVDKSLPKNFRCLISLSIFQCKLVNI
MGISVTRPDGLLEPSNRAGSLSLLDRELERLRFKLQFEEGGPIEVYYLYIKLMICCFAFLPGTPIE
DQVKYVSFAYLSATRIVTIVSKMVNDISLIELPIYIRQAVTYSVFMLFKLHLSRYLIDKYVDSARQ
SIVTVHRLFRNTLSSWKDLQNDISRTAKVLENLNMVLYNYPEIFLNDSENEDSSIITRMRSHLTAS
LFYDLVWCVHEARRRSVLDKGKRQAQPNKKILPLPFYNQITKDDFKTITTTSPNGTTITTLVPTDQ
AMNQAKSKSFDSSKPLEINGIPLPMLEATGSTREVLDSLPSQSLPSQAPTLQQYPMQQDQQQEPS
QQQQQKHSQQSQQYQQQQQSNQQQPHLQHQRQFQQSPPPQFSMISSTPPLQQPPFILANSPLPQTY
LPKIDEMNMSPEVKQENSVAPFASQITNFFDQQTSGWFNNDNQDDDFLGWFDVNMMQEK

YBL078C_homolog 908bp public: 1..908; exon 1: 417..449, intron 1: 450..533, exon 2: 534..908 (SEQ ID NO 291) CTTTTTTTTTATTTATTTTTGTATTTTGTATATTAATCAAACTATTATCATCATCATCTATATA TACATCCCCATCGATTCATCTGACATAATAGTATGTATGATCATACAGAGGGAAAATCACCCTTTT TATTATTACCAAGGTCTCAATGATTAGTGTGGCTAGCGTCTGTTACTACTTACCCCGTGTTTGTAG ATAATTGCCACTCAATCTTTAATTGACCATCGACCACAAAATAATATGGAAATAATACTAACAGA TGATTTTTAGTCCTCTGAATCTTCTTCCGATCATCATATACTAACATTTTCGTGGGTGTTATTCTT TAATAGAAAAGAGACAAGCCGAGGCAGCCAGAATTGCTCAGAGGTTCAAGGATAGAGTACCAGTCA TCTGTGAAAAGGTTGAGAATTCCGATATCCCCGAAATTGATAAACGTAAATATTTAGTGCCAGTGG ATTTGACTGTTGGTCAATTTGTTTACGTTATTAGAAAAAGAATCAAGTTACCAAGCGAAAAAGCCA TTTTCATCTTTGTCAATGACATATTACCCCCAACCGCTGCATTAATCAGTACAATCTACGAAGAAC ACAAGGACGAAGATGGTTTCTTATACGTTTTATACTCTGGAGAGAATACTTTTGGCGAGAAACTAG CAATTGACATTTCATCATTAGATTTCAGTGATATCCCTGATTATGTTTAA

YBL078C_homolog 135aa (SEQ ID NO 292)
MRSQFKDEHPFEKRQAEAARIAQRFKDRVPVICEKVENSDIPEIDKRKYLVPVDLTVGQFVYVIRK
RIKLPSEKAIFIFVNDILPPTAALISTIYEEHKDEDGFLYVLYSGENTFGEKLAIDISSLDFSDIP

YBR073W_homolog 2891bp PathoSeq: 1..2891; CDS: 501..2888 (SEQ ID NO 293)

GTGGCACATCCCAGGAAGTAGAGCATGGACAGTTCGTATGGTATTGCTGTGCATACGATACAAAAA AAACAGAAACGAGAAAAAAATCGATCGTCAACCTTTATCAACTCATCTACAGCAGCAGCAAAGTT CGTCCCTAAATATGAGTCAAGTCCAACAGAAACCCAAATCGTTTGGTAGATTGTATACCATGTACT ACTTTCATTTTCCATTTGTTATGCTTACGACAACTGAAACCATGCTACTTCATACGTTTGTATTGA TGTTTGCCTTATTGGTTGCCTATGGGATCTACGCTTATTTGCCTTCAAGTATCATGTTTTGCAATCT CCAGAGCATACTATTATGTTTTTGGCATGGATATTAGTACCATCAACGGTTATGCAAAGTAGCGCT GTCTACTTAGTTTATAGTTTAAAAATTTGTTAATAAAACCCAAAGTTTCTAACAGGCTCTGTTT ATCAAATGAATGTTCGACCTAATGCTCCGTTTCGGCCTCCTAGACCAATAAAGGGGGGGTGTTGCGG TGGTGCAGAAAGTAGTAAAACGAAAATTGCCCACTACCACCAATCCTAAACCTGCAAAGATTTTGA CTACCGATCCCGGCTCAACAAAATACGTGATCCAATGGAGAAAAGAAAACTTCAAAGAAGAACAAAA AGAACTCTGATGGCAAACCTATGGGGAAAAGAGTGTTTACTGCGACACCTAACCTTGACGACGTGA TTAGTGTGGGACCCTATGAATTAGAATTAGACGAAAAAGTAGGGTCTAACTCAACTCCCCAGACAG TGACACGTGTTACCCACCAGTTCAAAAAGGTTGCTCCTCCCACAGCTAGTAGTCGGAAACCGCTTT ATGACGACTGTGCCGATGCCATCGCGTTGCCTCCTCCAAAAGCCAAAGATTATGTCAAAGTAA GTGCAGTGGTAAATAAGGTATTGGTGGTGTCTCTCACGCTTATTTCCAATTGGAGACAGGAGT TTAGGAAATGGTTAGGTGCTAATAAGCTAAACGTGTTGACGCTCAACAACCCAATGTCAAACGAGA AACAGGATATACTCAATTTTGGAAAGTTGAATGTGTACCAAGTGTTAGTGGTGAATTATGAAAAAC TTGTGGCACATTTTGATGAACTCTCAGCGGTCAAGTTTGATTTGTTAGTGTGTGACGAGGGCCATC GTTTGAAGAATAGTGCAAATAAAGTATTGAATAATCTTATCAAGCTCAATATTCCGAAGAAAATTG TTTTGACGGGTACGCCGATTCAAAACGAGTTGGTAGAGTTTCACACGTTGATCTCGTTTCTCAACC CGGGTGTGCTTCCCGAGCTAAAATTGTTTCAGCGAAACTTTATAACACCTATATCTAGGGCCCGAG TGACTCAGAGTTTTATTCTTAGACGTACACAGCGATTTTGGCTAATTACTTGACACAGAAAACTG ACATTTGTTGTTCCACCTACATCGTTGCAGCTCAAGTTGTTCGACTATATAACCAACTTGA AGAAATTTAATCAGTTTGAGGCATTTACCATGATCAATTTGTTTAAAAAAGATTTGCAATTCCCCTT CGTTGTTGGCCGACGACGAGTTATTTAAAAAGATTGTTGAAGAAAAGTTTAATTTGGGGATGGCAT CCGGTAAAATAAACATTCTTGTGCCGTTGCTATTGGAAATTGCTTCGCTTGGGGAAAAGATTGTCT TAATTTCCAACTACACCAAGACTTTGGACTTGTTGGAACAGGTTTTGCGCCAAGGTCAGCCTAACAT TTTCGAGATTAGATGGGTCGACCCCCAACAATGTGCGTAGCAAGTTGGTTAATCAGTTTAACACGA ACCCCGACATAAACGTATTTTTATTGTCGTCGAAATCTGGCGGGATGGGGGATCAACTTGGTCGGGG CTTCGAGGTTGATTTTGTTTGACAATGACTGGAACCCAGCGACCGATTTGCAATCGATGTCGCGAA TTCACAGAGACGGACAATTGAAACCGTGTTTCATTTATAGGCTATTCACCACGGGGTGTATTGACG AGAAAATCTTTCAGCGACAGCTCGTGAAGAACAAATTGAGTTCCAAGTTTTTGGACAATGACGCCA TATCCAATACTCATGATTTATTAGAGTGTGTGTGTGAGGGCGACGGGTCGATGTTGAGTCAGCCAA CCATAGAGGAAAGCACCCCCCAAAACAAGCATGGGTTACTGCATTAGAGCTTAAGAAGAAGA TTGACGATGGTGAGGCGCTAAAGAGGCGCTGTTAAATTTGCCTTGAACGATTATCGACACTACA ATCCAGAGGTGAACCGTAATTTGGATTTTGATTCTGCGCTACACCGAATTGCTAACAATTCAAGCT ATGAAAATAAGCAATTGCCAATTACATTTATAATGCTGAGAGTAACTAATTAA

YBR073W_homolog 796aa (SEQ ID NO 294)
MFTLFFFTTDQMNVRPNAPFRPPRPIKGGVAVVQKVVKRKLPTTTNPKPAKILTTDPGSTKYVIQW
RKKTSKKNKTWDGDGYAVIKQLENGACEISIKNSDGKPMGKRVFTATPNLDDVISVGPYELELDEK
VGSNSTPQTVTRVTHQFKKVAPPTASSRKPLYDDCADAIALPPPPKAKDYVKVNIDPHLAKVLRPH

QVEGVKFMYECLMGYRGFGGHGCLLADEMGLGKTLMTITTIWTLLKQNPFMEKGAVVNKVLVVCPV
TLISNWRQEFRKWLGANKLNVLTLNNPMSNEKQDILNFGKLNVYQVLVVNYEKLVAHFDELSAVKF
DLLVCDEGHRLKNSANKVLNNLIKLNIPKKIVLTGTPIQNELVEFHTLISFLNPGVLPELKLFQRN
FITPISRARDINCFDPEVKKRGEEISQQLIELTQSFILRRTQAILANYLTQKTDILLFVPPTSLQL
KLFDYITNLKKFNQFEAFTMINLFKKICNSPSLLADDELFKKIVEEKFNLGMASGKINILVPLLLE
IASLGEKIVLISNYTKTLDLLEQVLRKVSLTFSRLDGSTPNNVRSKLVNQFNTNPDINVFLLSSKS
GGMGINLVGASRLILFDNDWNPATDLQSMSRIHRDGQLKPCFIYRLFTTGCIDEKIFQRQLVKNKL
SSKFLDNDATSKSDVFDNDDLKNIFEIDTSTISNTHDLLECVCEGDGSMLSQPTIEESEPPPKQAW
VTALELKKKIDDGEALKRTAVKFALNDYRHYNPEVNRNLDFDSALHRIANNSSYENKQLPITFIMS
RVTN

YBR086C_homolog 2643bp PathoSeq: 1..2643; CDS: 501..>2643 (SEQ ID NO 295)

CTTTGTGTACTCATACGATGGTTGTTATTAGTTAAAGTTGCTTTGCTTTGCTTTTCAATTTCAATT GGTTATTGGTGTTTATTATTTTTTTTTTGGTTCCTCTTTTTACCCCCCCTTCCGTCTAATTGAGTTA ATTGGATTTGAATTGTTACAATTGAATACTTCAACGAGATGACTTTACCAATTCAGGATTTAGAAC CTGATTATTATATTCCGTCAATTATCCTACCACCGATAATGGATCACCAACCCCACAAGCTGAAA AATCATTGAAAACATTAATTGATTTATTATACGATAAAGGGTTTGCCGCCCAAATTAGACCTGGTG ATTTAGACCATTTGTTAGTCTTTGTTAAATTGTCTTCATACAAGTTTTCTGAAGAAGCTGAAAAAG ATTTAATTAAAAATTATGAATTTGGTGTCACGGGTAAAGATGACGTGTTAGCTTCTAAACTTAGAA TTATTATCAATACTTAACTTATCCACAATCAGTTGGTGGATGTGGTATTACTCCTAATTCTGGGG ATTGGAAATTTGTCACCAGTATTGTTCCAATTACTAATGCCTTTAATGAAACCACTTTAGTTGAAG ATTTAAAAATTAATGTTACTCAACCAAATTTATCAATTGCCACTATCAAAAAGACATATGGAGTTG AAGTTGCTCTTTATTTTGAATATAAAACATTACACTTTTTTGGTTATTATTGCTTTTCTATTATTG GTCTTGTATCTCATTTTAGAAAAGATAAACGATTCCTGTTAACTTTTGCCTTTATCAATTTGCTTT GGGGGGTTTTATTCCTTGCATCATGGCATAGAAGAGAACAACATTTGGTTAATGTATGGGGTGTTC AAAATAGTCATTTAATTGAAGAACATAATTCCGAATTGGCTAAAGTCAATGAAAGATATGAAGAAA AATCAACTTATTCCATGCAAATAATACCAATGGATTCAGATTTTTAAAACAATTGGCATTTATCC CCATTGCCTTGGTGTTTGGTGGTGTTTTGATTAGTTATCAATTGAGTTGTTTCTGTATTGAAATCT TTTTAACCGATATTTATGATGGCCCCGGGAAATCTTTATTGACTTTATTACCAACGGTTTTAATCA GTGTATTTGTGCCAATTTTGACCATTGTTTATAATGCTGTCACGGATATTATTATTAAATGGGAAA ATCATGATAACCAATATAGCAAAAATAATTCTATTCTTGTTAAAACCTTTGTGTTGAATTTCTTGA CTGGTTATGTTCCATTAATCATCACTTCATTCATATATTTACCATTTGCTCATTTGGTGCAACCTC ATTTAGGTGATATTAAAACCACTATTGCCACATATGCTGGTGAAAAATAGATTCTACACCAAATACT ATTTCATTGTCACAAATCAAGTTATACAATTGGTATTGAAATATATTCTCCCATTGGGTTTAAGAT TTGTATTTAATTTTATTGAAACGAAAATTCAGAAGAAACCTCAATTACAAACTAAAGATGATAACC CTGATGAATCTATTTGGTTACATAATGTCAGATTATCGTTGAAACTTCCTGAATATAATGTTGATG ATGATTTTAGAGGATTAGTTTTACAATTTGGATATTTGATAATGTTTGGTCCAGTTTGGCCATTGG CACCATTGGTTTGTATTATTTCAATTTAATTTTTTCAAGTTGGATAATTTTAAATTATTGAATG GTAAATATTTCAAACCACCAGTTCCAAGAAGAGTTGATTCTATTCATCCATGGAATTTAGCCCTTT TCTTGTTAGCATGGATTGGATCAATTATTTCCCCCGTGGTCACGGCATTTTACCGTCATGGTACTG CTCCACCAAAATCTATGGGTCAATTTGCCCTTGATAAAGCTAGTGTTCATGTTTCATCCTCAGTTT TCTTGGTTTTATTAATGTTTGTTTCAGAACATGGATTTTTGATTTTGAGTTATCTTTTATTTGAAT TCTCTTCTTGTTCAAGAGTCAAGTTGAATGGGAAAATGATTTTGTTGATAATGATATTAAATTGA GACATGATTATTATTCTGGGAAAGTAAAACCAACTTATAAAGTCCACTCGGATGAGTTGTGGGAGA TTGAAAAAATTGCTTCTACCGAAGATGCTTATCTGACTTCTGCAGAAAAATCTACTACTACTGCTA CTT

YBR086C_homolog 714aa (SEQ ID NO 296)

103/161

MTLPIQDLEPDYYISVNYPTTDNGSPTPQAEKSLKTLIDLLYDKGFAAQIRPGDLDHLLVFVKLSS
YKFSEEAEKDLIKNYEFGVTGKDDVLASKLRIIYQYLTYPQSVGGCGITPNSGDWKFVTSIVPITN
AFNETTLVEDLKINVTQPNLSIATIKKTYGVEVALYFEYIKHYTFWLLLLSIIGLVSHFRKDKRFS
LTFAFINLLWGVLFLASWHRREQHLVNVWGVQNSHLIEEHNSELAKVNERYEEKSTYFHANNTNGF
RFLKQLAFIPIALVFVGVLISYQLSCFCIEIFLTDIYDGPGKSLLTLLPTVLISVFVPILTIVYNA
VTDIIIKWENHDNQYSKNNSILVKTFVLNFLTGYVPLIITSFIYLPFAHLVQPHLGDIKTTIATYA
GENRFYTKYLLKLKSQEEFKINQGRLDAQFFYFIVTNQVIQLVLKYILPLGLRFVFNFIETKIQKK
PQLQTKDDNPDESIWLHNVRLSLKLPEYNVDDDFRGLVLQFGYLIMFGPVWPLAPLVCIIFNLIFF
KLDNFKLLNGKYFKPPVPRRVDSIHPWNLALFLLAWIGSIISPVVTAFYRHGTAPPKSMGQFALDK
ASVHVSSSVFLVLLMFVSEHGFLILSYLLFEFSSLFKSQVEWENDFVDNDIKLRHDYYSGKVKPTY
KVHSDELWEKFTPQSTLNFTGPKPTAETDDKVEKIASTEDAYSTSAEKSTTTAT

YBR093C_homolog_1 1784bp public: 1..607, PathoSeq: 608..1784; CDS: 399.1781 (SEQ ID NO 297) CGGTAATTATGTCACAAAAACAACAATCAACATATTAAATCGTTATCCCAACTTTGTCAGTTTTA GGGCTCTGTTTAGTTTAACTTCTTGTAGTTTTATTATTCCGATTGGGTTAGCTCAATAACTGCATT TCGTACAATAATGTTAATTCAATTCTAAATTCCGATGAACCGAACACACAAAAAACATCCAGTTCT GGAGAGATTTTTCAAAACTTCTATTATAAATAGAACCCTATAAGTCCATAATAATTCAATTGAAGG TCATGGTTTCTGTTTCTAAATTAATCAATAACGGGTTGTTATTAACTAGTCAAAGTGTTTTCCAAG ATGTTGCTACTCCGCAACAAGCTTCTGTGCAACAATACAATATACTCAATTTTCTTGGCGGTAGTG CCCCTTATATTCAAAGAAACGGATATGGGATTTCTACTGATATCCCTGCTGGTTGTGAAATTGCTC AAATTCAATTGTATTCAAGACATGGTGAAAGATACCCAAGTAAAAGTAATGGTAAAAGTTTAGAAG CAATTTATGCTAAATTTGAAAACTACAAAGGTACTTTTAAAGGTGATTTGTCATTCTTAAATGATT ACACTTATTTTGTCAAAGACCAGAGTAACTATGCTAAGGAAACTAGCCCAAAAAATTCTGAAGGAA CCTATGCCGGTACAACCAATGCCTTGCGTCATGGTGCGTTTAGAGCCAAATATGGATCCTTAT ACAAGGAAAACTCAACTTTACCAATCTTCACATCCAATTCTAACAGAGTACATGAAACTTCAAAGT ATTTCGCTAGAGGGTTTTTAGGTGATGATTATGAAGAAGGTAAAACTGTCAAGTTTAACATCATCT CTGAAGATGCTGATCTTGGTGCCAATAGTTTGACTCCTAGAAGTGCATGTTCCAAGAACAAAGAAC TGAGCAGTAGTACTGCCAAAAAATATAACACAACATATTTAAATGCTATTGCTGAAAGATTAGTTA AACCAAACCCAGGTTTGAATTTGACTACAAGTGATGTCAACAATTTATTCAGTTGGTGTGCTTATG AAATCAACGTCAGAGGAAGTTCACCATTCTGTGATTTATTCACCAATGAAGAATTCATTAAGAACT CTTATGGTAACGATCTTTCCAAATATTATTCTAATGGTGCTGGTAATAATTACACCAGAATCATTG GTTCAGTGATTTTGAATTCATCCTTGGAACTTTTGAAGGACACTAAGAACTCTAATCAAGTATGGT TATCATTTGCTCATGATACTGATTTGGAAATTTTCCATTCTGCTTTAGGATTATTGGAACCAGCTG AAGATTTACCAACATCTTACATCCCATTCCCTAACCCATACGTCCATTCTTCTATTGTTCCACAAG GTGCCAGAATATACACAGAAAAACTTCAATGTGGAAACGATGCTTATGTTAGATACATTATCAACG ATGCTGTCGTGCCAATTCCAAAATGTGCTACTGGTCCAGGGTTCTCTTGTAAACTTGATGATTTTG AAAATTTCGTTAAAGAAAGAATTGGAGATGTTGACTTTGTTAAACAATGTGGTGTCAATAGTACCT ACCCATCTGAGCTTACTTCTACTGGGATTATAAAAATGTCACTTACAGTGCTCCTTTAGAATTGT

YBR093C_homolog_1 461aa (SEQ ID NO 298)
MVSVSKLINNGLLLTSQSVFQDVATPQQASVQQYNILNFLGGSAPYIQRNGYGISTDIPAGCEIAQ
IQLYSRHGERYPSKSNGKSLEAIYAKFENYKGTFKGDLSFLNDYTYFVKDQSNYAKETSPKNSEGT
YAGTTNALRHGAAFRAKYGSLYKENSTLPIFTSNSNRVHETSKYFARGFLGDDYEEGKTVKFNIIS
EDADLGANSLTPRSACSKNKESSSSTAKKYNTTYLNAIAERLVKPNPGLNLTTSDVNNLFSWCAYE
INVRGSSPFCDLFTNEEFIKNSYGNDLSKYYSNGAGNNYTRIIGSVILNSSLELLKDTKNSNQVWL
SFAHDTDLEIFHSALGLLEPAEDLPTSYIPFPNPYVHSSIVPQGARIYTEKLQCGNDAYVRYIIND
AVVPIPKCATGPGFSCKLDDFENFVKERIGDVDFVKQCGVNSTYPSELTFYWDYKNVTYSAPLEL

GAAGAAATTGGTCAAAATTTGACAATGTTTAGTAACTTTATATCTTGGTGTTGGGATGGTGCCACA AATGGAGATTGTTGAGTGTACATGAAAAATACGTAGTTAAATTTTGTTTCTTGTTTTTATTATTATTA GCCACTTTTTTATCCGATTCTTCATATTACCTTTGGTAAAGTGATAAGATTAATATCATATTAGTA AAACACCCCCAATGATGAATGTTTGTATTTATAGCCAGACTATAAAAATTACGGGGATTTAATTCG CGACTCACCACGTTCTCACACAGTATGTGCTTTTTTCATAAGTATGATTTGAACCCTAAAATATC CTGGGTTTATTCTAAGTGGACAATCTGTTTTCCAGGATGTTGCTGCCCCACATCAAGCATCAATTG AACAATATAATATTGTCAAGTACCTTGGTGGCAGCGGTCCATATATTCAAAATTCAGGGTATGGGA TTTCTACTGATATACCAGAAAAATGCACTATTGAACAAGTTCAAATGATTAGTAGACATGGTGAGC GATTTCCTAGTAAAGGAGATGGGAAATACTTTAATTCAGTGATGGAAGTTTTCAAGAGATATGGTG AATTTCATGGAGATTTATCTTTTTTAAATGACTATGAGTATTTCGTTACTAATCCAGATTATTATG AAAAGGAGACTACTCCTAAAAACTCAAAAGGTCCATATTTTGGAACTACAAATTTATTACGACATG GAGCTTATTTTAGAAAAAGATATCAATCACTATTTGACCAAAAGGAGGAGCTTGTTGTGTTTACTA GTAATTCTGGAAGGTGTTATCAAAGTGGTGTCTATTTCGCTCGAGGATTTTTTAGGAGATGATTACT CAGAAGATACAGTTGAATTTGTTGTTGTTGATGAAGACAAAAAAATGGGTGGTAATTCATTGACAC CAAGATACGCTTGTAAAACTTTGAATCAAGATTTACACAAAGATTTGGTGAATCAGTACGATAAGA CTTATTTGGACGATATTTTATCTAGATGGCTAGTAGACAATCCTGGATTAGATTTAAGTGCAGATC AGGTCTCGTCATTATTTCTTTGGTGTGCCTTTGAGATTAACGTTAGGGGGGTATTCTCCATTCTGCA ATCTATTTACAAAAGATGAATTTATCAGAAGTGGGTACCGAAACGATGTTGGTAATTACTATCAAA CTGGTCCAGGTAATAATATGACAAAGGTAATTGGCTCACCTATGGTGGAAGCGTCGTTGAAAATGC TTCAAGAAGATTCAAAAATTTGGTTGACATTTACCCATGATACTGATATTGAGATGTATTTGACAT CTTTGGGATTGATTGTTCCACCAGGGGATTTGCCCGTTGATCGAGTACCATTTCCCAATCCATATA ATGCAGCAGAATTTTTCCCTCAAGGTGCTAGAACTTACACTGAAAAATTGAAATGTGGTGAAAAGC AATATGTTAGATTTATTGTGAATGATGCAGTTTATCCATATCCGGATTGTAGTGGAGGTCCTGGGT TTACTTGTGAATTGATTTTATCAAATTAGTTAAAAGTCGTTTACATGATGTTGACTATAAGC TTCAATGTGAAGTGGACGGACCAGCGGAATTGACATTTTATTGGGATTATAAAGACAGAAAGTATA ATGCGCCGTTAATAGATCAGTAA

YBR093C_homolog_2 456aa (SEQ ID NO 300)
MVGLSRVLNAGFILSGQSVFQDVAAPHQASIEQYNIVKYLGGSGPYIQNSGYGISTDIPEKCTIEQ
VQMISRHGERFPSKGDGKYFNSVMEVFKRYGEFHGDLSFLNDYEYFVTNPDYYEKETTPKNSKGPY
FGTTNLLRHGAYFRKRYQSLFDQKEKLVVFTSNSGRCYQSGVYFARGFLGDDYSEDTVEFVVVDED
KKMGGNSLTPRYACKTLNQDLHKDLVNQYDKTYLDDILSRWLVDNPGLDLSADQVSSLFLWCAFEI
NVRGYSPFCNLFTKDEFIRSGYRNDVGNYYQTGPGNNMTKVIGSPMVEASLKMLQEDSKIWLTFTH
DTDIEMYLTSLGLIVPPGDLPVDRVPFPNPYNAAEFFPQGARTYTEKLKCGEKQYVRFIVNDAVYP
YPDCSGGPGFTCELNDFIKLVKSRLHDVDYKLQCEVDGPAELTFYWDYKDRKYNAPLIDQ

YBR093C_homolog_3 1888bp PathoSeq: 1..1656, public: 1657..1888; CDS: 500..1885 (SEQ ID NO 301) TCAATATATATCTTGTGAATAATAACTTCGTTCTAATTCACTATACACAACTAGACGTGTACACGC TCAATCTCAGGTAAAGAAAGTTTATATTCCATCACTATATAACAACAATCAGGCTTTGCAAAAAAA CATTTAAAACTAATACTGGTAATATGGAAATATAACGCCTCGTAGTTCTACGCACGTGGCATCCTT TATCTATTATTCAATTTACCCCTAATTTATGAATTAGCTTAATAAGAGCAGTCAAATTAACACGG CTCAATTAATAGTACTTAATAATATGAAGCCGATCAATTAACCGATCCTTTGAATAATTTGAAAAAT TTTCCTAAACAGCAACAACAACTGAAATTCAAAAATGGTTTCTGTTTCTAAATTATTGAACAA TGGATTGTTATTAGCTGGTCAAAGTGTCTTCCAAGATGTTGCTACTCCACAGCAAGCTTCTGTGCA ACAATATAACATCGTCAATTCTCTTGGCGGTAGTGCCCCTTATATTCAAAGAAACGGATATGGGAT TTCTACTGATATCCCTGCTGGTTGTGAAATTGCTCAAATTCAATTGTATTCAAGACATGGTGAAAG ATACCCAAGTAAAAGTAATGGTAAAAGTTTAGAAGCAATTTATGCTAAATTTGAAAACTACAAAGG TACTTTTAAAGGTGATTTGGCTTTCTTAAATGATTATACTTATTTTGTTACTGATAAAAACAATTA CGAAAAGGAAACTAGCCCAAAAAATTCTGAAGGAACCTATGCCGGTACAACCAATGCCTTGCGTCA CGGTGCTGCGTTTAGAGCCAAATATGGATCCTTATACAAGGAAAATTCAACATTACCAGTTTTCTC TTCCAATTCAGGTAGATGTTACCAAACTTCAAGATATTTTGCTAGAGGATTTTTAGGTGATGACTT TAAAGAAGGTAAAACTGTCAAGTTTAACATCATTTCTGAAGATGCTGATGTTGGTGCCAATAGTTT YBR093C_homolog_3 462aa (SEQ ID NO 302)
MVSVSKLLNNGLLLAGQSVFQDVATPQQASVQQYNIVNSLGGSAPYIQRNGYGISTDIPAGCEIAQ
IQLYSRHGERYPSKSNGKSLEAIYAKFENYKGTFKGDLAFLNDYTYFVTDKNNYEKETSPKNSEGT
YAGTTNALRHGAAFRAKYGSLYKENSTLPVFSSNSGRCYQTSRYFARGFLGDDFKEGKTVKFNIIS
EDADVGANSLTPRSACSKNKERSSSTAKKYNTTYLNAITERLVKPNPGLNLTTSDVNNLFSWCAYE
INVRGSSPFCDLFTNEEFIKYSYGNDLSNYYSNGAGNNYTRIIGSVILNSSLELLKDTKNSNQVWL
SFAHDTDLEIFHSALGLLEPAEDLPTSYIPFPNPYVHSSIVPQGARIYTEKLQCGNDAYVRYIIND
AVVPIPKCATGPGFSCKLDDFENFVKERIGDVDFVKQCGVNSTYPSELTFYWDYKNVTYNAPLGDF

YBR093C_homolog_4 1886bp PAthoSeq: 1..102/1038..1062/1078..1886, public: 103..1037/1063..1077; CDS: 501..1883 (SEQ ID NO 303) ACTACTTAAATTGGCATATCCAAACAAACTTGAAGTAGGAGTTTCCTTATTTTTATTTTGTATTTA ACATATTAAATCGTTATCCCAACTTTGTCAGTTTTACTAACACCTTTTATTTTGTGTTATACAAAT TGCACAATCAATTACTATAACTTTTTTTTGAAACGTGGGCTCTGTTTAGTTTAACTTCTTGTAGTT TTATTATTCCGATTGGGTTAGCTCAATAACTGCATTTCGTACAATAATGTTAATTCAATTCTAAAT TCCGATGAACCGAACACAAAAAACATCCAGTTCTGGAGAGATTTTTCAAAACTTCTATTATAAA TAGAACCCTATAAGTCCATAATAATTCAATTGAAGGATTATTTTCTTTTTCCCTTTTCTGATTACTT TCACCAATTTTCTTCTCCCAAAAAAAACACCTTCTTCATGGTTTCTGTTTCTAAATTAATCAATA ACGGGTTGTTATTAACTAGTCAAAGTGTTTTCCAAGATGTTGCTACTCCGCAACAAGCTTCTGTGC AACAATACAATATACTCAATTTTCTTGGCGGTAGTGCCCCTTATATTCAAAGAAACGGATATGGGA TTTCTACTGATATCCCTGCTGGTTGTGAAATTGCTCAAATTCAATTGTACTCAAGACATGGTGAAA GATTCCCAACAGCAAGTAGTGGGAAAGATTATGAGAAAATTTATGCTAAATTTAAAAACTACAATG GTACATTCAAAGGTGATTTGTCATTCTTAAATGATTACACTTATTTTGTCAAAGACCAGAGTAACT ATGCTAAGGAAACTAGCCCAAAAAATTCTGAAGGAACCTATGCCGGTACAACCAATGCCTTGCGTC ATGGTGCTGCGTTTAGAGCCAAATATGGATCCTTATACAAGGAAAACTCAACTTTACCAATCTTCA CATCCAATTCTAACAGAGTACATGAAACTTCAAAGTATTTCGCTAGAGGGTTTTTAGGTGATGATT ATGAAGAAGGTAAAACTGTCAAGTTTAACATCATCTCTGAAGATGCTGATCTTGGTGCCAATAGTT TGACTCCTAGAAGTGCATGTTCCAAGAACAAGAACTGAGCAGTAGTACTGCCCAAAAAATATAACA CAACATATTTAAATGCTATTGCTGAAAGATTAGTTAAACCAAACCCAGGTTTGAATTTGACTACAA GTGATGTCAACAATTTATTCAGTTGGTGTGTTATGAAATCAACGTCAGAGGAAGTTCACCATTCT GTGATTTATTCACCAATGAAGAATTCATTAAGAACTCTTATGGTAATGATCTTTCCAAATATTATT CTAATGGTGCTGGTAATAATTACACCAGAATCATTGGTTCAGTGATTTTGAATTCATCCTTGGAAC TTTTAAAAGACACCGAGAACTCTAATCAAGTATGGTTATCATTTGCTCATGATACTGATTTAGAAA TTTTCCATTCTGCTTTAGGATTATTGGAACCAGCTGAAGATTTACCAACATCTTACATCCCATTCC CTAACCCATACGTCCATTCTTCTATTGTTCCACAAGGTGCCAGAATATACACAGAAAAAACTTCAAT GTGGAAACGATGCTTATGTTAGATACATTATCAACGATGCTGTCGTGCCAAATTCCAAAATGTGCTA TTGACTTTATTAAACAATGTGGTGTCAATAGTACCTACCCATCTGAGCTTACTTTCTACTGGGATT ATAAAATGTCACTTACAATGCTCCTTTAGAATTGTAA

YBR093C_homolog_4 461aa (SEQ ID NO 304)

MVSVSKLINNGLLLTSQSVFQDVATPQQASVQQYNILNFLGGSAPYIQRNGYGISTDIPAGCEIAQ IQLYSRHGERFPTASSGKDYEKIYAKFKNYNGTFKGDLSFLNDYTYFVKDQSNYAKETSPKNSEGT YAGTTNALRHGAAFRAKYGSLYKENSTLPIFTSNSNRVHETSKYFARGFLGDDYEEGKTVKFNIIS EDADLGANSLTPRSACSKNKESSSSTAKKYNTTYLNAIAERLVKPNPGLNLTTSDVNNLFSWCAYE INVRGSSPFCDLFTNEEFIKNSYGNDLSKYYSNGAGNNYTRIIGSVILNSSLELLKDTENSNQVWL SFAHDTDLEIFHSALGLLEPAEDLPTSYIPFPNPYVHSSIVPQGARIYTEKLQCGNDAYVRYIIND AVVPIPKCATGPGFSCKLDDFENFVKERIGDVDFIKQCGVNSTYPSELTFYWDYKNVTYNAPLEL

YBR181C_YPL090C_homolog 1635bp public: 1..938, PathoSeq: 939..1635; exon 1: 500..505, intron 1: 506..930, exon 2: 931..1632 (SEO ID NO 305)

ATATATATATATTTTATGTATTTTTTTTTTTTGTTGTTCAGGAATTTTAAACATGTTCATGAATAATGA TAATCTATGAACAAATTAAAGAACTCTTTGGTTTCATTTGCAACCAATGTGCGTGACTTAGGGCTA TAGCCCTACTTTTACTTGTACGATACTGCATATTTTGTTGTTGTGCGAATAGTTAGCGTAATAATC AGTTGTTTGTATAGTGAGAGTTTCACTAACACAAAGCTTCAACAATACTAACAAATTTTTCGCACGC TGTGGAAGGAGAACTTACACTGTACACTACACTACACTGTACACTATACACCACCAACAGAAAAA AGTTAATTTCAGACAGGCACAAAGGAATTAATCACCATGAAGGTATGTGATTGAATATAACCTAT AGAGTAGGAGTTTTAAACAGGATAATTGGATTCAATAAGAGGAAAAATTTTTTTATCGTCGTGATTA TAACAAATACAAAGAAATTAAGCAATGAAGTGATATAAGCAAATGAAGGACTAGTTTATTAGGGGT AACTACAAATCAATTTAGTTAACTTCAATAATGACAATAATTTTAATCACTGAAAACAATAAACAT TTTTAGTTAAACATCTCATATCCAGCCAACGGTACTCAAAAATCTATGGATATCGATGATGACACA AAATTACGTGTTTCTACGGAAAAAAGAATGGGTCAAGAAGTTGAAGGTGACTCAGTTGGAGATGAA TTCAAAGGTTACATCTTCAAAATCACTGGTGGTAACGATAAACAAGGTGTCCCAATGAAACAAGGT GTTATGCACCCAACCAGAGTTAGATTATTATTATCTAAAGGTCACTCTTGTTACAGACCAAGAAGA ACTGGTGAAAGAAAAGAAAATCCGTTAGAGGTTGTATTGTTGCTCAAGATTTGTCAGTTTTTGGCT TTGTCTATTGTTAAACAAGGTGACAATGAAATTGAAGGATTAACTGACACCACTGTTCCAAAAAGA TTAGGTCCAAAGAGAGCTAACCACATTAGAAAATTCTTTGGTTTAACTAAAGAAGATGATGTTAGA GATTTCGTTGTTAGAAGAGAAGTTACTAAAGGTGACAAAACTTACACCAAAGCTCCAAAGATTCAA AGATTAGTTACTCCACAAACTTTACAAAGAAAGAGAGCTTTGAAAAGCTAAAAAAGTCAAGAATGCT GAAGAAGACTGAAATTAAAAAGAAGAGAGCTGAATCTTTAAAGAACTAA

YBR181C_YPL090C_homolog 236aa (SEQ ID NO 306)
MKLNISYPANGTQKSMDIDDDTKLRVSTEKRMGQEVEGDSVGDEFKGYIFKITGGNDKQGVPMKQG
VMHPTRVRLLLSKGHSCYRPRRTGERKRKSVRGCIVAQDLSVLALSIVKQGDNEIEGLTDTTVPKR
LGPKRANHIRKFFGLTKEDDVRDFVVRREVTKGDKTYTKAPKIQRLVTPQTLQRKRALKAKKVKNA
QQQRDAAAEYAQLLAKRLHERKEERAEIKKKRAESLKN

YCL016C_homolog 339aa (SEQ ID NO 308)
MSEYSVYQQLNEDTNATKYTYKLLQLPSKILNQLESKSTNLYIKSDINSLALCTDSETFKLRQMNH
SNTVLLLNKEPDNKLIGFQKTSYEYELTEIKGSIDTSDIPIFNGQTAQQPIDLIALEDNSICSHQE
FLSNWYELGGCEIDNGAYIMSADIITELLYLLITKLMSLQVHEFSPEDVSSIITPPYNDSMVTSII
HKFCTIESEKYQLNDLKITQWFGIVEMSKINHKMTDISEFLLNWKTSLPSFYNPPLDISQLAGYYC
SPIENKILYVDPESLSENLSQRFKELFELDKSWNYDEFIPFIKKFVPAGKKVDSIILKYGKKKKVG
RDRFIVCPR

YCR073WA_homolog 710bp PathoSeq: 1..710; CDS: 315..707 (SEQ ID NO 309)

YCR073WA_homolog 131aa (SEQ ID NO 310) VKLPLFDLFLLGCAPDGHIASLFPNHGEQLREKLAWVLPVSNAPSGPENRITLSIPVICHSARVTF VVEGLTKAPIIKTIMERPEKGLPSSIVNEGAAGRVSWFVDDDALNDLFDITKKKYKYLSIPEPSH

YDL010W_homolog 1190bp PathoSeq: 1..1190; CDS: 501..1187 (SEQ ID NO 311)



YDL010W_homolog 229aa (SEQ ID NO 312)
MAGVRQLRIIALTAFVLGLIFTLHKVGSNAASLVHAQASDQQPNKHNTKSTTYTATNDESVANLID
SKNDPQTDDKINQKISQDQDEAINGNKDTNKDTTKVKPDNGEYDPISDLIKIRSLSPMTIFSKSYC
PYSKKIKQLLLEKYDITPAPNVVELDRYEYGAELQSYLTEKSGRRTVPNVLVGKSFESRGGCDEFE
KLHKDNDLIKLLVEWGSGRLQVAKKNTPSNA

YDL083C_YMR143W_homolog 1256bp PathoSeq: 1..1256; exon 1: 501..521, intron 1: 522..848, exon 2: 849..1253 (SEQ ID NO 313) AGTGGTTGTTCAATAATGGTAAGTTCTTGGAAATAGCCATTGTTGCTTTCTGGTGGTTAGACTTGT AGGAAGTAGAACTGTTTTCCAATGAAAAGTAGTTTTAATTAGAAAAATTTTCAAAGTGCGTGAAGC TGCTCAAAACTATATGTACTGTACACAATCTAGGGCTATAGCCCTAATATTGTACAGGAAGAACTT TGTTGTTAGTAGAGAGTGTCTCGCACTAACAGAACATTTTTTTCAGAACAGGAAAATTTTTGAAAT CTAACATCTTTTACTGAAAGCCAAGCATCAACACAATAATGTCAACCCAATCTGTTCAAGTATGTA AACGAATTGAAATAAAGAGATAGAGAGATGTTTTATTATCAAAATACGAAAGGAAAGGCAATTAAA AATAACCAGAAAACGATAATATTTTAGCGACCATTAAATGACACTTGAAGGCTCACTGGGCCAATA GAATATCTCCATATACACTTTTGAACTATTTACTAACAATTTACTTTTGTTTCTAGACTTTTTGGTA CCCCAATCACCTTGGTCCAACCAGAAATCTTAAGATTCAAAGTTTACGAACCATTGACTTTGGTTG GTTTAGATAAATTCCAAGGTATCGACATCAGAGTTAAAGTCACTGGTGGTGGTCACGTTTCTCAAG TCTACGCCATCAGACAAGCTATTGCTAAAGGTTTGGTTGCTTACCACCAAAAATACGTTGACGAAG CTTCTAAGAACGAATTAAAGAAAATTTTCGCTTCTTACGATAAGACCTTGTTAGTTGCCGACTCAA GAAGAATGGAACCAAAGAAATTCGGTGGTCGTGGTGCCAGAGCAAGATTCCAAAAATCTTACCGTT AA

YDL083C_YMR143W_homolog 142aa (SEQ ID NO 314) MSTQSVQTFGKKKTATAVAHVKAGKGLIKINGSPITLVQPEILRFKVYEPLTLVGLDKFQGIDIRV KVTGGGHVSQVYAIRQAIAKGLVAYHQKYVDEASKNELKKIFASYDKTLLVADSRRMEPKKFGGRG ARARFOKSYR

YDL125C_homolog 959bp public: 1..959; CDS: 501..956 (SEQ ID NO 315)

GTGTTGGTTGGCCTGAAGCCACTGATTTTGATAAATTAGGAAAATTGCATGAGAAATTAAAGG AAGAATTGGCTAAGGTAGATAATGAAAAATTATAA

YDL125C_homolog 152aa (SEQ ID NO 316)
MASHASCIFCKIIKGEIPSFKLIETAKTYSFLDIQPIAEAHVLIIPKHHGAKLHNIPDDYLSDILP
VVKKLTKVLKLDENNTPEGEGYNVLQNNGRIAHQVVDHVHFHLIPKKDEATGLGVGWPAEATDFDK
LGKLHEKLKEELAKVDNEKL

YDL133CA_YDL184C_homolog 25aa (SEQ ID NO 318) MRDKWRKKRVRRLKRKKRKVRARSK

YDL136W_YDL191W_homolog 1303bp PathoSeq: 1..1303; exon 1: 501..503, intron 1: 504..943, exon 2: 944..1300 (SEQ ID NO 319) TATTGTCTGATGCTATACGGAATGGGCGTTACAAATATACAAACTTATATTTGAAAGTAAATTCTA TTATTTTCTTCTATCGTATGCATACCGATTATTATCACAAGGACAATTGCCTATTGTTGTGGGAA TAAATTTAAAATCCTTCTTATTGGTGTCTAGACTTTGCTTTTTTGTGGTGATTAGGGCTTTAGCCCT CAATTAACGCTTAGATCCAATACAGTTTTGGTAACTTGTACACGAACAAAATCTCAAATTTGTTAC TGTGTGAACCAACAAGGAAGAAAAAAAACCCATACAAAAATTTTTCAGTATCAAGGAATTAGA ${\tt AGAGACGTTTAAATCAACAAAGTTCAAATCTATCAACAATGGTATGTTTAATATCGATATTATCCA}$ TAGATGTACATGTATCCTAATGGGTTTCATTATTTGGAAAGTTATGTTTATGGGAGTTCTATTTAT TAAGATATGGGATAAGAATTAAAGTATTGGATGAGTACAAGACCAACAAAGAGAAAATAGCCCC CTTTCCCTCCACTATTCAATATACTCAACAACATTATCAAGTTAAAAGTTCAGAAGATACACGTAA ATGAAAAGTTAATACCAAGAAGAATACAAATTACCAGTCCATACCGTGTTTGGGTTTAGATTACTA TATTTTACAAGAAACATATTATATGAAATGATACCCAATCCACAGCGACTTTTCAGATAGCCAAAT CTTTTTTTTTATTAGGCCGGTGTTAAAACTTTCGAATTAAGAACTAAATCTAAGGAACAATT AGAATCTCAATTGGTTGAATTGAAACAAGAATTGGCCACTTTAAAAAGTTCAAAAATTACAAAGACC AAGTTTACCAAGAATTCACACTGTTCGTAAAAACATTGCTAGAGTATTGACTGTTATTAACTTGAA TCAAAGAGAAAATGTTCGTGCCTTTTACGCTGGTAAAAAAATACATTCCAAAAGATTTAAGAGCTAA AAAGACTAGAGCTTTAAGAAGAAAATTGACTAAATTTGAAGCTTCTCAAGAAAACTGAAAAAAGCTAG AAAACAAAGAATTGCTTTTCCACAAAGAAAATTTGCTATTAAAGCTTAA

YDL136W_YDL191W_homolog 120aa (SEQ ID NO 320) MAGVKTFELRTKSKEQLESQLVELKQELATLKVQKLQRPSLPRIHTVRKNIARVLTVINLNQRENV RAFYAGKKYIPKDLRAKKTRALRRKLTKFEASQETEKARKQRIAFPQRKFAIKA

TTTCTACTACCTGTGATGACTCGCCGACATTTGTCACTAAGGATTCTTCCGAGTTAATTGAATTTG CTTGGGAAACAGTCGATAGTGTCACTTTGGAAACTTTATACAAAGGATCAAACTTGGTTCGTCCAA CCAACACCTATCACACCTTACTGCTCGAAGATTCATAGAATAACATGGGACAATGTCAAAAAATG CTGGGTCGTTCAAAGACGCCATCACAAACTTTGATCAATACGTACAAGAACACATAATTTCCAAGA AAAAGGAGTTTTCAATTGTGATGTTTGACATTTCCAAATTGAGAGTTCAGTTGGTTCGTGAAGCTA GAGACAAATCCGTGGTTTTACCCTCGTATCTACAACATCCAAGGATTTTTGATTTACCAAGAGAAT ATTTAAATTGGCAATCTAGCCACCCTGAAACATTATCATACCCCCCAACTTCTTTAACTAATATTA TTACTGCATTAGAAGTTGAGGTTGAGAATATATCTGAATATGTCGACTTGCCAAACTTTTCTTCCA CACCATCACCATCAAAAGCTTCAGCAACAACGACGACGACAACTGCAAATGTCACAGCCATTGACG TCCTTTCCAGTGAAACAGAACCAAATGGTAAAGTCATTGCAAATTTGCACGCCAAAATTGCCCAAAC AATTGATCAAAAAATCCATCCCTGTTGAGAATCACCCTAATGTATTTACAAGACCTTTTGATTCGG CTCAAGATATCACTGCTTTTACATCAGAAAGATCAAAAGTACTCTATCTTTCCAACTTGCCAAACG ACACCACACAATCAGAGTTGGAATCATGGTTCACTCAGTATGGTGGAAGACCAGGTGGGTTTTTGGA CTTTTAAGTCTGCAGATGATAACAATAATAATAACAACAACAATAGCAATGGCGGGAAAGGATATC AGAATGCGAGAAAATATGGTATTTCAGGGTTTGTGGCCTTTAATACTCATGAGGAAGCAGTTGATT GTTTAGCTTTGAATGGGAGAGTGTTGAATGATCGTCCTATTGAAGTTCAAGCGTCTTCTAGTAAAG TGTTTGATATGGCCATGGATAAATTGTTGTTGACTCTGTTCCCACTCTCAAAGAACAGACCTAGAC CCGGGGATTGGACTTGTTTATCTTGTGGGTTTTCCAATTTCCAGAGAAGAACACACTGTTTCAGGT GCTCTTTTGCGGCAGTGGCGTTTCAGGATGTTTTTAACAGTAATACAGGCAATGCCAACGGTAATG GCAATGTTAGCGGCAACCACAACCACAACCACAATAGTGGAGCTCGCCGTGGCATGAATTTACAGC CTGCTCAAGCTAATGAGAAAATTGGAACAGGCAATATTAGTATTCCTTCTTACAACGATCCAATCA AGGGTCCAACAGGTAATGTCACTAATCACCTCAACAATTCTGAGACCAATTTACTGAACAACACTA ATCTTAACAACAACAATCATCATAGTAATAATTATCACAATAACTACCATCACCACAACAACAATA ATAACAATCATGGGAATAGCAATGGTAACACCATACATGGTCGTTCCCATTATAACAATAGTGTTC CATTTAGAGCAGGTGACTGGAAATGTGAAAATTGCATGTATCACAATTTCGCCAAAAATTTGTGTT ATTCAACGCCGCTGCCATAGCTGCAGCAACAGCCAGTGGTCAACCTTTAAACTTGAATAATAATG ATTCTCGTAACAACAATGCTTCTGGGGCATCAAAGTTCAACAATGGCTACAACCCAAAGAATCAGT ATTACAATAATAATAGCAAGAATCTTAGCAACAATTTTGGTCTTAATGGTATGCATCAGCAAAACC ATGGAAGTAGCTCTTCCCATCAACTGAAACTTCAATTGAATAATACTTGA

YDL167C_homolog 729aa (SEQ ID NO 322)
MSDIYIIIHISTTCDDSPTFVTKDSSELIEFAWETVDSVTLETLYKGSNLVRPTNTPITPYCSKIH
RITWDNVKNAGSFKDAITNFDQYVQEHIISKKKEFSIVMFDISKLRVQLVREARDKSVVLPSYLQH
PRIFDLPREYLNWQSSHPETLSYPPTSLTNIITALEVEVENISEYVDLPNFSSTPSPSKASATTTT
TTANVTAIDVLSSETEPNGKVIANLHAKIAKQLIKKSIPVENHPNVFTRPFDSAQDITAFTSERSK
VLYLSNLPNDTTQSELESWFTQYGGRPGGFWTFKSADDNNNNNNNNSNGGKGYQNARKYGISGFVA
FNTHEEAVDCLALNGRVLNDRPIEVQASSSKVFDMAMDKLLLTSFPLSKNRPRPGDWTCLSCGFSN
FQRRTHCFRCSFAAVAFQDVFNSNTGNANGNGNVSGNHNHNHNSGARRGMNLQPAQANEKIGTGNI
SIPSYNDPIKGPTGNVTNHLNNSETNLSNNTNLNNNNHHSNNYHNNYHHHNNNNNNHGNSNGNTIH
GRSHYNNSVPFRAGDWKCENCMYHNFAKNLCCLKCGVAKPAINNQQNNTIHSVNSTAAAIAAATAS
GQPLNLNNNAFLNLQQQQSQSQPQGQHHYNQHSRNNNASGASKFNNGYNPKNQYYNNNSKNLSNNF
GLNGMHQQNQNQILMYSQQLQQQQQQQQQQQQQQQQQQQQQQQQQQQQDDLNGSSSSHQSKLQL
NNT

AGAACAACAAATCAAAGTTTCAAGACTATCTCAAATCTTGTTGTCACCATAACTATCAATTGTTCA CCTCTTGAACCAACATCAAATTGAATAAACATAGGATCATGAGTGACAGTGGTTATACATTAATCT ATGAGCCTAATACGGCTACGAAAGTATCTGTCAATGAATTTAAAAATTTGTTGGAAAAGGGTAAAG ATGATGTGAAAGTAGATACCATGAAGAAGATTTTGATTACCATATTAAATGGAGACCCCTTACCTG ACTTGTTGATGCATATAATCAGATTTGTCATGCCTTCCAGAAATAAAGAATTGAAAAAGTTGTTGT ATCATTATTGGGAGGTTTGTCCAAAAATGGATGAATCAGGTAAAATGAGACATGAAATGATTCTTG TGTGTAATGCCATCCAACGTGATTTACAGCATCCAAATGAATATATTCGAGGCAATACTTTGAGAT ATTTGACGAAATTGAAAGAGCCAGAATTATTGGAAACTTTAGTTCCTAATGTCCGTCAATGTTTAG AACACCGTCATGCCTATGTCAGAAAAAATGCTGTTTTCGCATTATGGTCTATTCATAAAGTCAGTG ATCATTTAGCTCCTGATGCTGACGAGTTAATTTACAGATTTTTTGTATGAGGAAAACGATTCTGTTT GTAAAAGAAATGCTTTTGTTTGTCTTGGAGACTTGAATAGAGAAGCTGCTTTGCAATATATTCAGG ATAATATTCAGTTATTGAGACTTTGGATCCATTGATACAATTGGCTTTTATTGAGTTTATCAAAA AGGACTCTATTCAAAATCCAGCTTTAAAGCAACAATATGCCCCAATTAATGACAGAAATTATTGAAA GCTCTTCAAATGTTGTTATGTATGAAGCTGCTAACACGTTGACTGTTTTGACTTCAAACCCACAAT CAATTTTGTTGGCAGGAAACAAGTTTGTTGAATTGGCTACTAGAGAGTCTGATAATAACGTTAAAA TTATCACTTTAGAGAGAATAAATCAATTACACAAGCAACATCCTGGTGTGTTACAAGACTTGTCAT TGGCTATTAAATTTGTGGAGGTTGCTGCCAATGTCATTGATTATTGTTGGATTCTATAGCCGATT TGAATACCACTGCCGCCTACGAGGTTATCACATTTGTTAAAGAAGTTGTTGAGAAATTCCCAGATT TAAGGGACGCTATTTTGAGAAGATTGATTTTGGCTTTGCCACATGTGAAAAGTGGTAAAGTTTTTCC GTGGTGCATTATGGGTTATTGGTGAGTATGCCTTAGAGGAATCATTAATACAAGAATCTTGGAAAT ATATTAGAGGAAGTATTGGTGAAGTACCAATTATTGCTAGTGAATTGAAACTGAAAAAGCGTGATG ATACTGAGGAATCACAAGAGGAAGAAACCGAGTATGATGGTAAACCTCGCAGAAAGGGTCCAGTTG TATTGCCAGATGGTACCTACGCTACTGAGTCAGCATTGACAAGCGAAACAACTGACTCTTTGGAAA GTGACAGCAAGACTCCTATCAGAAAGCAAATTCTTGCTGGTGATTTCTACTTAGGTGCTGTATTAG ACGGATTAAAAGCAGAAGCATTGTTGATTATGGTTTCGATTTTAAGAGTTGGGGAATCTAGCTTGG TTTCTAAGAAATTGATGAGGATTCTGCTGACAGAATTTTGTCTTACATCAAGATTTTGAACGATG AAGAAGACCTTCAGGAAATCAAGACAAGCTTCCTTGAAGATACTAAAGATGCATTTAAAGCACAAA TTAATAATGCTGAATTGAAGAAAGCAGAAGCATTGGCTAAGGATTTGCATGATAACGCTGAACAAA TTGACGATGCAATTGTTTTTAGACAGTTGGATAAAGATAACAAAAAGAGTAAAGCTTCTGTGGATG TTATACAATTGACTGGGTTTTCCGATCCTATTTACGCAGAGGCATTTGTCAAAGTTCATCAATACG ATGTTGTGTTAGATGTCTTGCTAGTGAATCAAACCACAACTACTTTAAGAAACTTATCAGTTGAAT TTGCTACATTGGGTGATTTGAAAGTGGTTGATAAACCAACTACCGCAAATATTGGACCTCATGGTT TCTACAAAGTTCAAACAACTATTAAAGTTACTTCGGCTGATACTGGTGTCATCTTTGGTAACATAG TGTATGACGGTCAACACTCGGACGATTCACGTATAGTTATTTTGAATGACGTTCACGTTGACATTA TGGATTACATTAAGCCAGCCACTTGTTCAGAAAGTCAATTCCGTAAAATGTGGAACGAATTTGAAT GGGAGAATAAGATAACCATTAAATCACCTATTGAAACATTGAAAGAGTACTTGGATGAATTAATGA AGGGTACAAATATGCAATGCTTGACACCGGGTGCGGTAATTGGAGAAGAATGTCAATTTTTATCAG CAAACTTGTACTCAAGGTCAAGCTTTGGTGAAGATGCATTGGCTAATTTATGTATAGAGAAACAGA GTGATGGACCAATAATTGGTCATGTCAGAATAAGATCAAAAGGTCAAGGTTTGGCTTTGTCATTGG GTGATAGAGTAGCTTCCATTTCAAGAAAAGGTAAGAAGGCAACTATTGCTCGTGTTTAA

YDR238C_homolog 952aa (SEQ ID NO 324)
MSDSGYTLIYEPNTATKVSVNEFKNLLEKGKDDVKVDTMKKILITILNGDPLPDLLMHIIRFVMPS
RNKELKKLLYHYWEVCPKMDESGKMRHEMILVCNAIQRDLQHPNEYIRGNTLRYLTKLKEPELLET
LVPNVRQCLEHRHAYVRKNAVFALWSIHKVSDHLAPDADELIYRFLYEENDSVCKRNAFVCLGDLN
REAALQYIQDNISVIETLDPLIQLAFIEFIKKDSIQNPALKQQYAQLMTEIIESSSNVVMYEAANT
LTVLTSNPQSILLAGNKFVELATRESDNNVKIITLERINQLHKQHPGVLQDLSLEILRGLSSQDLD
VKKKALDVTLQFITTRNVEDVVKLLKKELQSTALSNDDKNADYRQLLINAIHQLAIKFVEVAANVI
DLLLDSIADLNTTAAYEVITFVKEVVEKFPDLRDAILRRLILALPHVKSGKVFRGALWVIGEYALE
ESLIQESWKYIRGSIGEVPIIASELKSKKRDDTEESQEEETEYDGKPRKGPVVLPDGTYATESAL
TSETTDSLESDSKTPIRKQILAGDFYLGAVLASTLVKLILRLQSLKQTQEKILNGLKAEALLIMVS

ILRVGESSLVSKKIDEDSADRILSYIKILNDEEDLQEIKTSFLEDTKDAFKAQINNAELKKAEALA KDLHDNAEQIDDAIVFRQLDKDNKKSKASVDDVAAASGSNELKKENLSSRLNKIIQLTGFSDPIYA EAFVKVHQYDVVLDVLLVNQTTTTLRNLSVEFATLGDLKVVDKPTTANIGPHGFYKVQTTIKVTSA DTGVIFGNIVYDGQHSDDSRIVILNDVHVDIMDYIKPATCSESQFRKMWNEFEWENKITIKSPIET LKEYLDELMKGTNMQCLTPGAVIGEECQFLSANLYSRSSFGEDALANLCIEKQSDGPIIGHVRIRS KGQGLALSLGDRVASISRKGKKATIARV

YDR294C_homolog 2270bp public: 1..278/280..2270, PathoSeq: 279; CDS: 501..2267 (SEQ ID NO 325)

AAAAGCAGAACACAAAACATGGAATTTGAAAACAATTTTGTAATTCAATCGATCCGAGACTTCCAT AGCAAAGTTAACAAGCACAATTGTCATTTTAACTTAATTGGTGGATTAATCGGGATCAATCTGAAT TGTTTCCCGTATTGTTTAAAACCAAAGAAAAAGGATAATCAAAACTAAATCTTTCATATTAACACT AAAGAAAAAGAAAGCTCTCTCCCCCAAAAGAAAAAGCAAAGGTAATTCCTTCATACACACCTT TGATATCTTTCCTCTTAGACTTTTCTTTTAATACTTGCATCAATTGGAATATTACTTGTTCATACT GGAGTTTTCATTGAACTAAATATTATTAAAATATTATTATTATGAATTGAATTCAATTACGATTC CTCGGAATTTCACTGAATTCCAACTCACAGCATTAAAGATCTACTATCAACTTAAGATTTTATTTC TTGCCACATACTGTGCTCAAGGATCATTTGGCTTGAACGGTTCAGTCTGTTTAGCAAGAGATATTT TTGTTGGCTATGTTGTATACACTCAATTATTAAAGCTTTATCGAGTATTAAGAGGGTACGGTATTG TAGATTCTATTCGAAGGTTATACCTATATGTTAGTTCTACGGTGTCATCTCAAATCTTTTCACTAC CATTTATTAAATCCAAAATTGACAAGGAATTGCAAGCGACTATTGGCAAAGTAGAAGAAGAGATTA TGAAAAACGATCCACAGTTATTACAGTTTCCCGAATTGCCAGAACAGGGTATTGACGCTGACAATG TTTCCTTGGAGTTGGATAAATTACAAAACTTGAAACATTCTGACTGGATCAATGGAAGAGTCAGTG GAGCAGTTTATCATGGAGGTGAGAATCTATTGTCATTACAAGTTGAAGCTTACAAGAAATACTCGG TGGCCAATCAATTGCATCCCGATGTTTTCCCAGGTGTGCGTAAGATGGAGGCCGAAGTAGTTCATA TGGTTTTGGATATCTTTAATGCTCCGAGTGACGGGTGTGGATCGACAACTTCGGGAGGTACTGAGT CGTTATTGTTAGCCGGGTTGTCAGCTAGAGAATATGGGAAGAAATATCGTGGAATAACTGAGCCTG AAGTCATTGCCCCCGTGACAATACATGCGGGAATTGAAAAAGCCTGTTTTTATTTTGGAATGAAAT TACATAAAGTTGACTTAGATCCGGTTACCTTTCAAGTTGACGTTAAGAAAGTAGAAAGATTGATCA ATAGTAATACAGTTTTAATCTGTGGATCAGCCCCAAATTATCCTCATGGAATAATTGATGATATAG AGTCCTTATCCAAGTTGGCAGTCAAGTATAATATCCCGTTGCACGTTGATGCATGTTTGGGGTCAT TTATTGTTTCGTTTTTAGAAAAATCAAAAGTACATGGCGATAGGAAATTGCCCATATTTGATTTTC GATTACCAGGTGTCACGTCAATCTCATGTGATACTCACAAATATGGGTTTGCTCCCAAGGGGTCAT CAATAATTATGTACCGTTCGCCAAAATTACGTGAGTGTCAATACTATATTGCAAGTGATTGGACGG GTGGAATGTATGGTTCTCCAACTTTGGCTGGTTCTAGGCCAGGTGCTCTTGTAGTTGGATGCTGGG CTACATTAATCAATATTGGGAAACAAGGATACACCAAGTTTTGTTACGATATTGTGCTGGCGTCAA TGAAAGTTAAACGAGCAATTGAAACTGACCCGATACTATCCAAACATTTACAAATTATTGGTGATC CAATTGGGTCGGTAATTTCGTTTCAACTTGCACCTCAGCAATCGGGAAATTTAAGTATTTACGAGA TTAGTGATTTGTTGACCAAAAAAGGTTGGCATTTTGCAACTTTACAAAACCCATCAGCATTACATT AAGAAGCGGTGGCAATTGCCGAGGAACACAAAAAGAATGGAGTGACCAAAGCTCCAGGTGATACTG CTGCGTTATATGGTATAGCTGGCAGTGTACATACAGCAGGGTTGGCTGATAGATTAATTGTTGCAT TTTTAGATACCTTATACAAAATTTGA

YDR294C_homolog 589aa (SEQ ID NO 326)
MLELNSITIPRNFTEFQLTALKIYYQLKILFLATYCAQGSFGLNGSVCLARDIFVGYVVYTQLLKL
YRVLRGYGIVDSIRRLYLYVSSTVSSQIFSLPFIKSKIDKELQATIGKVEEEIMKNDPQLLQFPEL
PEQGIDADNVSLELDKLQNLKHSDWINGRVSGAVYHGGENLLSLQVEAYKKYSVANQLHPDVFPGV
RKMEAEVVHMVLDIFNAPSDGCGSTTSGGTESLLLAGLSAREYGKKYRGITEPEVIAPVTIHAGIE
KACFYFGMKLHKVDLDPVTFQVDVKKVERLINSNTVLICGSAPNYPHGIIDDIESLSKLAVKYNIP
LHVDACLGSFIVSFLEKSKVHGDRKLPIFDFRLPGVTSISCDTHKYGFAPKGSSIIMYRSPKLREC
QYYIASDWTGGMYGSPTLAGSRPGALVVGCWATLINIGKQGYTKFCYDIVSASMKVKRAIETDPIL
SKHLQIIGDPIGSVISFQLAPQQSGNLSIYEISDLLTKKGWHFATLQNPSALHFAFTRLTVPVVDE
LIADLVEATKEAVAIAEEHKKNGVTKAPGDTAALYGIAGSVHTAGLADRLIVAFLDTLYKI

YDR430C_homolog 3605bp PathoSeq: 1..330/1927, public: 331..1926/1928..3605; CDS: 501..3602 (SEQ ID NO 327) AATTTATAAAACCGGATAGGGCCGTTATCGCAGGACGTGTCCCATGATCAATCTACAATGAAATGA TTCACATGAAATATGTTACAATTCCACACTTGCTGCTAAAAAGCAACAGTTTTGCAATAGAGAAAA GCATGATATACTATCGATAATATCTTTCGATAAGAACTTAAATGTAGCAACGTTGAATTTTAAAAT CTCGTTGAAATCATCTCCATTCTTTTCCACGTCTTTGTTGAAAACTTTGCAACCTAAAAAAAT AAGAATCACTCCAACAAGTTTAAACTACATTATCAATTATGTTGAAAACTAGATTAAAACAAAGCA GGGCCATAAGTCGGGTTGTAAGAAGATATGCATGCTCACACCCCATTTCTCCCAATCTTGATAAGT ACCCAGTTGGTCTAAAATTGCATGGTTACGAAGTTACCCAAACATCACCTATCCCAGAATTTTCCC TCACTGCTGTATCATTAAAACACACAGAGAGTGGTGCAACTCACTTACATTTGGATTCCCCTAATG ACAGTAATAATGTATTTCTGATTGCCTTCAAAACAAATCCTCCAGATAATACTGGGGTTCCCCATA TTTTAGAACATACAACTTTGTGTGGTAGTAAAAAGTTTCCGGTCCGTGATCCATTTTTTAAAATGA CCAACAGGTCGTTGAGTAACTTTATGAATGCAATGACAGGCCATGATTACACATTTTATCCATTTG CTACCACCAATTCAAAGGATTTTGAAAACCTAATGGATGTGTATTTATCGTCAGTGTTTGAACCGC AATTAAACCATACCGATTTCTTGCAAGAAGGATGGAGAATAGAAAATCAAAATGTTCATGACATAT CGTCCAAGCTTGAATTCAAGGGAGTTGTATATAATGAAATGAAGGGCCAGTATTCGAACTCTGCAT ATGCAAAAACATTTACTTATGGAAAATTACCATTGGAAGACAGTTTAAGTAAAATAAGCAAATACT ATGAATCATTCGAAAAAAAGGTGTCTTCAGTTGACGTCAAACAACCTATATTTTCTACAGATAAAT AGTACTGCACATCTATCACCTGGAACTTGGGTAATCCATTGGATCCAAACATGCAGTATGATATTT TTAAATGGAAAATATTGAGCTCATTATTGTTTGATGGACACACTCTCCTTTCTATCAAGAGTTAA TTGAAAGTGGATACGGTGACGATTTTTCTGCAAATACTGGGTTGGACTCAACCACCGCGTTGCTTT CGTTTACTGTTGGTCTCAACTACTTAACCAAGCAAAAAGTTGATAATTTTAATGAAAAAGTTATGG **AAATCATTAATAATAAATCATTCCCGAATTAAGTAACGAAGAGTCCTCTTCATATCATGGTAGAA** TTGATGCTATATTGCATCAAATAGAAATAGGATTCAAAAGACACAAGCCCGATTTTGGATTTGGAT TATTGAGCTCTATTGTTCCGTCATGGGTGAATGGAGTTGATCCAATTGACACCTTGCAAGTGGAAA AGATATTGTCGCATTTTAAAGAAGATTATAAACAAAATGGTTTAAGGATCTTTAAAGAATTATTAG AAAAGACATTGTGTAACCCTCATTCGCAAAAATTTAAATTCACCATGGAGCCAAGAGAAGATTTTA CCAAACAATTGGTAAAAGATGAGAATTTGATGATCGAGAAAAGAGTAAGTGAACTCACAGAAGATA ACAAGAAGCCAATCTATGAGCAAAACTTGGAATTAGCTAAATTACAATTGGAGGATCAAAATACAG AAGTTTTACCCACATTGACTATTGATGACATTCCAAAGAGAGGTGATTTTTATGCCATTGATTTGG GCCAAGTAAATAAGAAAGTTGTACATGAAAGGGTAGTTGATACCAATGGCTTGGTTTATGCCAACG CTTTAAAAGATATTTCCTATTTACCCACCAAACTTTACAAGTACCTTCCATTGTTTAACAACTGTT TGACGAACCTTGCTGGAACAGAAAACACACCCATTACGGAGTTGGAAACTAAAATACAAATGTTAA CTGGCGGGATAACATTTAGTTCTAAAATATCGACTGACCCCTATAATATTGAGCAACTAAAATTAC AGTATGTGTTAAGTGGAATGGCTTTGAAAGAAAAGTCATCCTCAGTTTATGATTTATGGTTGGAGA TTTTAACTACTACCAAATTCGACACCAGTGATGAGGTATTAGAAAAGTTGTCAGTTTTGATTAAAA ACATGGGACAAAACCAAATCAATAATATTGCTGATCGCGGTCATTCTTATGCGGCTGCTGTGAGCT CACTGAAATTGACACCGCTGAAATACATCAGTGACATCGTTTCAGGTTTGAGTCAAGTTCAATTTG TAATGGAGTTGAACTCCAAATTAGAATCAGAAGGGAAAGAGTACTTGGCCAAAGAGATTATTCCGA TATTGCAAGAAATACAAAAGTATGTATTGCAAGGTGAATTCAGGTATAGACTAGTTGGAAATCAAG AGATTATTGTTGAAAAACGAAAAGCTTATTGAGAAATTTGATAAGGATATTTCTTCGAACAGACCAA CTTTATCGTTAACAGTAACAGATGGTTTACTGGCATTGTTGAACTCATTCAATTACAATCATACAA GTGAAAATGTCTTAGTTAACTTACCATTTCAAGTGGGATACTCTTCATTAGGTAAGATTGGCTCTT CGTATTCATCAAAGGATGGTGCTTCTTTACAAATATTATCTCAGTTATATTCCTTTAAAAATCTAC ATTCCAAAATAAGAGAAAGCAATGGTGCATATGGAGGTGGTTTGACATATGATGGGTTGAACGGGA CATTAAACTTTTATTCGTATCGTGATCCTAATCCTGTTAAGTCGATTCAAACTTTTAGAGATTCCT TACTGTATGGACTTGATGCTAATTGGAACGATAAGGATTTACAAGAGGCTAAGTTGCGGGTTTTCC AAAGCGTCGATGCTCCAATTAATATCTCTCTCAGGGTGCTAGTGCCTTCTTTGAAAATATAGATG

ATTACTTGAGACAGGAAAGAAGAGAAAACTTTTTGGGTACCACTTTAAAGGATCTCAGAGATGTGA

CTGAAAAGTATCTTGTTGATAACCAAAACAACCTTGTCACTGTTATTGGTGACAATGAAATTTTAA ATGTCGATAATAAATGGCAAATTAGAAATTTTCAAGTATAG

YDR430C_homolog 1034aa (SEQ ID NO 328) MLKTRLKQSRAISRVVRRYACSHPISPNLDKYPVGLKLHGYEVTQTSPIPEFSLTAVSLKHTESGA THLHLDSPNDSNNVFSIAFKTNPPDNTGVPHILEHTTLCGSKKFPVRDPFFKMTNRSLSNFMNAMT GHDYTFYPFATTNSKDFENLMDVYLSSVFEPQLNHTDFLQEGWRIENQNVHDISSKLEFKGVVYNE MKGQYSNSAYYFYIKFLESIYPSLNNSGGDPKKIVDLSYEGLLEFHSKNYHPSNAKTFTYGKLPLE DSLSKISKYYESFEKKVSSVDVKQPIFSTDKSEIFDVTIPGPVDTMNGKETSEQYCTSITWNLGNP LDPNMQYDIFKWKILSSLLFDGHNSPFYQELIESGYGDDFSANTGLDSTTALLSFTVGLNYLTKOK VDNFNEKVMEIINNKIIPELSNEESSSYHGRIDAILHQIEIGFKRHKPDFGFGLLSSIVPSWVNGV DPIDTLQVEKILSHFKEDYKQNGLRIFKELLEKTLCNPHSQKFKFTMEPREDFTKQLVKDENLMIE KRVSELTEDNKKAIYEQNLELAKLQLEDQNTEVLPTLTIDDIPKRGDFYAIDLGQVNKKVVHERVV DTNGLVYANALKDISYLPTKLYKYLPLFNNCLTNLAGTENTPITELETKIOMLTGGITFSSKISTD PYNIEQLKLQYVLSGMALKEKSSSVYDLWLEILTTTKFDTSDEVLEKLSVLIKNMGONOINNIADR GHSYAAAVSSSKLTPSKYISDIVSGLSOVOFVMELNSKLESEGKEYLAKEIIPILOEIOKYVLOGE FRYRLVGNQEIIVENEKLIEKFDKDISSNRPTLSLTVTDGLSALLNSFNYNHTSENVLVNLPFQVG YSSLGKIGSSYSSKDGASLQILSQLYSFKNLHSKIRESNGAYGGGLTYDGLNGTLNFYSYRDPNPV KSIQTFRDSLSYGLDANWNDKDLQEAKLRVFQSVDAPINISSQGASAFFENIDDYLRQERRENFLG TTLKDLRDVTEKYLVDNQNNLVTVIGDNEILNVDNKWQIRNFQV

YDR450W_YML026C_homolog 1366bp public: 1..1366; exon 1: 501..548, intron 1: 549...976, exon 2: 977...1363 (SEQ ID NO 329) TTAAGAACTAGCAGATGTAAAATGTTTTATGTCATTATAATATTTGTTAATACATGTATATAGATT TTTTAATGAATGTATTCCCTAAATAGAACAGAATTATGATGCTGTTACAGCAAAAACTGGTTTGAG GCGCGCGATTCTTCCTGCTAGAGGTTTTTCTTTTTGTATGTCTGTAACAGTGCGACTCACATAGTT AAGTAATTTTAAAGCCAGAGATTGTGTACAGTCGCACGCCCCTAATCACATAGTTAATTCTCAAA TTTTGTATAGTTCAGTTTAACAACACCAGTAATCAAACATGCCATTAGTTGTCCAAGAACAAGGTT CATTCCAACACATTTACGGTATGTGAGTGTATTATAAGATTATTTGAATGAGATAGAAAAGGGTT AAGGAAGGAAAGAAATTATCCAACTACTGTTTTGGGAAAGATTAATCAGAAATTTGAATGCAATGA AAAAACTTTTTCAAGAGATGGATATGGAACAAGATTCGATTGTTATCAACAAATATAAAGAAAAGC AATGATTTACTACTGTTTGGGAAAGATTTTGGATATGTGTATCAACAATACTACTATTTACTTTGG AGTAATATGTTTTCAATATTATCAGAGACTTATCAAAATTTATGAGTTTATTATTATTGAAGTTCA ATACCATCAAGCCTTTTTTTTAACCATCACTCTATTCAACAATCATTTAAATATTAAAGTCTTTTT TTTCCCTGTTTAAAGTATTCGATTTACTAACATTATGAATTATTATTATAGTTTGTTAAACACCAA CATTGATGGTAGAATCAAGATCATGTACGCCTTGACCAAGATCAGAGGTGTCGGTAGAAGATATGC CAACTTGGTTTGTAAAAAAGCCGATGTTGAATTAACCAAAAGAGCTGGTGAATTGACCCAAGAAGA CAGACAAAAAGATCAAGTTGATGGTAAAGATTACCATGTTTTAGCTAACAACTTGGAATCTAAATT GAGAGATGATTTGGAAAGATTGAAGAAAATCAGATCTCACAGAGGTATTAGACACTTCTGGGGATT GAAAGTTAGAGGTCAACATACTAAAACTACTTCTCGTGGTCGTTAA

YDR450W_YML026C_homolog 145aa (SEQ ID NO 330)
MPLVVQEQGSFQHILRLLNTNIDGRIKIMYALTKIRGVGRRYANLVCKKADVELTKRAGELTQEEL
ERIVTIMQNPTNYKIPAWFLNRQKDQVDGKDYHVLANNLESKLRDDLERLKKIRSHRGIRHFWGLK
VRGQHTKTTSRGR

TTTTCACACTAAGTTAAGGAGAGTGCGAAAAATTTAGTACTAACAAAATTGTATTGTGTTGTGTGT TTATTGTATTAACATTTTAAGATATCAAGAAACTAAAAATGGCTAAGTTCATCAAATCTGGTAAAG TTGGTATGTAAAAATGAGTACCTATATGGGTAGACAATGATAGATTTATTGGCCAACTATGAATGG GATAGATATATGATATGGGAGAGAATTTTGAAGGATTGAAATATTTTATAAAAGAGAGAGAGC GAAGATTTAAATGATTACCATCGTAATAAATTTATTGGAATTTTGGAGATTCTTTTTGGAGTTAAGA AAAAAGCAAGTGATTGATCAATCACTATGGAGCCGTCACAAGACATCAACGAATCCCACAACATTT ATTATACTAACTAAATTTTTTAGCTATTGTTGTAAGAGGTCGTTACGCTGGTAAAAAAGTAGTCAT TGTGAAACCACATGATGAAGGTACCAAATCTCACCCATTCCCACATGCCATTGTTGCTGGTATTGA AAGAGCTCCATTGAAGGTTACCAAGAAGATGGATGCTAAAAAAGTTACCAAAAGAACTAAAGTCAA GCCATTTGTTAAATTAGTAAACTACAACCATTTAATGCCAACTAGATACTCATTAGATGTTGAATC ATTCAAATCTGCTGTCACTTCTGAAGCTTTAGAAGAACCATCTCAAAGAGAAGAAGCTAAAAAAGT TGTCAAGAAGGCTTTTGAAGAAAAACATCAAGCTGGTAAGAACAAATGGTTCTTCCAAAAATTACA

YDR471W_YHR010W_homolog 136aa (SEQ ID NO 332) MAKFIKSGKVAIVVRGRYAGKKVVIVKPHDEGTKSHPFPHAIVAGIERAPLKVTKKMDAKKVTKRT KVKPFVKLVNYNHLMPTRYSLDVESFKSAVTSEALEEPSQREEAKKVVKKAFEEKHQAGKNKWFFQ KLHF

YDR486C_homolog 1157bp PathoSeq: 1..1157; CDS: 501..1154 (SEQ ID NO 333)

TTCCAGTCATTCCGAAATGCATAAGCAAGACGTTAGTTGTATTGTGGTTGTTTAGTCTAATCCAAA AATACTTGCCATGACGACCCACTGAAGTAACAACTGCATTTGTTAAGGCTTTTCTCATCTTATTCA ATTCTTTTTCAGCATCATTCGTATCTTTAAGCACAGGGAATAGCAATGGATCATGTAACAAATTCA AGTTAGTCGTCAAGAAAATAATTCAGTGTTAAAGTCTGTACCTTAAGCGTCAAACGTACTTCTGCA GGAGGTTTTAGAAGGCAAAACCAAATCTAGACAAGGAGATGAACAGATTATTCGGAACGAAAAGCA CTGCGCCCAAACCATCTTTGAATGATGCAATCAAGGGAATCGATGAAAGAGTGGGGTCTTTGGATG TTAAATTAAGCAAGATCAACTCGGAATTATCCACATACCAACAAAAGATAAGCAGAATGAGAGACG GACCCGGGAAGTCGGCACTAAAACAAAAAGCAATCAAGTTACTAAGACAGAGGAAGCAGATAGAAG CTCAAAAGGATCAGTTAGAGAATCAATCTTGGAATATGACACAAGCTTCCATGACAACAGATAACT ATGAACTACAGGAGGCACTTCTGACGAGCTATGATGTACCCGATGACATCAGTGAGCTGGAGTTGG ATGCTGAATTAGAAGCTCTTGGCGAAGAAATTGATTTTGAAAATGAAATGGCAGAGAGTGGGATAG GTGCACCTAGTTACTTAAATGATACAGAACCTACAGCAGCAGATAAATTGCCTACATTTATTGACG AACAACCAGAAGAAGCTCAAAAAAATCGCAAACTAG

YDR486C_homolog 218aa (SEQ ID NO 334)
MNRLFGTKSTAPKPSLNDAIKGIDERVGSLDVKLSKINSELSTYQQKISRMRDGPGKSALKQKAIK
LLRQRKQIEAQKDQLENQSWNMTQASMTTDNLQNTMVTINAMKTANKSLKQTYGKINIDELEDLQD
EMLDLIDKSNELQEALSTSYDVPDDISESELDAELEALGEEIDFENEMAESGIGAPSYLNDTEPTA
ADKLPTFIDEQPEEAQKIAN

TCATTTGTTGACTTTTGAAAGTTTTATTCATCCATATTCTTCAAGTTAAAATAGTGTTCAATATCT GTCCAACCAAGAAGAAAACCAATAAACAACATCAATTCCAACTTTGTTTACATCAAACAGAAACAA AAAACAGATAATTTATAGACACCTTCATTCATTCGTTATTTTTTTCCAAGTACTACACGTCTTTAT CGTCATCGATTATGTCCCAATCAAATCATAATCATCCACAGAAGATCGGACCTTGGAAATTAGGTA AAACTTTAGGAAGAGGTGCCACCGGTAGAGTCTTATTAGCTACTCATCAAACTACTGGTCAAAAAG CTGCCGTTAAAGTAGTTTCCAAATCCGAATTACAAGACGAAGAAACCGAGAAAAATGGAGATGGAT TATATGATGTATGGGAAACATCTAAGGCTCTTTATCTTGTTCTAGAATACGTTGAAGGTGGAGAAT TATTTGATTTATTGGTGGAACGTGGTCCATTACCTGAAGTCGAGGCTATCAAGTATTTCCGTCAAA TCATATTGGGTACGGCTTATTGTCATGCTCTTGGTATATGTCACAGAGATTTAAAACCAGAGAATT TGTTACTAGATTCTCAATTGAATGTAAAATTAGCCGATTTTGGAATGGCAGCTTTAGAAAGTAACG GCAAATTATTAGAGACTTCTTGTGGTTCACCTCATTATGCTGCTCCAGAAATCGTTAGTGGATTGA AATATCATGGAGCTGCTTCTGATGTTTGGTCTTGTGGGGGTTATATTATTTGCCTTGTTGACAGGTA GATTACCCTTTGATGATGAAAATATTAGAAATTTACTTCTTAAAGTCCAGGCTGGTAACTTTGAAA TGCCCGTTGATGAAGTTAGCAGAGAAGCTAGAGATTTAATTGCTAGAATGTTAGAGGTTGATCCTA TGAGAAGAATATCTACTGAAAAAATCTTAAGACACCCATTGTTAACCAAATACCCAATGTCAAACG AAGATTTAATCAGTGAAAAATCATTACCACATCCACATACTGGTTACAAATCTTTAGGGTCAGTTA GAAACATTGATAAACAGATTTTATCAAACTTGACAATTTTATGGAATGATAGACCCGAAGAGGAAA TTGTTGATTGTCTTTTGAAAGATGGATCCAATCCAGAAAAAACATTCTATGCATTATTGATGAGAT ACAAGCATAATCAAGACGATAACACTAATAACAATTCACCAAAGAAATCAACGAGTTTCAATAATA AAGTGGTACGCAGTGGGTCCAAATACAGTCTTAATGGAACCCCTAGAAGAAAAAAGAGCCAGTCACA TAAGTGTGTCAAGACCAACATCTTTCCAATACAAGTCTAATCCTGGCGCTGGTGCAACAGCAAATA GAAACTCCGTTGCCAGACATTCTGTGGCTTCCTCGGCCAACAATTCTCCTCGTAAATCACCATACA AGTCACCATACAGATCACCTTATAGATCACCATATAAATCGCCTTCTAAGAGATATTCATATAATC AATCCCCAACTAAATCTCCTTACGGAAGAAGATCAAATTCACAAAGACAATTTGAAAAATGAACCAT TAAAGGCAAAGCCAAGAAATATTTACAATGAGATTGTTGATGCACAAAGCAACTTTTCTCTACCTC CATCGCTTCCACCTTACCTTCAAAAGATTCTCGTTATATGATCGATGAACCCAATCAACCCC AGTTGCAACAACCTGCTTTAAGTCAAGTCCCTGAAAATCCTATTGTTGATGAATCCCCTGATTTAA TGCAGTCAGCAAAAATTTCTAGTGGAAAGAGAAATTCAATAATAGGAAAGAACAACAACAACAACAGCA ACAGCAACAAGAGAATGTCTAAGAGAAAATCAATTCGTGCATCTATGACCACGGGATTGAAAAAGAA ATTCCATAACCATGAAATTGTTATCTACTTATGCTAAATTATCAGGTGATGACGACTGGGAATACA TGGATAAACAAACAAAAGAACATCGGCTACTTTTGCAGCATTGTGTGACAAAATATTTAATCAAG <u>AAGACTATGACGAAGAAGACGAACAATTAGTTGATCCTGAAGAAAAGGAAGCCAAGGAATATGAAA</u> GGTTAATGGAATTGGAAAGAAAGAAACATGAAGCTGAGTTGAAAGCTAGAAGAGAGAATTAGAAAAGA AGAAAAGAAGACAAAAGAGACGTTCCATTTTGAGTTCTAAGAAATTAAGTATTATTGTCAAGAATG ATGCTGATCCAAATAATAGTGAACAAGAGTTGGTCGATGAAGGTATAAAACAACCAAAACGTCAAT CCAAAAACTTGACCGCTTTAAGAGCATTATCTGAAGGAAATCATGCATCTGAAGAATTGACATTGG **AAGACGTTGAGAATTTGAAGAGACGATCAGCATCACAGCCGGTTCCAAAAAGAAGACAAACTCCGG** TTTTGACAAGAAGACCTGTATCAAGATTAGATCCATTATGGCAAGCACACGAGAATGAACAGTTAG ATAGAGCAAAAGATGCCTTGGAACAAGAATGGAGGGATTCACAAAAGAGAAGTTCTACTGTTAGTC GTAAAAAGTCAACAGAGAGTCGATGATATCAGTTATGGATGATATTGTTGAAGAGGACCAAGGCC GTGTCAACAGGAGATCAACACGAAACACTTACTATGAAAGGGAAAGAGACTATGAATTACCAGAAC CAACTGTGGAAGATTCCAACTTGACTGATGACTACATGACAGAAATCAGAAAATCAAGACTTTTGA ACAGTCAGTTAAATGTTAGGGATCCACTTAATGAAAAAAGAAAATCTGAACCCAAGACTCTTATTA GCAATGTTCAAATACCGAGTGTTACTAGAAAATCAAGAAATTTCACTACTTCCAACAAAAGGTTGT CGGTATTGTCTATGTATTCAACAAAGGAATCATACCGTGATTTGAATTCTATAATTAACTCACCAG ATGAAAACCCCGAACAGCATCAAAACATGAACAAGCCAGCGTTACGAACCAGTATTGCTGATCGTT TGGATAAAGCTGGATTGGCTGAACCAGAATATGAAACTGAGACTGATGGTGAAGATAAAGTGTCTG TTATTGATTTGGATGATCATTTAGCTGATAGAAGGACTTCCTATTATGATGGATCTGGAAAGAGAG CATCTAGAGCTTCAACAACTAAACGTTACAATGTTCATTCCAGTTCAGAAAAAAAGACCAAAATCCA AAGTTCCTGATTTGCCAAAGAATGATTATGATGACACATTTGTCAGTAATAGTGATGAAGTTCATA AGCGTCAGTATAAATCGATGGTTTCTGATGAGTCTAGTGCATCTGATGATGTATTTGATAAGATTA AATTACCAGATGGTAAATCAACTAAATCTTCCATTGATGAATTGGCTAACGGCACGTCTACAAGTG GTCATAGAAAACCAAAGATAAGACATTCTCAACCGGGCCCAGAAATGTTGATTCCTCATTTGAATG GAGGTATTGAGTCGTCTCAACCAATGTCTAAAGTTCGTGGTAACAATTCAAGTGGTCATGATGATA



YDR507C_homolog 1349aa (SEQ ID NO 336) MPHSRQPSISSSIMSQSNHNHPQKIGPWKLGKTLGRGATGRVLLATHQTTGQKAAVKVVSKSELQD EETEKNGDGLPYGIEREIIIMKLLTHPNVLRLYDVWETSKALYLVLEYVEGGELFDLLVERGPLPE VEAIKYFRQIILGTAYCHALGICHRDLKPENLLLDSQLNVKLADFGMAALESNGKLLETSCGSPHY AAPEIVSGLKYHGAASDVWSCGVILFALLTGRLPFDDENIRNLLLKVQAGNFEMPVDEVSREARDL IARMLEVDPMRRISTEKILRHPLLTKYPMSNEDLISEKSLPHPHTGYKSLGSVRNIDKQILSNLTI LWNDRPEEIVDCLLKDGSNPEKTFYALLMRYKHNQDDNTNNNSPKKSTSFNNKVVRSGSKYSLNG TPRRKRASHISVSRPTSFOYKSNPGAGATANRNSVARHSVASSANNSPRKSPYKSPYRSPYRSPYK SPSKRYSYNOSPTKSPYGRRSNSQRQFENEPLKAKPRNIYNEIVDAQSNFSLPPSLPPSLPSKDSR ${\tt YMIDEPNQPQLQQPALSQVPENPIVDESPDLMQSAKISSGKRNSIIGKNNNNSNSNKRMSKRKSIR}$ ASMTTGLKRNSITMKLLSTYAKLSGDDDWEYMDKQTKRTSATFAALCDKIFNQEDYDEEDEQLVDP EEKEAKEYERLMELERKKHEAELKARRELEKKKRRQKRRSILSSKKLSIIVKNDADPNNSEQELVD EGIKQPKRQSKNLTALRALSEGNHASEELTLEDVENLKRRSASQPVPKRRQTPVLTRRPVSRLDPL WQAHENEQLDRAKDALEQEWRDSQKRSSTVSRKKVNRESMISVMDDIVEEDQGRVNRRSTRNTYYE RERDYELPEPTVEDSNLTDDYMTEIRKSRLLNSQLNVRDPLNEKRKSEPKTLISNVQIPSVTRKSR NFTTSNKRLSVLSMYSTKESYRDLNSIINSPDENPEQHQNMNKPALRTSIADRLDKAGLAEPEYET ETDGEDKVSVIDLDDHLADRRTSYYDGSGKRASRASTTKRYNVHSSSEKRPKSKVPDLPKNDYDDT FVSNSDEVHKROYKSMVSDESSASDDVFDKIKLPDGKSTKSSIDELANGTSTSGHRKPKIRHSQPG PEMLIPHLNGGIESSQPMSKVRGNNSSGHDDSVPPPPPAHKVNKKPLDDKTNFPPPEVDPKRKGSF FRKLSWGSKKTIENNTNAATNTTTQQQLPSPAESKEEKPKSSFFRWFSSSNTPSAAEIRKFNTILP KHEMSTALFALLNSWSNFGLKDLRNDQVGYYITGAISKHNSFNLKSCKFRIKINQRDFNQKSEIVC VRVKGSKVTTDTLFCEIEKVLLKEGGLDK

YER102W_YBL072W_homolog 1121bp public: 1..1121; CDS: 501..1118 (SEO ID NO 337)

AAAATTTTCATAATTTAGAAGTTTCATTTACAGTCTTTTTTCAATTAACAGTGATACAAGAGTGTA TGTAAAGACAACATGTACTAGCAACTATAATATGATTTACCAATGATTGGGATCACAATAAATGTG TTAATATGAATGAGAGAAGGATAGTGAATAAGAGATTACGAAAGAATAGATTCAACAAGTTCAGAA TGGTATACAACTAAAATGGAATTATTTTCAAATATGCAACTATCATTATGACTACTACGACAACAA TTTTAATCGAGAGAAGATCATTAGATCAAGAGTTGGGAAACTAATACCAAGGAAATATCATTAAGA ATTAATAGCTTTGCAAAAATTGGTTTTACTCATATTATTTGTTTTAGTTGGAAAGCGATTACATCA TGGAACAAGTTTACTAACAACATTGTTATAGGTAAAAATGGGTATTTCTAGAGATTCACGTCACA AACCAGCCAACACCAAGATTGGTCCAAAAAGAATTCACTCTGTCAGAACCAGAGGTGGTAACCAAA AATTCAGAGCTTTGAGAGTTGAAACCGGTAACTTCTCTTGGGGTTCCGAAGGTGTTTCCAGAAAAA CCAGAATTGCTGGTGTCGTTTACCATCCATCTAATAACGAATTGGTTAGAACCAACACCTTGACCA AATCTGCTGTTGTTCAAATTGATGCTACTCCATTCAGACAATGGTACGAAAACCACTACGGTGCTA CTTTAGGTAAAAAGAAGGGTGGTGCTCATGCTGCTCACGCTGCTGAAGTTGCCGATGCCAAGAGAT CAAGAAAAGTCGAAAGAAATTGGCTGCTAGATCTGGTGCTGCTGCCATTGAATCCGCTGTTGACT ${\tt CTCAATTCGGTTGGTAGATTATACGCTGTCATTTCTTCAAGACCAGGTCAATCTGGTAGATGTG}$ ATGGTTACATCTTGGAAGGTGAAGAATTAGCCTTCTACTTGAGAAGATTAACTGCTAAGAAATAA

YER102W_YBL072W_homolog 206aa (SEQ ID NO 338)
MGISRDSRHKRSATGAKRAQFRKKRKFELGRQPANTKIGPKRIHSVRTRGGNQKFRALRVETGNFS
WGSEGVSRKTRIAGVVYHPSNNELVRTNTLTKSAVVQIDATPFRQWYENHYGATLGKKKGGAHAAH

AAEVADAKRSRKVERKLAARSGAAAIESAVDSQFGSGRLYAVISSRPGQSGRCDGYILEGEELAFY LRRLTAKK

YFL014W_homolog_1 819bp PathoSeq: 1..819; CDS: 419..816 (SEQ ID NO

TTCTCCTGTGAAAAGTTTCGAGATGTAACGTTTCGCAGTAATAGAGAGCCAGAATCCATTTTTGTG TACTACAGACAAATTCAGAAGTTTCAACTGCTGCATATCGCCTTAAATGACTGTAGCATTCGTCCA AATTGAGACCCTCAATTACATTTTGTCAAAAAAATTGGTCCCTAGTGTTGCTATCGATAACGAAGG TGAAGGCAGTTTAGCTTGGAGACATTTAGAGAACTTAGTTACATCTCATCTTCCGTTTCGAGAAAT CGTTGATTTACCGTGCAGCGCTTATATTGATTGCTACTTGTTCCCAGCACCACAGCAATATAGCAA TCATAAATAAATTGCCCCGCGGTTGACAGTGTATATCTTCGAGGAATGGCAACCTTTGCCCCCCTC TCGAAAAACAATATAAATAGAGTCAATTTCTCTAGTAGAGGTAAATTCTTTGAATCTTGTTTTTTT TCGACATACACCATAAATCCCATAGAAAACTGCAAAATGTCTGACGCCGGAAGAAAAAACATTTCT ACTAAAATCAACGAAGCTATAACCCCCGAATCCGAAAAGTCTACCTTGGAAAAGGGCAAGGAACAA GTCACCAGTACCCTTGACAAAGCTGTTGGCTCAAATGTTCCAGATAACCAAAAATCTTTCACTCAA ACTGTTGCAGACAGCGTGCAACAAGGTTCCGATAATGCTAAAGCTGATTTGAAGAAACAATCCGAA CAAGCAGAGGGCGAACAAGACCCTTGCTGAAACAGCTCAAGAATATGTCGAGGTTGCCAAAAACTG AAATTGGAAAGGCTGCTGAATACGTGA

YFL014W_homolog_1 106aa (SEQ ID NO 340) MSDAGRKNISTKINEAITPESEKSTLEKGKEOVTSTLDKAVGSNVPDNQKSFTQTVADSVQQGSDN AKADLKKOSEQAEGEORPLSKOLKNMSRLPKSKLERSSNT

YFL014W_homolog_2 884bp public: 1..884; CDS: 501..881 (SEQ ID NO

CCTTCTCCTGTGAAAAGTTTCGAGATGTAACGTTTCGCAGTAATAGAGAGCCAGAATCCATTTTTG TGTACTACAGACAAATTCAGAAGTTTCAACTGCTGCATATCGCCTTAAATGACTGTAGCATTCGTC CAAATTGAGACCCTCAATTACATTTTGTCAAAAAAATTGGTCCCTAGTGTTGCTATCGATAACGAA GGTGAAGGCAGTTTAGCTTGGAGGCATTTAGAGAACTTAGTTACATCTCATCTTCCGTTTCGAGAA ATCGTTGATTTACCGTGCAGCGCTTATATTGATTGCTACTTGTTCCCAGCACCACAGCAATATAGC AATCATAAATAAATTGCCCCGCGGTTGACAGTGTATATCTTCGAGGAATGGCAACCTTTGCCCCCC TCTCGAAAAACAATATAAATAGAGTCAATTTCTCTAGTAGAGGTAAATTCTTTGAATCTTGTTTTT TTTCGACAAACACCATAAATCCCATAGAAAACTGCAAAATGTCTGACGCCGGAAGAAAAAACATTT CTACTAAAATCAACGAAGCTATAACCCCCGAATCCGAAAAGTCTACCTTGGAAAAGGGCAAGGAAC AAGTCACCAGTACCCTTGACAAAGCTGTTGGCTCAAATGTTCCAGATAACCAAAAATCTTTCACTC AAACTGTTGCAGACAACGTGCAACAAGGTTCCGATAATGCTAAAGCTGATTTGAAGAAACAATCCG AACAAGCAGAGGGCGAAGCAAAGACCCTTGCTGAAACAGCTCAAGAATATGTCGAGGTTGCCAAAA CTGAAATTGGAAAGGCTGCTGAATACGTGAGTGGAGTTGTCACCGGTGCTACCGAAGGTGCCAAAA CCGGCGCTGATAGTACTAAAAAATAG

YFL014W_homolog_2 127aa (SEQ ID NO 342) MSDAGRKNISTKINEAITPESEKSTLEKGKEOVTSTLDKAVGSNVPDNQKSFTQTVADNVQQGSDN AKADLKKQSEQAEGEAKTLAETAQEYVEVAKTEIGKAAEYVSGVVTGATEGAKTGADSTKK

YGL011C_homolog 1244bp PathoSeq: 1..1244; CDS: 501..1241 (SEQ ID NO 343)

GAAGGGCACCATAATGAAATCGACTCACTTCAGGATTATAATGGTATGAAACATTGTACTTGTTAT TAGTGCCAGGATGATTAGGATCATATATTGGGGTGTTTTCTCGAGTCTTGGTATCGGTTGTAAACG TATCTGTTTCACTTATCAGTATCGTCATTTATATTAACTACTTTTCTCCTATGGTTATATATTGGT AAACAAAGAAACAAAACAACAAAAAAAAGAAGTAGTAGTTTTGAAAATTGTCAATAAAAGAAACAAAG AATGAAAGAATGAATGAAAGAAAAAAAAAAAAATATGAAAGTGAGTGCGACATAATGTAGAAAAA TGTCGAATGTCTTGAACTTTACCCATTGAGTAGTTGTTGTAGTGTAGGAGGAAGAAAACAACAGAA AGAAAGAGAAAAGAAAAATTTCGCCACTACAAATATTCAACAAGTTTCATATAGTAATAATACC CAATTGATCATTACTTTATTCCACACAATTCATAAACAATGTCCAATTCAGCAGGTTTTGATAGAC ATATCACTATTTTTTCTCCTGAAGGTAGATTATACCAAGTAGAATATGCTTTTAAAGCTATCAATT CAGCAAATATCACCAGTTTAGGAATCACAGGTCAAGATTCTGCCGTTATTATATCACAAAAGAAGA

TCCCAGATAAGTTATTAGATCCTAAAACCGTGTCATATATTTTTAAAATCACTCCTAGTATAGGAA
TGGTTGCCACTGGATCAATTGCTGATGCTAGAGCTCAAGCCATGAGAGCAAGATCTGAAGCTACAG
AATTTAGATATAAATATGGTTACGAAATGCCGGTGGAAAGTTTATCAAGAAGAATGGCGAATATAT
CTCAATTGTATACTCAAAGAGCTTATATGAGACCATTGGGTGTTGCTTTAACTTTTATTCAAGTTG
ATTTTGCTGATGAAGGTAGAGGTCCACAAATTTTTAAATGTGATCCTGCTGGATATTTCACTGGGG
TGAAAGCCGTGGCCACTGGTCCAAAACAACAAGAAGCAACGACTTATTTAGAGAAAAAATTCAAAA
AAACCGATGCTGTTAAAGGAGATTGGCAAAAAAACTGTTGAATTTGCAATAATTGCCTTGAGTTCTG
TGATTGGAACTGAATTCAGAAAAAAATGATATTGAAATTGGTGTTGCCACTGAAGGAGAATTTAGAA
TTTTGACACCAGAAGAAATAGACGAAAGATTGATTTCAATAGCTGAACAAGATTAG

YGL011C_homolog 247aa (SEQ ID NO 344)
MSNSAGFDRHITIFSPEGRLYQVEYAFKAINSANITSLGITGQDSAVIISQKKIPDKLLDPKTVSY
IFKITPSIGMVATGSIADARAQAMRARSEATEFRYKYGYEMPVESLSRRMANISQLYTQRAYMRPL
GVALTFIQVDFADEGRGPQIFKCDPAGYFTGVKAVATGPKQQEATTYLEKKFKKTDAVKGDWQKTV
EFAIIALSSVIGTEFRKNDIEIGVATEGEFRILTPEEIDERLISIAEQD

YGL031C_YGR148C_homolog 968bp PathoSeq: 1..968; CDS: 501..965 (SEQ ID NO 345)

YGL031C_YGR148C_homolog 155aa (SEQ ID NO 346) MKIEVDSFSGSKIYPGRGTLFVRGDSKIFRFQSSKSASLFQQRKNPRRISWTVLYRRHHKKGISEE AAKKRTRKTVKHQRAIVGASLELIKERRSQKPSDRKAARDSKLAKDKEAKKAAKAARKAEKAKAVA SGASVVSKQQAKGSFQKVKATSR

YGL043W_homolog 1418bp public: 1..436, PathoSeq: 437..1418; CDS: 501..1415 (SEQ ID NO 347)

YGL043W_homolog 305aa (SEQ ID NO 348)
MDTKEIRSTVSNLEKAVDDTTILKLLNILNDGVKPSEKLLRETKVGVAVNKFRSHDSAEINGLVKK
MIRNWRDAVQAEKNNKKKLAIAAGTGTGTPSSSAISPSSSGSGSTTPKPSESTTPSAARKGPRNPK
TDGVNTQLYENDTRNASVSALYTSLAVDRDDSPKHILRIAIEIEAEVYKSEYSKVSDSYRNRLRSF
TMNLRNKKNPELRERILSKQILPAAFIKMTPNEMAPEALKKEIEKLHKQNLFDAQGATEKRAVTDR
FTCGKCKHKKVSYYQMQTRSADEPLTTFCTCENCGNRWKFS

YGL103W_homolog 1301bp public: 1..688, PathoSeq: 689..1301; exon 1: 501..548, intron 1: 549..899, exon 2: 900..1298 (SEQ ID NO 349) ACATTTATTGTTGGCTATACTTTCCCAGTTTTAAAGGAATGGTTAGGCGGGTCAGTCTACTTTATT TTTACTGTAATGTGTGTGCCAGTGTATGGTTTATCAAGACTAAAGTTCCTGAGACAAAGGGTAAG CATTCGTACCAGGAAGTCTGGAATTAAACGGTAGTTACTTCCAGTATATATGGTGTTCATTGTGTT ${\tt CCATACACTCTCGCAGTCGCACGCTTGACAAAAGTTAATTAGAAAATAGAAAAATTTCTCATTCCTT}$ TTGAGTTTTCCACCATAATCAACTAGTAATAACCAACAATGCCTACTAGATTAACTAAAACCAGAA AACACAGAGGTAATGTTTCTGGTATGTACAATTTCACTAAAGTTTTAACGGATGAAAGAGTATTGA TCATACAACCAAAGCAATGAATATGAGTAGTTTGGGAAACCACAACATACGAGTTATTTTCAGAA CAATCAAGTTTATCATTTACAGAAGACAGTTCCATCAATATGTCCAAAATACTCTTTGAAGTCAAT ACAGAAAGCACCCGGGTGGTAGAGGTAAAGCTGGTGGTCAACATCATCACAGAACCAACTTGGATA TGAGCAAATCATCTGCTTCTGCTGCTCCAGTCATCGACACCTTGGCTCACGGTTACGGTAAAGTTT TGGGTAAAGGTAGATTACCAGAAGTTCCAGTCATTGTCAAAGCCAGATTTGTTTCTAAATTAGCTG AAGAAAAATCAGAGCTGTTGGTGGTGTTGTCGAATTAGTTGCTTAA

YGL103W_homolog 149aa (SEQ ID NO 350)
MPTRLTKTRKHRGNVSAGKGRIGKHRKHPGGRGKAGGQHHHRTNLDKYHPGYFGKVGMRYFHKQQN
HFWRPEINLDKLWTLVDSEKKDEYLSKSSASAAPVIDTLAHGYGKVLGKGRLPEVPVIVKARFVSK
LAEEKIRAVGGVVELVA

YGL147C_homolog 423bp PathoSeq: 1..423; CDS: <1..420 (SEQ ID NO 351)

GCTATCAAAATCACTGTTCACAATGGTGACAGAAAACACGTTGCTGCTTTAAGAACTGTCAAATCT
TTGATTGCTAACTTGATCACTGGTGTCACTAAAGGTTACAAATACAAGATGAGATTTGTTTATGCG
CATTTCCCAATTAACGTTAACATTATTAAAAAAGATGGTCAAGATTACGTTGAAATTAGAAATTTC
TTGGGTGAAAAAAGAGTTAGAGAAGTTAAAATCCATGAAGGTGTCACCATGGAAATTTCTTCTACT
CAAAAGGATGAATTGATTGTTTCTGGTAACTCCTTGGAAGCTGTTTCTCAAAATGCTGCTGATATT
CAACAAATCTGTCGTGTCAGAAACAAGGATATCCGTAAATTCTTGGATGGTATTTATGTTTCTGAA
AGAGGTACCATTGTTGAAGAAATCTAA

YGL147C_homolog 140aa (SEQ ID NO 352)

AIKITVHNGDRKHVAALRTVKSLIANLITGVTKGYKYKMRFVYAHFPINVNIIKKDGODYVEIRNF LGEKRVREVKIHEGVTMEISSTQKDELIVSGNSLEAVSQNAADIQQICRVRNKDIRKFLDGIYVSE RGTIVEEI

YGL213C_homolog 1655bp PathoSeq: 1..1655; CDS: 501..1652 (SEQ ID NO 353) GATGATCGCTAACAAGGTACCCGATTTATTCATCAACAAAGAAGCTACTTCATAGAATTGATTCTC AACCTTAAATAGCTTGTAGTTTTTATGATTGGGACTAATTGTGCAGCATCGAACAATATTGCCAGT

TGCATAGAATAAATCGGTATTATTACGGCATACCAATCGATTGTAGGGGGTTGAAGCTGGTGCTAA TTCTGGGGTTGTTGCATTTCCAGTCCATAAACGTTGAAACACAAATTGCTGTGTAATTTGGTGAAT GAATTGATCAGATGATCCTATGGGTGGCATTGTTAAGGTTGTTCGCTACGATGTATTTCTAGGATA TTGTCGTTGTAGCAAGAAGAAAAAAAAAGTGTCTTCACAAGTCTTGGACTCAATTTTCACCCCT CCACAAACTCAATTCAATTAACTATCAATAATCCAATATGGGTAAACAGTATATATCTACCGTCA GTGCATCTCAGGCTCATAAGCTGGATATTCTTGGTGTAGCTATTACCAATAAGTTCACTGTATCCG TTGTCCAACTGGTATTTATAGATAAAAGCGGAATCCATGCGGTGGCTGCTTACGAAAATGTTTTGC CAAGCTCTACATTGAAAGTGACATTATTAGCATTTGCATGTTTCAATGGATCTATCATCTTCAGAT ATTATATCAATGATGACTTTTCAACTATCGAAAGTCTAACTGATGATATAAAATCATTTGAAAGCA ATTGTTGGACCCCTGGCTTTTATCGCGATCCAGAATCCAAACAAGACTATTTTATTACAACCAAGA CCAATGGCACTACAGAGGTTCATTTATTGAATATTGTTGATGAAAATGAGAAGGCTGTAATCACAT TTGAAAAGTTTGGGCAATTAAAAGGAAACTCTTCTTCTTTCCCAAATTCTTTGGCTATATGTCCAA CAGAGAATAAAAAATGTGCTGTGGGGTACATCAATGGTGATGTCTTGTTATATGACTTTGTTAGCT TGAAATTGATATACACATTTCGTTCGAGTGATTTGGTGACCAGTAGAAATTCCCAATCGACGTCTA TACCTAGGGTGTTGGCATTTTCCCCTGGTGGAACCTTGTTGGCTGTGGCAAGAGACAATCAAGCTG CTGGGTCAATTACATTATACGACGTTGAGCATGGTGAGAATGTGGGGGTCTTTGGCCACACCCTCAC ACTCGGCCAAATCTGTTGGTGGGGTTTGCACATCAAGGCTGGATTTTGGGGGTTGAGTTTTGATG AGGAAGGTAAGCACTTGGCTAGTTGTGGATTTGACAAATGCATAAGAGTCTGGAATTTAGAAACAA GCGAAAGGGAAGCAACAATTAGTATATCTATATCAGACTTAGATGATACTACACATAATGATCAAG ACGAGAGTGTCGCTTCTGGTGTTTTTTTTAAAAAGGGGGGTTAGAGGTGGCTCTGGTGGTGACA GCAATGAAGGATTATGTGTCGTGAGTTTCGATAGAGGAATAAGATGGTACCGAGAGGCAGGAGGAA TATAG

YGL213C_homolog 384aa (SEQ ID NO 354) MGKQYISTVSASQAHKSDILGVAITNKFTVSVSSDGYAKFWDNKQDEVHSPKEFVQSVFIDKSGIH AVAAYENVLPSSTLKVTLLAFACFNGSIIFRYYINDDFSTIESLTDDIKSFESNCWTPGFYRDPES KQDYFITTKTNGTTEVHLLNIVDENEKAVITFEKFGQLKGNSSSFPNSLAICPTENKKCAVGYING DVLLYDFVSLKLIYTFRSSDLVTSRNSQSTSIPRVLAFSPGGTLLAVARDNQAAGSITLYDVEHGE NVGSLATPSHSAKSVVGGFAHQGWILGLSFDEEGKHLASCGFDKCIRVWNLETSEREATISISD LDDTTHNDQDESVASGVAFIKKGVRGGSGGDSNEGLCVVSFDRGIRWYREAGGI

YGR085C_YPR102C_homolog 1418bp public: 1..1418; exon 1: 501..503, intron 1: 504..896, exon 2: 897..1415 (SEQ ID NO 355) ATAGAGATGCTTATTCTGGTGGTTCAGTTAATTTATATCATGTCACTGAACAAGGTTGGACTTATC ATGGTAATTTCAATGTTGGTGATCTCTTTTGGGAAGTTAAAGAAAAGGAACAATCATTTGTAAATG TAGATGGATAAAGTAAGTTGATTGTATAAAAAAAAGAATGGATTCATTAATAATATAAATTTACAAATCT GATAATAAACTACAGTAACTATTATGCAACAATTGAAAGTATCCTGTGTCACGTGATTAGGGCTCA TGGTGAAAATTATTAGTGAGACGATGTTGTTCGCATTTTACCACACTCTCACACTGAGTGTAGT CATACTAACAATCTTCTCACACTATACACAAAAAAAATCTTTCGTTTGAAAAGTTTTGAAAGGTTC GTTTTCTCAATAGTATATCCATACAATAACTGCCAAAGATGGTATGTTCAAGTGTTTAAAGAGATC GAAATGTTTTGTTTTAATTGGAAGTGATATCATAATGAGAAAATATGGGAAATAGAGATAGGACCG AATTAATTGAAAGAGTTTTCTTTTTGGGGAAATGGGTTCAATAAGATTTTTCAAGATTGGAATCAAA TTATGTCAGATGTGAAGAAGAGTAAATATAACAAGAAGTTCAAATCATTAAAAATTTTATGTAAAT ACAACGATTATCAATTACAGTCAACGAATAGAATAAAACAAAAGCCAGCATATAACAGATACCAGT GATTCATCCCAGTGATATAAATAATGATATTCAATTAAAAACAATATTAAGACATTTTTTATTAT

WO 01/02550 PCT/BE00/00077

YGR085C_YPR102C_homolog 174aa (SEQ ID NO 356)
MSDKSQNVMRELRIEKLVLNICVGESGDRLTRAAKVLEQLSGQTPVQSKARYTVRTFGIRRNEKIA
VHVTVRGPKAEEILERGLKVKEYQLRSKNFSATGNFGFGIDEHIDLGIKYDPSIGIYGMDFYVVMG
RAGARVTRKRARSTIGNSHKTNKEDTIQWFKTRYDAEVLDK

YGR118W_YPR132W_homolog 919bp PathoSeq: 1..919; CDS: 482..916 (SEQ ID NO 357)

YGR118W_YPR132W_homolog 145aa (SEQ ID NO 358)
MGKGKPRGLNSARKLRVHRRNNRWADQAYKARLLGTAFKSSPFGGSSHAKGIVLEKIGIESKQPNS
AIRKCVRVQLIKNGKKVTAFVPNDGCLNFVDENDEVLLAGFGRRGKAKGDIPGVRFKVVKVSGVSL
LALWKEKKEKPRS

YGR277C_homolog 1164bp PathoSeq: 1..724, public: 724..1164; CDS: 196..1161 (SEQ ID NO 359)

TTGAATCCAGTTATATTCATTAAAGATCCTATAAAATACGATTATTCACAATTTATTATATCTTTA CTCCCGAAATTCATTAATTGTAATCGTATTGATTTAGTTATACTTTGTCAAATCACCGAATCAAAT CAATTGAATGAAATTTTATGTTTTTATTATCAATTAATTCGTAATCATAAGAATAATGGAGATACT GATGGAGATACCGACAGTTTGCCTATGTTTGATTATCGATTTGAAATTAATATATTATTTAATTTA TCAACAAAAAATTGAATCAATTATGTTTAAATAATTGGAATCATGGATATATTGCGGAAGGTGAT AATGATAACAGTACTAACTTGTCATCTTTGCCATTGTCAATAACACAAATATCAAACATTGAAATT CCAACAATCCAATCAAGAGCAAATAGTAGTAGTGCTTATAATGATGAGGATGATAAAATTACTACT AGTCGGCAATATCAACAATTTAAAACTACTGCTGTAGGTGGAACATTTGATCATTTACATGATGGT TCTAATTTATTAATTAAAAAAATTTAAATCTCAATTACAAACTTTTAATCAAAGACAAAATTTA ATTAATGATGTTTGTGGTCCAACTGGTTATATTAATGATATTGATAATTTAATAATATCTCAAGAA ACTAAATCTGGTGGTGAATTTGTTAACAAATTTCGTAAAGATCATGGATTTAAATTATTAGATATT ACAATAATTAAAGTGATTGGTGGGAATATTGAAGAAAATTCATGGAAAGGTAAATTAAGTTCAA

CTGATATTAGAGAACAAGAATATAATCGATTATTAAATCAATAA

YGR277C_homolog 322aa (SEQ ID NO 360)
MLNPVIFIKDPIKYDYSQFIISLLPKFINCNRIDLVILCQITESNQLNEILCFYYQLIRNHKNNGD
TDGDTDSLPMFDYRFEINILFNLSTKKLNQLCLNNWNHGYIAEGDNDNSTNLSSLPLSITQISNIE
IPTIQSRANSSSAYNDEDDKITTSRQYQQFKTTAVGGTFDHLHDGHKILLSMAIFLTSNKLIIGIT
GSNLLINKKFKSQLQTFNQRQNLVIQFINLLLLSETSVIFFEIYEINDVCGPTGYINDIDNLIISQ
ETKSGGEFVNKFRKDHGFKLLDITIIKVIGGNIEENSWKGKLSSTDIREQEYNRLLNQ

YGR284C_homolog 1427bp public: 1..1427; CDS: 501..1424 (SEQ ID NO 361)

CAAGAGTAAAATCTAAATCGTTCCAATGATTTTGGACAGCTCATAGGTTAAGAGGTCTACATGTGT TGGTGGCAGTAGTATTGGTATTAAGTGGGTGGGTCATGGTATTAGAGAGTGGGTGTTATAAAAGAA GGTTGTGATTTTTTTTTTCCACTGGTGGTGGTGGTGCTGATTGTACTGCTGTTCACTTTATTGTTT TTTGTATTAGTTGTTCTTTTTTTTTTTTTTTTCTTCAAAGTTTCATATAATAATAATATTCT TGTTTTCATATTTTTTTTTTCAGAACAAGAACAAATACAACTTATATAATTTGATCTTACTCTTAT TTGAGGAGTATCATTAATTTAAATTATCAGTTAACAATGTCGTATCGTGGTCCTAATCAATTTG GTAATCAACCTCCACATCATGGAATACCTTCTCAACCTCAACCACATATTGGTCCAATATCTTCCA GCAAAAGTCCTTTAGAACAATTTGAAGATGTTGCTAAAAAAGTTGAAGATTGGATCGATGATTATT TTAAAGTCTTGAAACCATACGTCCCAGCAATTGGTAGAGCATTTTTGGTGGCCACTTTCTATGAGG ATACTTTAAGAATCTTCACTCAATGGAATGAACAAGTTTATTACTTGCACAACTATAGACACTATT GGCGTTGGTTGACCGTTTTATTCTTGATCAATAATATGGTGGTTATGACAGTTGCATCCACTTTAG TAATTGCCAGAAAAAAGAATAACATTGCTACTATTGCATTGATCGTTGTTGTTATTATACAAGGTA TTGGGTATGGTTTATTGTTTGATGCTCAATTTGTTTTGAGAAACTTGTCCGTTGTTGGAGGGTTAG TATTAGCATTTTCCGATAGTATTGTTAGAGATAAAAGATCCTTAAACATGCCAGGTTTACCGATGT TGAACAATCAAGACAACAAAAGTATTTCCTTTTAGCTGGTAGAATTTTGTTAGTATTATTATTTT TGGGATTCGTCTTTTCTTGATTGGTCATTGGGTAGAGTTTTCATTATTATAATCGGGTTAACTT CTTGTGCTTCAATTGTTGGTTACAAGACAAAGTTTTCAGCTGCTATCATGCTTATTGTTTTAT TCTTATACAATGTGTTCACTAACCAATTCTGGGCTTATGCATCTCAAGATGCTAGACGTGACTTTT TGAGATATGAATTCTTCCAAGTTTTGTCAATTGTGGGAGGATTATTGTTAGTGGTTAATGCAGGTG CTGGTGAATTCTCCATCGATGAAAAGAAAAAGATTTATTAA

YGR284C_homolog 308aa (SEQ ID NO 362)
MSYRGPNQFGNQPPHHGIPSQPQPHIGPISSSKSPLEQFEDVAKKVEDWIDDYFKVLKPYVPAIGR
AFLVATFYEDTLRIFTQWNEQVYYLHNYRHYWRWLTVLFLINNMVVMTVASTLVIARKKNNIATIA
LIVVVIIQGIGYGLLFDAQFVLRNLSVVGGLVLAFSDSIVRDKRSLNMPGLPMLNNQDNKKYFLLA
GRILLVLLFLGFVFSSDWSLGRVFIIIIGLTSCASIVVGYKTKFSAAIMLIVLFLYNVFTNQFWAY
ASQDARRDFLRYEFFQVLSIVGGLLLVVNAGAGEFSIDEKKKIY

AACATCATCCAGATAAAAAATCCGCTAGTGGTGGATTAGAAAACGATGGATTTTTCAAAATTATTC AAAAAGCCTTTGAAGTTATGTTGGACCCAGTCAAGAGAAGACAATACGATTCTATTGATGTTGAAA ATGATCCAAAACCACCAGCTCCAAAATCCAAATACGATTTCTTTGAAGCTTGGGGTCCAGTATTTG AAAGTGAAGCAAGATTTTCTACTAAACAACCAGTTCCATTGTTGGGAAATTTAGAAAGCACCAAAG AAGAAGTTGATGCTTTCTACAGTTTCTGGGGAAGATTTGACTCTTGGAAGACTTTTGAATTCAAAG ATGAAGATGTTCCAGATGACACTGCCAACAGAGATCACAAACGTTATATTGAACGTAAGAATATTG CCCAACAGAAAGAAATTGAAGCAAGAAGATCACAAGAGATTATCGAATTGGTCGAAAGAGCTCATG AAAAAGAATCTGGATCAAGAAAAGCTGCTGAAGAGGCTGCTGCCAAAAAGGCTGCTGAAGAGGCCG CTGCTAAGAAAGCCGCCGAAGAAGCCGCCGCTTTGAAAGCCAACTCTAAAAAAGCTAAAGAAGCTG CTAAAGCTGCTAAAAAGAAAAACAAGAGAAACATCAGAGCTGCTGTTAAAGACAATAATTACTTTG GTGACTCAGCTAAATCTGCCGACATTGATGCTGATGTCGATTTGTTAATCGAAAAATTCGACGATG TCAAATTAGGTGAAGTTGCTGATAAAGTTAAAGATGCTGATGCTTCAGTGAAATCTACTTTTG TTGAAGTTGCAAAGGAATTGGTTGGAGCTGGTTCTTTAGATGCTTCCTATTTGAAATATTTTTAACT AGATTTTTTTTTTGTAGGAAAATAATATATATAGAATGTAAACTATCAAAAACAATTATACAGAAG CTGAACTCAAACAAGACTAAACAGCAAG

YGR285C_homolog 427aa (SEQ ID NO 364)
MSIVLPSGTTDGFKAVSKYSAPVRRPIEPVGRYFLAHASRTLRGHTWSEFEKLEAEKNVKQIEVNE
DEDLGDEEQSEELLEHDPREWKTANLYAVLGLSHLRSKATEDQIRRAHRKQVLKHHPDKKSASGGL
ENDGFFKIIQKAFEVMLDPVKRRQYDSIDVENDPKPPAPKSKYDFFEAWGPVFESEARFSTKQPVP
LLGNLESTKEEVDAFYSFWGRFDSWKTFEFKDEDVPDDTANRDHKRYIERKNIAQQKEIEARRSQE
IIELVERAHAEDPRIKLFKEKAKKEKAAKKWEKESGSRKAAEEAAAKKAAEEAAAKK
ANSKKAKEAAKAAKKKNKRNIRAAVKDNNYFGDSAKSADIDADVDLLIEKFDDVKLGEVADKVKDA
DAASVKSTFVEVAKELVGAGSLDASYLKYFN

YHR021C_homolog 1178bp public: 1..537/917..1178, PathoSeq: 538..916; exon 1: 501..503, intron 1: 504..932, exon 2: 933..1175 (SEQ ID NO 365)

ACATCTCAAATTGGTAGTAGAAGAATTCAACCTTGGGACAGTATTCTCTGCTTAAAATGAGTTTAC TGATCAAATAAAATATTGGCTCAACCATTGAAAAGCTATTCTTGACACTTTTTTGCAGTTTTAGTTT TGGTTGTTTCACAATTGAAAAAAAAAATGTTGAGCCCTAATAGCCCTAATTGTTTGCACGTGATGT AGTTTTTGAATTATACATATTAGAGAAACAAGTTAACAATGGTATGTTCATTAGATTTACCATGAG TTATGGAGGGATATTCCTGGATGATCAGAATATCATAATATAGGAGTATACTATTTTACTGGAATC AAGATATAATTGAATTGAAATAAAAATTGAATAAGAGGAAGCATAGAATACGGAATGATGATTAAC AAATCAGAAAACATTGTACTACCGAATAATGAATTAGGATCAACATATTAATATCAACTACTACTT TAAAAGAACAGGAAAATGAGAAGAGAATCAGCATGAAAGTTACCACCTCAGAAAACGTCAAAGAAA TATACTTTTGGTGTGGATCCATGTGTTATTACTGAAATCATCGAAACGAATATAACCCTCCTTTTC TCGTATAGGTTTTAGTTCAAGATTTATTACATCCATCTCCAGCCACTGAAGCTAAACAACACACAAAT TGAAAACTTTAGTTCAACAACCAAGATCTTTCTTTATGGACGTTAAATGTCAAGGATGTCTTAATA TCACCACTGTTTTCAGTCACGCTCAAACTGCTGTCACTTGTGACTCTTGTTCTACTGTTTTGTGTA

YHR021C_homolog 82aa (SEQ ID NO 366)
MVLVQDLLHPSPATEAKQHKLKTLVQQPRSFFMDVKCQGCLNITTVFSHAQTAVTCDSCSTVLCTP
TGGKAKLTEGCSFRRK

YHR141C_YNL162W_homolog 1179bp PathoSeq: 1..1179; exon 1: 501..503, intron 1: 504..861, exon 2: 862..1176 (SEQ ID NO 367) TTTATATTGTTTTTGTTTCTATGTATAGTAATTATTTAATTTGATGTTCCATTATTCATGTAATT GTGATGTATTTTTTTTTGTGTCCTTCTTTGTGTTTTTGATATTTTGCAGCTGGTCGGATCATACAA TTAGGTGAACAAAATTAATGTGTGAGCGTGTACATGCACAATTTTCAATTGGTTATTCTCACGCA TTAGTTCACTAGTAACTTTCGAAGACAACATAGACAAGATGGGTATGTTCCAGTATAGCAATATTC AACAATGAGATACAAGATATTCCTCCAATACAAGAGATTAATGGTGTTTTTGATAGAGTGTAAAG CCATGTGTTTAATAAGAATGATTTGTCAAGGGATAAGATGAAAAGTGGAAATTGTCCAAACAACAT TGAAACGAATTTTCTGGGATAGCGTTCAAACAATCAAACCTATCCAGGTTTCTTATGACAATTAAG AAAACAAGTCAATATTATCAAAGATGGAGTTTTATAAGGAGAGATATTGAAACATCAAATTGTTGA AAGAAATAGCCAACTATTTGGCACCATTTCCTGTGATCATAGAAATACTAACAATCCTCTTGTGTT ATAGTTAACGTTCCAAAAACTAGAAAGACCTACTGTAAAGGTAAAGAATGCCGTAAACATACCCAA CACAAAGTTACCCAATACAAAGCTGGTAAAGCTTCTTTGTTCGCTCAAGGTAAAAGAAGATATGAC AGAAAACAATCCGGTTATGGTGGTCAAACCAAACAAATTTTCCACAAGAAAGCCAAGACTACCAAA AAAGTTGTTTTGAGATTGGAATGTGTTGTCTGTAAAACCAAGGCTCAATTACCATTGAAAAGATGT AAACATTTCGAATTGGGTGGTGACAAAAAACAAAAAGGTCAAGCTTTACAATTTTAA

YHR141C_YNL162W_homolog 106aa (SEQ ID NO 368) MVNVPKTRKTYCKGKECRKHTQHKVTQYKAGKASLFAQGKRRYDRKQSGYGGQTKQIFHKKAKTTK KVVLRLECVVCKTKAQLPLKRCKHFELGGDKKQKGQALQF

YIL112W_homolog 3583bp PathoSeq: 1..3583; CDS: 365..3580 (SEQ ID NO 369)

GTGCGAATAATACAAGCGATCGTTTGAATAATCCAATGATTAGCTCTGATCAACGAATTCAAAATT TTCCCCTCAAGGACGTAGTACAACAAGAGATGAGAAGGGGTTTGAACTGTTTGATTTCAGAGGAGA TGACGGTGCAAAAAGATCTACCACCAAAGAAGCACATAATTTTTTGAATGATTCACGAAAGAGTTC CATTAGTGATATCTCAAGCCAAAAATTTTCAAGGGAAAGTTCCCGTAATGTTTCACGGGAAAGCAG CAGGCGAAGTTCAATAATAAAATTGATCATCATACTAATGTGGACGTGTCAACGAAACCGGAAAA TATAAATAGCAGAGATAACAAAACTGAGAAGAATATGACTTTGAGTTCAGAGTCAACCAAACCGAG AAAATCTGCCAAAACTAAGGCTAAAGAAGAAAAGGTAACAATCGAAAAAAGTGACAAAACGATTAA TTCAGAAGAACGAAAAACGGAACCAATTCAACAAAGCGAGCAACTTTTAACGGACAAAAAGGATAA TAAACTGGAACCCAATAGTGAAGTAAATTTGAAAGACAATAATGACGACCTGAAAGCTACAGCTGG CTGTGCCCTAGGACCTGATAAGAATACTGGAAAAAACGATTCAGATAAATCAGAAACGACTCAACC AAAACTTGCCCGCTCAGAATCATTTGCCCGATACATCATTATTGTCTCCAGTTAATGAAAGTGATAC TGATTTCAATTCAATGAGTTAGCAGAGATACCGGAAGCAAAGGATGGTTCAGTTGTGGCAGCAAA TGTGCTGGAGAACATTGATGAGAATGAAAATATTTCAGAAGCTGAAACTGTTATAGCAGATGACCT GAAGAAAACAAAATTGAATACTATTTTTAGTTCCGATGAAGAGGAGGAGGAGATTCAAGAACCAGA TTTCAAACTCCAAGAACCAGAAAAACTACCAGAAGATGACCAACATCCTGATTTTCAAAATTCAAA AGCAACAACAGAAATCAGTAACGATAAAACAGAAGTAAATAAGCCAGAAGTGAAAGAGGTTGGCGA GAAAGAGAGAAATCACCAACTAGAAGATAGATTACCAATTAAAAAAGAGAAAATGCGGTCGGAGAA TGCAAAGACATCTGAAAACGGTGTCAGTTCAAAATCAGAATCTAAGATTTCAAAGTCGAAGAAACT ACCTTACAAAGTTAAACGTGATTCAAGTGGTCGATCATTATTACAACGAGCTTGCAAGAAGGGTAA TTTTGCAGATGTCCAAGATTACATAGAGAGGGGTGCTAGTGCCAATGAAAAGGATTTCTGTGGATT CACATGCTTGCATGAGGCAGCATTGGAAGGTCATACACAAATTGTGAAAATATCTCATCGAAAATGG TGCTAATGTAAATGCGAAAGCTGATGAAGCTGGTGATTCCGAGACACCATTGATCGATGCAGCTGA AAACAAACATCTTGATTGTGTTAAAGTGTTACTAGAAAATGATGCTGATCCTACTATTTTCAATAT TGATGGATTCACCGCTTTAACTAAGATTTATAATGAACATGAAGGAGAAGAAGGATATGATGAAAT TATTCAAGTTCTAGAAGAAGCAACTGCAAACTATAACAGTCGTTTACCAAGAGAAGTTCAGTTTGT

ATCAGATGCTCCTATTGGTAGTGGACCAATCATGGAGGATCCAAATGACAACTATTTTGCAGAGCT AATTAAAGGTAAGGGAATATATAAATACGCTGCAGAGAATTCAAAAGAGAAAACAGCAGAATATTT TGTTGCTGGTCATAATTTAGAAGGAAAACCAGATATTTTAATTTTAGCTGCTAGAAACGGCCACAC AGAACTTGTTGATATTATACTAGGGCTAAACCCTACACCTTTTAATATTGATACCGAGTCAAGTTG TGGTGTTACTGCATTATTGGCCAGTATTGGACGCGGTCATTTTGAAGTTGTCGATTCCTTGTTGTC CAAAGGTGCTGATCCATTCAAGACAAGAAAAAAAGATGGGTTGAATGCTTTAGAAATTGCACAACA CTCGCCACATTTTGATTCACGGGAAGTTAGTGTAATAATGAAATTCATGGAGAAGAAGAGTGGAAC CAAAATTTTGTCTGGTATTCCGTCAAGGGTAGTATCTCGTGCAACATCTCGTGCACCTTCTGTTCC TGCTGAAAAGAAGCTGGAGGATAAAATCACGAAAACAGTTAATGAGCATGTCAGCAATCGGAAACC ATGGTCAGACGATGAACCTAAAGAACCACATCTTTTGAAGAAGTCAAAGTCTGATTTGAAATTGAA ATCACTACATAGAGAATTCACTTCTGATGATCACCACCACCAGTGAAAGCCATTCAGATTCTTTTGC AGAAAAAAGAAAACATTTATCGGCAACGCCACCTGCTCCTCCGCCACCACCACCACCACCACCTTC TCAAGCAGTTATCAAGGCACAAGAAGAACAAAAAATCAAAGATGCTGAAGAAGCTAGATTGTGGCA AGAAAAGGTCGAAGCTAAAAAGAGGGCTCGAAGAGAAATGTTTTTAAAGTCCGAGAAAGAGAAAAGA GCAGAAACGGAAAGAAGAAGAATTGCGAGCACAAGAAGAAAACGAATTGCCAAAGCAAAACA GGGGTTGCGACAACAGTTGACATTAGATCATTATCCGGTTGGATTGCGTTATTGCAAGTTTGATGG AAACCCAAATATCTCGGCTGTTGATAAATTTTTGCCTTTCTATGTATTTGTAATCGACGATAAAAA GTATGCTGTTGATTTGCAAGTCTCCTTGATCACGTCAACGGTTGTCAGCAAGGTTATCAATACTGT ACAACCTCATCAGAAGAGAGAAATAAATGCAACTGAAAAAAGCAAATTGTGGAAGCTCTTTTTCAA GTTTATTGGTATTGATCCTAGGAATCCAAATTGTGATCAAAGAAGCTCAATAACAAATGGTCAAAA ACAGTTTCAAAATTTGTTGCTTCATTTTGTGGAGGTAGATTTTAGCTGAAGAATTTTTAAAGGAATT TCCAGAAGTACACTCAAAAGCAAAAGATAACCAAATTGATGTTAGTTTAGAGTCTTTGAGTGGGTT TTCTGATTGCGTCAAGGATGATAATAGTTGATGGAAATCTTGAAATTGATATTGATTCCAAGAA AATCGAAAAGTTTATTCCTCCTCATTTGAATACTAGGAAAGACATTATTAGGACTGTCAGTACTTT AGCACACCCACTATGGTGA

YIL112W_homolog 1072aa (SEQ ID NO 370) MTLSSESTKPSVEEVSKSLKPTITKKTSFTDYLKSAKTKAKEEKVTIEKSDKTINSEERKTEPIQO SEQLLTDKKDNKSEPNSEVNLKDNNDDSKATAGCALGPDKNTGKNDSDKSETTQPKLARSESFADT SLLSPVNESDTDFNFNELAEIPEAKDGSVVAANVSENIDENENISEAETVIADDLPRLDEGKKLLR EQTADVKRHKLKKTKLNTIFSSDEEEEEIQEPDFKLQEPEKLPEDDQHPDFQNSKATTEISNDKTE VNKPEVKEVGEKERNHQLEDRLPIKKEKMRSENAKTSENGVSSKSESKISKSKKLPYKVKRDSSGR SLLQRACKKGNFADVQDYIERGASANEKDFCGFTCLHEAALEGHTQIVKYLIENGANVNAKADEAG DSETPLIDAAENKHLDCVKVLLENDADPTIFNIDGFTALTKIYNEHEGEEGYDEIIQVLEEATANY NSRLPREVQFVSDAPIGSGPIMEDPNDNYFAELIKGKGIYKYAAENSKEKTAEYFVAGHNLEGKPD ILILAARNGHTELVDIILGLNPTPFNIDTESSCGVTALLASIGRGHFEVVDSLLSKGADPFKTRKK DGLNALEIAQHSPHFDSREVSVIMKFMEKKSGTKILSGIPSRVVSRATSRAPSVPVSSDEDDVVEE KEITAHTENKSAEKKSEDKITKTVNEHVSNRKPHESTGRKLEKTHSNEERKRKREWSDDEPKEPHL LKKSKSDLKLKSLHREFTSDDHHTSESHSDSFAEKRKHLSATPPAPPPPPPPPPPSQAVIKAQEEQK IKDAEEARLWQEKVEAKKRARREMFLKSEKEKEQKRKEEEELRAQEEKRIAKAKQEEQERLAREAE EKSKELEEKKVGLRQQLTLDHYPVGLRYCKFDGNPNISAVDKFLPFYVFVIDDKKYAVDLQVSLIT STVVSKVINTVQPHQKREINATEKSKLWKLFFKFIGIDPRNPNCDQRSSITNGQKQFQNLLLHFVE VDLAEEFLKEFPEVHSKAKDNQIDVSLESLSGFSDCVKDDIIVDGNLEIDIDSKKIEKFIPPHLNT RKDIIRTVSTLAHPLW

YIL148W_YKR094C_homolog 659bp PathoSeq: 1..659; CDS: 501..656 (SEQ ID NO 371)

YIL148W_YKR094C_homolog 52aa (SEQ ID NO 372)
MIEPSLKALASKYNCEKSICRKCYARLPPRATNCRKRKCGHTNOLRPKKKLK

YIL150C_homolog 2297bp PathoSeq: 1..1162, public: 1163..2297; CDS: 501..2294 (SEQ ID NO 373) ACTCAGCCTTTTGAAATTCACTTTTGGTAAAAGGATATGTAATTGAATCCGCATAATGGACTTTCT CTAACTCCATATTGTTGTTCCTACCCTCTTGCGATAGAGACTTTGATCGTGACATTTTGTAAGTGG TAGAGGTATGGGTAAGATTATTTTCACCACCGTTTTCCTTTAGCAAATAGTCTAAAGCATTTTCTG AATTGTTGAGTTTCGGTACATCATTAGCTATCTTTTGTACAATTGATTTGCTTCTACCTCTAGTCA TCTTTTCATAGTTTTTTTTTTTCCATACATAACTTCTGACGCGTGCACTATATCTGCTAACATACTC GGCAACAACAAAGAAAGAATTTGAACTAATCCGAAGATGAACGACCCCAGAGATGAACAAATTG ACTCCGATGATGTATTAACAGAAGATTCATCTGATGAATTGAAGGACTTGGTGCAGGAGTTTGAAT TGAAATATGCAGAATTAAAGAAGAACAAAGCCTTGAAAAAACGTCGTTCACAGTCACCACTGGAAG ACATGCTGAATAAACAGAAACCCCATCAACCGGAGGTCCCCAGAACCCCAGAAAAAGCTAAAGTCC ATTTGGATAAGGTAGTAGAAGAACCAAAGCAAAGAATTTTTACCAAGAAGGAGCCTCGGGATTCCA AGATAAAAGAATCAAACTTCTTAAACAAACTCTACGAGACAAGTAATAAGCATGATAAAGAAGATG CCCATAAAATAGATTTCAGTAAAAGAAGGTTTGAGTTTCAATTGGATAAGTATACTTTTACGCCAA AAGACGTTGTTGATGATTTAGAACCGATATCCAAGCTTTACTTGCGCAGAAGATACCTTGCCCAAC TGCAAATTGCCGACATTATTGCCGAAACTGATAGCAACATGAAATTCCTTAAAATTGACAAGTTTT TAGCGAAAACCCATAAATCAAACAACTATGCTGAACCCAAGTATTGTAATTGGTGTCTTGTTGCCT TTGTGGTGCGCAAGGACCCAGTGCAGGTTGCTGCCAACAACTCTAAATACATCAAGTTGAAGGTTG GAAATTTTATGAATTCTGTAGACTTGATGCTTTTTGATAAGGCTTTTCAGAAAAACGGGAAAATCC AACCGGGTGATTTATTATTCATTTTGAATCCATTGATCAACAAGTATGAAATACAAGTTGGCAAGG GCCAGTTTCAGTCTGGGTTCAATTTGAAAGTAGAAAACACCAATGTGTCAAGTATTTTAGAGATAG GATCGTTAAGAGATTTTGGGTTTTGCAAGTTTACTAGAAAGCTAGATAATAGCAGATGCAAAAGGG CCATCAACAAGGACGCAAGAATTCTGCGATATACATTTGGATATGAAGTTTAAGTCTAGTACAA GAATGGAATTAAATGGAAGTGTTTCGATTAGATCCCCGCAAAAAAACAAGAAAAAGATGTACATGA ATAAAAATGGGTCTGGCTTTATTAAGCAATATAACGAGGAGAGTACTGTTATAGGAACAAGCTACG GTTCTCCTCTTGATCCAAAAAGGTACCAAGACCCGAAAGTACTCCAGAACCAAATCAAGCGGCGCA AACTAATAGACGACAAGGCAAAGGAGATGCTTGAACAAAAGCTATCGAAACTAGGTTCGGCTTCAT TATTGAACAATTTACAATTATCTAAGAAAGAAGCAACAGATAAACTTGCGAGTGATCGTCTGAAGA GCAAAGGATTCACCAACACAATGATTTCACATATTGGGTTTGATCCAACAGGTACATCTTTGAACC AAAATAGTACCCTGCTTGGCAGCAAGCTGATGGAAAAATCTCGAGCACGGGAATTGCATGATTTGA GTGTTGAAACATCTGGTCATAAGTCGTTGTCTTCGTCTAAACAAGATCGCCAGTCGAAAGTTGCAA CCTCTCGTCGGTTACAGAATCTTGTAGGAAAGCAAACACACGCTACACTAGTAGATAAAAGGAAAA GAGTGGTTGTCTCAGATGAACAACCGGGGATGGAAGAAGATGAAGAAGACATTGAAATCCAGT TTGACGACGAAAAGTCTAAGATGTCCTACATGAAAATGACTGGAGCCAGGTAA

YIL150C_homolog 598aa (SEQ ID NO 374)
MNDPRDEQIDSDDVLTEDSSDELKDLVQEFELKYAELKKNKALKKRRSQSPSEDMSNKQKPHQPEV
PRTPEKAKVHLDKVVEEPKQRIFTKKEPRDSKIKESNFLNKLYETSNKHDKEDAHKIDFSKRRFEF
QLDKYTFTPKDVVDDLEPISKLYLRRRYLAQSQIADIIAETDSNMKFLKIDKFLAKTHKSNNYAEP
KYCNWCLVAFVVRKDPVQVAANNSKYIKLKVGNFMNSVDLMLFDKAFQKNGKIQPGDLLFILNPLI
NKYEIQVGKGQFQSGFNLKVENTNVSSILEIGSLRDFGFCKFTRKLDNSRCKRAINTRTQEFCDIH

LDMKFKSSTRMELNGSVSIRSPQKNKKKMYMNKNGSGFIKQYNEESTVIGTSYGSPLDPKRYQDPK VLQNQIKRRKLIDDKAKEMLEQKLSKLGSASLLNNLQLSKKEATDKLASDRSKSKGFTNTMISHIG FDPTGTSLNQNSTSLGSKSMEKSRARELHDLSVETSGHKSLSSSKQDRQSKVAKWNTNIRTLQNYD RRVASHSLSTSRRLQNLVGKQTHATLVDKRKRVVVSDDEQPGMEEDEEDIEIQFDDEKSKMSYMKM TGAR

YIL167W_YIL168W_homolog 1499bp public: 1..1499; CDS: 501..1496 (SEQ ID NO 375)

TTTCTTCATCAACTTGCTCAAATGTCTTTGAAAGTGAAAGCTTACTTTTTTGGTTTCGTTTAGGTG GCATCAAGGTAAAGGAGGGAGTTTTGGTATAGTTAGGTTTTTGACTTATTTCCTTTTTTTGAGTAGA TATAACAGAACTACCAAAAGTGAGCCCACATCTGTTAATCTTGAAAAGCAAAATTGAGAAAACCAT TTATGCAAGTCGTGTACTGGTGATATTCTTGGTCAATTGCTACACTTTTGTAATGAATACTGTAAT GTAGCCGACGTGGGTTGAANAATATATTTAAGTATATAGAATCAGGTCAATATAAAATGTTTGA AATATAACAAAATGTTTCAATGTAAACTGATGGTTAAGGGATTATAAATCAAACTGAGTAGTGCTT TTGTTCCTAAAAAACCCATCGTGGTGGTAACGTCAGGAGACCGCGACATCAAATGGAATTCACACA TTGTTGAGGTTACAGACAAACTTCCTACAAAGCCTCCGTGCAGGGTGTTTTTCAAGAATGAGTATG CCAGAAAACTTGGCAAATCGAACGTAGCAGTTTTTTCGTCATCTGGTGGTAATGCAGGATTAGCAG CTGCTTATGCCAGCCAGTTTTTTGGAGTATCGTGCACTGTGGTGTTGCCTGAAAGTTCGAAGCCAA CTGTTATAGAAAAGTTGAAATCCTTGGGTGCAGATGTCATTATTCATGGGAAACATTGGGGAGAGG CCGATAACTATTTAACTGATTTTGTTATTAAAAATCTTGACAAAACAGTCTATCCGGTCTATTGTC ACCCTTTTGATGACCCATTGTTGTGGGAGGGTCATAGTAAGATCATCACGGAAATCATCGATCAAA ACGGAATAGTTGAAGGTTTGGAAAATCATAAGGAGATACCAGTGTTGGCAATTGAAACTAAACAAG CGGCCACGTTTCACGAGGCGGTCAAAGAAGGTAAAGTTGTTCATTTACAAAAAGTGCAAACTTTGG CCACTTCTTTGGCTTCGCCGTACCTTTCTTCCAAGGCATTAGCAAACTATATTGAGCGTCCTACAG TTCTTGCTGAAATTGATGACTTGGACGCTGTTAAAGGTGTTGTTGATGTATACGACCATTTCGGAT ATATGGTTGAGCCTGCATGTGCATCCGTTGCATCAGTGATGCACAGGCAAGATTTATTGAATA AATTTGGTACATTAAGTCCAGATGATATTATCATTGTTGTCATATGTGGTGGATCGGCTATCAACA AGTATATTATAGACGAATATAGAAGTTTATTAGAAAAAGACTCTTGA

YIL167W_YIL168W_homolog 332aa (SEQ ID NO 376)
MKEPSITTTFVEVTDKLPTKPPCRVFFKNEYEQPSGSVKLRGMGHLVGQSIDVARKLGKSNVAVFS
SSGGNAGLAAAYASQFFGVSCTVVLPESSKPTVIEKLKSLGADVIIHGKHWGEADNYLTDFVIKNL
DKTVYPVYCHPFDDPLLWEGHSKIITEIIDQKQLPNFDKVKGVICSVGGGGLYNGIVEGLENHKEI
PVLAIETKQAATFHEAVKEGKVVHLQKVQTLATSLASPYLSSKALANYIERPTVLAEIDDLDAVKG
VVDVYDHFGYMVEPACGASVASVMHRQDLLNKFGTLSPDDIIIVVICGGSAINKYIIDEYRSLLEK
DS

GTTTGAAATATAATGATGACACTGTGCAAAAGGAACTTAAACATTTGCCTTACAAAATTGAAAATA AGGGTAACAAACCAGTTGTTAAAGTTGAATACCAAGGTGAAGAAAAAACTTTCTCCCCTGAAGAAA TTTCATCTATGGTTTTGGGTAAAATGAAGAGTATTGCTGAAGATTACCTTGGCAAAAAAGTTACTC ATGCCGTTGTCACTGTTCCAGCTTATTTCAACGATGCTCAAAGACAAGCTACTAAAGATGCCGGTA CTATTGCTGGTTTGAACGTTTTGAGAATTGTCAATGAACCTACTGCTGCCGCTATTGCCTATGGAT TAGACAAAGGCGACCAAGAAAAACAAATTATTGTTTACGATTTGGGTGGTGGTACTTTTGATGTTT ${\tt CTTTATTGTCCATTGAAGGTGTTTTTCGAAGTCTTGGCTACTGCTGGTGATACTCACTTGGGTG}$ GTGAAGATTTTGATTTCAAGATTGTCAGATACTTGGCCAAACAATTCAAGAAGAAGCACAATATTG ATATCACTGCCAATTCTAAAGCCATTTCCAAATTGAAGAGAGAAGCCGAAAAGGCCAAGAGAACTT TATCTTCTCAAATGAGTACTAGAGTTGAAATCGACTCCTTTGTTGATGGTATTGACTTTTCTGAAA CTCTTTCAAGAGCCAAGTTTGAAGAATTGAACATTGCTGCTTTCAGAAAGACTTTGAAACCAGTTG CCACCAGAATTCCAAAAGTTCAAGAATTATTGGAAGGATTCTTTGATGGTAAAAAGGCTTCTAAAG GTATTAACCCAGATGAAGCTGTTGCTTATGGTGCCGCTGTTCAAGCAGGTGTTTTGAGTGGTGAAG AAGGTGTTGATGACATTGTTTGTTGGATGTTAACCCATTGACTTTAGGTATTGAAACTTCTGGTG CTGCTGCTGATAACCAACCAACTGTTTTGATCCAAGTCTATGAAGGTGAAAGAACCATGGCTAAAG ACAACAACAGATTGGGCAAATTCGAATTGACTGGTATTCCACCAGCTCCAAGAGGGTGTCCCACAAA TTGAAGTCACTTTCTCATTGGATGCCAATGGTATCTTGAAAGTTGAAGCTGCTGATAAGGGAACTG GTAAATCTGAATCCATTACTATCACCAACGAAAAGGGTAGATTATCCAAGGATGAAATTGATAGAA ACTCATTAGAAAACTATGCTCATGTCTTGAGAGGTCAATTGAGTGATACTTCTGAAACCGGTTTAG GTTCTAAATTGGATGACGATGACAAGGAAACTTTGGATGACGCTATCAAGGAAACTTTAGAATTTA TTGCTAACCCAATCACAGCAAAATTATACGGTGGAGCTGCTGGTGAAGGTGCTGGTGGCGCTGGGG ATGCCAAATTCGGTGATGATGATTCAGATGATGAATTCGATCACGATGAATTGTAG

YJL034W_homolog 687aa (SEQ ID NO 378)
MRSSQSSWLPRIGLLYVALVILIPFLVSPKHAFAVAAVSDDESSTDNYGTVIGIDLGTTYSCVGVM
KNGKVEILANDQGNRITPSYVSFNGDERLVGDAAKNQASSNVNNTVFDIKRLIGLKYNDDTVQKEL
KHLPYKIENKGNKPVVKVEYQGEEKTFSPEEISSMVLGKMKSIAEDYLGKKVTHAVVTVPAYFNDA
QRQATKDAGTIAGLNVLRIVNEPTAAAIAYGLDKGDQEKQIIVYDLGGGTFDVSLLSIEGGVFEVL
ATAGDTHLGGEDFDFKIVRYLAKQFKKKHNIDITANSKAISKLKREAEKAKRTLSSQMSTRVEIDS
FVDGIDFSETLSRAKFEELNIAAFRKTLKPVEQVLKDGGVKKSDIDDIVLVGGSTRIPKVQELLEG
FFDGKKASKGINPDEAVAYGAAVQAGVLSGEEGVDDIVLLDVNPLTLGIETSGGVMTTLIKRNTAI
PTKKSQIFSTAADNQPTVLIQVYEGERTMAKDNNRLGKFELTGIPPAPRGVPQIEVTFSLDANGIL
KVEAADKGTGKSESITITNEKGRLSKDEIDRMVEEAEKYAQQDQELKEKIEARNSLENYAHVLRGQ
LSDTSETGLGSKLDDDDKETLDDAIKETLEFIEDNFDTATAEEFEEQKQKLIDVANPITAKLYGGA
AGEGAGGAGDAKFGDDDSDDEFDHDEL

ACTATAATGATTTAATTTTGTATGTGACAGTGGAGCCTTGTATTATGTGTGCATCTTATTTACGTC
AGTTGGGCATCAAAAAAAGTAATATTTGGTTGTGGGAATGATAGATTCGGAGGAAATGGTACCATTT
TATCAATACATAGTGACATCACCTTGCCTAACGCAGCTTATTCCAGTATCGGGGGTATATGTAGGA
CAGAAGGAATCCAACTATTACGAAATTTTTATATTCAACAAAATGAGTCGGCACCAAATCCAAAAA
TCAAAAAGAACACAGATATTGAGAGTAAGGAATACCCAGAGAATCAGTTTTGTAGCATTTCAAAGG
ATGAATTTATAGAGTTTTACGGAAATGAAAGAGTGCATATTTACGATGGGAAGATTTTTGAAATCA
CTCCATTACAAAACAAGGGTTATGATATAAAAAGAATTGATATCGTTGGATATGATGCAAAAAGTTC
CATTTCTAGAGGATGAGTTGGGACAAATTACAGATGAGCAAATAATTCACAACTTATTTT
TCAACATAAATGATGATGGAACGGTTAATTATAAAAAAACCAATAGGCAAAATATAACAGTAAAAAGA
GACACTTTGCAAACGATGAAGAATAG

YJL035C_homolog 281aa (SEQ ID NO 380)
MSTDLTSHFQYMAISLFVGYKALLNNETPVSCIVVDSKSDKIISIGYNYTNHSLNGTQHAEFIALQ
RFGEQKSSIDYNDLILYVTVEPCIMCASYLRQLGIKKVIFGCGNDRFGGNGTILSIHSDITLPNAA
YSSIGGICRTEGIQLLRNFYIQQNESAPNPKIKKNTDIESKEYPENQFCSISKDEFIEFYGNERVH
IYDGKIFEITPLQNKGYDIKELISLDMMQKVPFLEDELGQITDEQIIEFHNLFFNINDDGTVNYKK
PIGKYNSKKRHFANDEE

YJL180C_homolog 1504bp public: 1..938/940..1504, PathoSeq: 939; CDS: 501..>1502 (SEQ ID NO 381) CTTTATCTAATTGATTTAAATAATTATTAACATTAGTACCAATAAATGCTTTACCACAACCTTGCC AAACTTTTCATTTGATTGGGTATTACATATTTTATTTAATTTAGCATTTGTAGTATCAATTATTG ATTGATTATCCATTCAAGTAGGACTTTTTTGTAATGCTTCTTGATTCATGATTAAATGAGACGAGT GTGTGTGTATGGGCGATGAAGCTGAAGGTTTTGCAGATGTGGTGTCTATAAGAGTAATTTGATGTG AAAAATATACAATCTATAATCAGTATGTTCAGTTTTGGAATGGAAGCCCCAAGAAGAACAACAGGG TCAAACGAAATATATCTTACCATCCCCCCCCCCCCAAAATGCTTAGATTTACTAGGACTACTGCTT GGAAATTAAGATCTATTCCAATTGCCACTATTCAATATAGACAATTTACTTATTCCACTATATGTT AAACTAATAGATTAGCTAAAACTGGTACTAGATTTTGGAAAAAAGGTGAAGTTAAATTCAATAATG AAACTCAAAAATATGAAATTCAATTAGATGGGAAAACTCTACGCACACCACTTGGATTCCCATTAG AATTACCAATCAATAAAAAACAATTGGCATATTTAATTGCTCATGAATGGACTCATTTACCTGATA TTAAAGTGAAATCAAGTACTTTACCATTAACAGCTTTAGCCACTAGAGCTATAGATTTGAGTCAAC AACATTTGAGTGATATGAAGACAGAAAAAGCTGAAGAAATGTTAGCATTGGAAGATATTAAATTAC AAATGTTAAGATATCTTGATACTGATACTTGTCTTATATTTGCTACCAACAAAGAATGTGATGGTA TTTATGCTCATAATAAAAATTTAATCCCTCGACAAAAATCTATTGAAATTGAAATATTTAGATTGTG AAACTGATGGATTAAGAGGTAATAAACAAGATGAAACCACTCAATTAGTTGTATTGGATTGGTTAA ATCAATTACCAATTTATGATTTAATTGCCTTGGAGAAAACAATCTTAACTACTAAATCATTTTTAT GTGGAATTACTTTATTAAGATCAAATGTTAATGATATTGAAACTTTAAAAGAATTATCAATTTA ATAAAAATTCCATTGATGAAGATTATTATCATAAAACTTTAGAAGAATTAGTTGAATTAGGAAATT TAGAAACTATTTATCAAACTGAAGAATGGGGTGAAGTAGAAGATACTCATGA

YJL180C_homolog 334aa (SEQ ID NO 382)
MLRFTRTTAWKLRSIPIATIQYRQFTYSTICYQLKTLTPSLGINNTIESNIPSETNRLAKTGTRFW
KKGEVKFNNETQKYEIQLDGKTLRTPLGFPLELPINKKQLAYLIAHEWTHLPDIKVKSSTLPLTAL
ATRAIDLSQQHLSDMKTEKAEEMLALEDIKLQMLRYLDTDTCLIFATNKECDGKLRKRQEEIYRPL
INEFNEFFTIYAHNKNLIPRQKSIELKYLDCETDGLRGNKQDETTQLVVLDWLNQLPIYDLIALEK
TILTTKSFLCGITLLRSNVNDIETLKELYQFNKNSIDEDYYHKTLEELVELGNLETIYQTEEWGEV
EDTH

TAACTGTATTGTTGGGCTGACAGTAGAGTATTGCGGTCATTTTTAGGAGTGATTATAATTCTCTGT CAGCCAAAACCACATATCTGTGCAATATTTACGCTCCAATGGATTCAAACCCGTGTCAAGACGTAT CGGGTGATACCAGTAGCACCAATGGCCAACAATAATCCCACTAATGACAGCACAATCTCCTCTC AGAACCATTCTAAAACTGGCTTGAGAAAACACCAACAACAACACTACCACCAACACCTGCACCTGC AAATGCATTCTCATTCACAGCAGTCACCTTATATTAATCAATTGGAATACTTTACCAATAACCAGT TTTCACGCTCTTTCAATAGTTTAATTTTGGAGGATGCCAATGATGCCCAACAACAATAGTTCAA CAACAACCTTAAATAAGAAAACCATTAACAAGTCACCACCATTCAATATCAAGCAGGACTTATTAA ACGATAGTATCGACACGTTTCTTGATAACTCCAACACGGAAACGATAGAAGATGGAGACGTCACAA CAACAGACGACGATCACGATTTTGATGATGAAGATATTGAAGATCCTGAAGCAGTGCAGTACACCC AGAGCAATAGTCAGATTACCTACAATCTGCACGTACGGAAGCCATCCGAAGAAGATACGTCATCAT CGATGGCTACAATAAGGTTATCTAACAACTCACAAAGTTCAATTAAGAGATCGTCAAAGTATTTGA ATTTATCTATTGATTCCAATTTGAAAACGGTTGATGGAGGTAAAATTCCCGATGAAATAGATGACA TTAGTTTGAACGAAATAGATGTTGCAGTGGCACCTAACGATTTTTCATCACCACTATCAGCAAGAA AGCCGGACATATTTGCTGCTATAACTGCAGCAAACGGGAATTCCAATAATCAATTTAAAAGGCCAC ACAAGTTGGTTAGTCAATCGCCTTCCCCGTCGTCAAAGAATAAGTTTCGCATATCATCATCAACCA CATCTTCGCCACAGTCTAACTTGCATTCACCTTCCAAGTTGGGACTGAAAGGATTCAAAATGTTTA AAAATGCAAATAGAGACGCGATAATGTCGTCAAGCAGAGTTATGACTCCAGAAAAACCGAAAATGG TATCTAAAATATTTGGCAAGTCAGCAAAAATAAGGCGAGCTTATACCCCAACCCATACATCTACCC CAATGGCTGTCTCATCACTCAACCCTTCTTCATCATCTACACTGAATTCAACAACGGCAGCAATAA CATCTACAAGTCCAGCAGCTGATGAGCATTATGATATTGACAATGACTGTGACAGTCCGTCAAAAA ATAGAAAACTGTCTAATATTTCTGCATCTTCAATTATTATTATCAAGATGAAAATCATATCAAGT TTTCTGCTTCTGTGGCTGAAACAGGGAAAGGGTCAACTACAACTAAAAGCAACCTATCTAAGGGTT GTCCCTTATTTGATGATAAAGAGAATAAAGCTTCTTATCAGTTTGTTAAACCATTGCAAACAGCTT TCAATTCCTCGGGGTTGGTCAAAAAGAATAGCATAAGTGGTCTGCTGGACAGGAAACTACCTCCAG AAACACCAATCAAAAGAAATCCATTAATGATTTTAAATACCAACAAAGTTGTACCTCCATATAGCA AAAATCAACGTTTTCCTGGCAGCGTGAATCCCAACACTACTACGAACAACAACAACACTCAACAGC ATCATGATAGTGATCTTTCTATTGAAGTTGGAAGGAATAATTCTTATGATGCCAGTAGTAGCACTA TCAATAACACAAGTTATATCAAAATTTTCCCTTCTTCGGAATTGAAAAAGGAGCAGGTGCTTCAGC GACCACAAGAAGATTTAGAATTAGTTTTCAATTCTGACATTGAACTAGATGATAACATAATACCAG AAACACCAACAAAGAAACTGCTACTACCGAATCAGCACCATCAACATCACTTACCCCTTTACACGC **AATCCAAGAGTCCATTGTTGAAGTTTGACACTGAGAAAGATGGAAGAAGGAATTTGTCAATAGTCT** TTGCAAAGAATAGTTTTAAGAAACCTATGAATAATGCTGAAAGAGGTGATGACCCTGATAGTATAA TTGCTCAACGCATAGATATTATGCCATCGTTAGATGAAGTTGACTCAGTGTCTGTTTATCCTTCAA AGATAGATGAACATTTAATTGAAAAGTTTGGAATGAAGAATATCAAGTATATTGGATCGGGAGCAT TTTCCATTGCTTTTGAATGTTTATTTAATAACGAAAAGTTTGCTATCAAAAGAACTAAAAAAACCAC TTATTGGAAAATTGGAGAAACAAACTATAAAACGAGAAATTGAAGCATTGAGAGTGTTGACAAGCA TTAAAGAAGATGAAGCAACTAATATGCAAGAACAAGAAGAAGGGGAAAGAGTATCTAGTTTATTTCA TTGAGGCCTGGGATTTTAATAATTACTACTATATAATGACAGAATTCTGTGAAGGTGGTACATTAT TTGATTTCTTAGAGGAAAATAAACATTACAAAATTGATGAATTTAGAATTTGGAAGATCCTAATTG AAATTCTAAATGGGTTAAAATTTATTCATCTGAAAAATTATTTACATTTGGATTTAAAACCAGCAA ACATTTTTATCACTTTTGAAGGGTCATTGAAAATTGGTGATTTCGGATTGGCTACTAAATTGCCTA TACTAGAAAAGGACTTTGATCTTGAAGGAGATCGTAATTATATTGCCCCGGAATTGATTAATGACA TAATTTTACCAGATAATGGAACGCCATGGCGTAAATTGAGAAGTGGAGACTTGAGTGATGCTGGCC GATTATCAAGTGATAATATTTCAATGTTTTTACAACACAATCCAAATACCAATAGCAATATCAGTG GCAGTGGAAGTAGAAGTGGTAGTGGCAGTACAGGAGGCAATGGTAGTGCTGGTGATTGA

YJL187C_homolog 1062aa (SEQ ID NO 384)

WO 01/02550 PCT/BE00/00077

132/161

MDSNPCQDVSGDTSSTPMANNNPTNDSTISSQNHSKTGLRKHQQQHYHQHSHSQMHSHSQQSPYIN QLEYFTNNQFSRSFNSLILEDANDANTNNSSTTTLNKKTINKSPPFNIKODLLNDSIDTFLDNSNT ETIEDGDVTTTDDDHDFDDEDIEDPEAVQYTPTLNILKSKKVDSFNIISSKHRKSNSQITYNSHVR KPSEEDTSSSMATIRLSNNSQSSIKRSSKYLNLSIDSNLKTVDGGKIPDEIDDISLNEIDVAVAPN DFSSPLSARKPDIFAAITAANGNSNNQFKRPHKLVSQSPSPSSKNKFRISSSTTSSPQSNLHSPSK LGSKGFKMFKNANRDAIMSSSRVMTPEKPKMVSKIFGKSAKIRRAYTPTHTSTPMAVSSLNPPSSS TSNSTTAAITSTSPAADEHYDIDNDCDSPSKNRKSSNISASSIIIYQDENHIKSNHARKSSNPIPY PPTEPLPTNI SASVAETGKGSTTTKSNLSKGCPLFDDKENKASYQFVKPLQTAFNSSGLVKKNSIS GSSDRKLPPETPIKRNPLMILNTNKVVPPYSSGFAEGKDVMGDQHDIYSHIPCQNQRFPGSVNPNT TTNNNNTQQHHDSDLSIEVGRNNSYDASSSTINNTSYIKIFPSSELKKEOVLORPOEDLELVFNSD IELDDNIIPETPTKKSLLPNQHHQHHLPLYTOSKSPLLKFDTEKDGRRNLSIVLDKSNATKREISE PPSTPINMSFAKNSFKKPMNNAERGDDPDSIIAQRIDIMPSLDEVDSVSVYPSKIDEHLIEKFGMK NIKYIGSGAFSIAFECLFNNEKFAIKRTKKPLIGKLEKOTIKREIEALRVLTSIKEDEATNMOEOE EGKEYLVYFIEAWDFNNYYYIMTEFCEGGTLFDFLEENKHYKIDEFRIWKILIEILNGLKFIHSKN YLHLDLKPANIFITFEGSLKIGDFGLATKLPILEKDFDLEGDRNYIAPELINDKIYTPFADIFSLG LIILEIAANIILPDNGTPWRKLRSGDLSDAGRLSSDNISMFLQHNPNTNSNISGSGSRSGSGSTGG NGSAGD

YJL189W_homolog 887bp public: 1..666, PathoSeq: 667..887; exon 1: 501..506, intron 1: 507..737, exon 2: 738..884 (SEQ ID NO 385) AGTCAAGAATTTTATGATGACTTTGGAGGATGGTCTGATTAAGACTTGTCTTTTTACCAGTTTTTTC AGCATTGTTGATGGCGTTTAAAGCATCAGCTAAGACGGAGGTTCTAGTCATGGTTGAATTGTCTGT TCCTCACTGTAACAGTAGTAAACACTAGTTACAACTGATGACCTGCATATTATAAATCTTTCTG AATGATGTCTTTCAGTCTTTTATTGGGTGATTATTATAATAAATGGCAGATGAGAAATATATTGGA TAATAAACCTTGCAAATGAAATCAGTTGACCATTTTGAAATAATGGACCATTAGCAATACCCAGAT TGCTGGAACAAGACGAGAGAACTAGACAACTCAGATATAATAGAACATCCATACTAACTTCACTC ATTTCTTATAGTCTCAAAAATCATTCAGAACTAAACAAAAGTTAGCTAAGGCTCAAAAGCAAAACA GACCATTGCCACAATGGATCAGATTGAGAACTGACAACAAAATCAGATACAATGCTAAAAGAAGAC ACTGGAGAAGAACTAAGTTGGGTATCTAA

YJL189W_homolog 51aa (SEQ ID NO 386)
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YJL190C_YLR367W_homolog 893bp public: 1..893; CDS: 501..890 (SEQ ID NO 387)

YJL190C_YLR367W_homolog 130aa (SEQ ID NO 388)

MTRTSVLADALNAINNAEKTGKRQVLIRPSSKVIIKFLTVMQKHGYIGEFEYIDDHRSGKIVVQLN GRLNKCGVIQPRFNVKINDIERWTDNLLPARQFGYVILTTSAGIMDHEEARRKHVSGKILGFVY

YJL197W_homolog 4619bp PathoSeq: 1..3041/3260..4619, public: 3042..3259; CDS: 501..4616 (SEQ ID NO 389) CAACGACAACAACAATAAGAAGAATCTTTTCCAGATATTGTAAAATCCTTATATTAAATGTTAATA GAAGCCTAAAAATTGCTTGAATTGATAGATTTGCTGATTCTTTTGCTAGAAACACGCGTTATATTA CTTATCCTTTCTGTAATTTCTTGATCTCTGTTTGAATCAACAACGCCTTTGTTTTCTCTTTCTGCC TTTTTTTTTAGTTTTTTAACAACAAAATTGAAATTACAATCCTTGAATTTACAACTTCATATTC AGCTCTAAATACTAATAATTATAACAATAATTAATTGAATTATTCTATAAACCACTGATATTTGAT AGATACCTTCTGATGCAAAGGAAATTGTGACTACAAATGAAATTGAAGCAACAGATTCAGAACATA ACAACCTTGCATCCAAACGTCAATTAATCAATGATTTATTACACAATGATCATTTTGAAGAAGGAA CAGAACGTTACATCATCCCTCAAAATTTCTTACATGAATTTTTGAATTTACCAATCGATAATTTTA GTGATTTGAAAGATCAACTTGGTCCTATTGATTTCCACTCATTACTTAATGAACAAGGTAATTTAT ATCCCGAGAATGAAGAACCAGTCACTTTTTGTCATGTATCGCCAGAAGTATTTCAACATTTGGGTG AATGGTTTGGAATATTGGGCCAACCAATTATTAGAGCTATCATTATTAATCCAGACACCAAAGAAA ACTTGCGACACCGTCATAATGGAAGCAACCACAATCATCACCATGGTCATCACGATTCACCAA TACCAGTATTGCTTTCCAAAACAAGCACTTTTCATAGATTAATGGATGTTATACGTTATAATGTTC TTAAAGCACCACGAAAATCGACGAAAGATTTTAGGATTTGGTTTATTGTCCCACAAGATAAAGGCT TACAGTATTTGATTTCAATACAAACTTTTATGTTTGATATCTCCAAAAAAACTTTGGTTTCACCAA ATATGCTTGAGGATGCTTTGAAAGATCACGGTATTGTGGCCAGTTCCTATAATATAATGGTAGAAG AAGAAGTATCACAGGGTGGTGGACACCTTGGATTATCAAACATGGGGAACACATGTTATATGAACT AAGAATTGAATTTTGACAACCCCTTGGGATATCATGGAGATGTTGCCAATGCATTTGGTTCACTTT TAAAACAAGCATTTGATCACGTGAAAAATAGTTCTAGTATATCTCCTCGAGAATTCAAATCAACTA TTGGGAGATATTCCTCGATGTTTTCTGGGTATCTTCAACAAGATTCTCAAGAGTTGTTGAGTTGGC TATTAGATGCTCTTCATGAGGATTTGAATAGAATTCACCAAAAACCATATTGTGAAAAGCCCGAAT TGAAAGATGACGAAATTGATGACCCCCAAGCCATCACCAAACTTGCCAATACTTGCTGGAATCAAC ATAAGGCAAGAAACGACTCGGTGATAATTGATTTATTTACTGGGTTGTATCAATCTACATTAATCT GTCCTGATTGTGGTAAGAAATCCATAACTTTTGATCCCTTTAATGATTTAACTTTACCTTTACCCA TCAGTAAGAAATGGTATCACACATTTACAATTGTTGATTTGTCCAATCAAGGCGTTATACCGGAAA GGATAATGAAGTTGGAAGTTGAATAAAACATCCAATTTCGATGATTTACTTAGCTATTTGA GTAATTTCTTGAATGTTCCATCTACTGAGTTGTTTGCTTATGAGATTTTTCAAAATGCAATCTATA GTGACTTCCAATTAGATTACACCAAGAACAAGTTTTTACCTATCAGTGATATTATCAGAGATACAG ATGATGTTATAGTGTACATTGTTCCACATAACCCTGCCGTTGACATCATTGTGCCAGTGTTCAATG CCGTTGAAGATGCTGATAGTTCATATCAAATGGTTAATTTTTTTGGAATCCCATTATTTGTGGTGA TATTGAGTAAAATTGATTTGGTTGATGAATATGAAAAAATAAAAAGGAGTAATGAAGATTACGTTG AAAAAGTATTTACAAAAAACTGGATTTCCCTGCATTGTCACAGCCATTAGAAACCTCCGATTGTG AAAAAAACAACAATAATACTAGCGACAACGACGACGATGAGGATGCTGACAACGATGAAGGCTATG ATGACTATAGCCCTAAATTGAATTCTAACCTTCGTAGCAGGTACAATCATGACCAAACAACCAAAT TCAAACAAACAGAGAGAGTTATTAATGTTCCTACACACAAACCTACTTTTAGCGATTTCAAACCTT ATGAGATGGACCAATTGGTGGAGGAAGTGAACCAAAATTTGGCAGAGCAANGAGAAGCGAGATCAT ATACTCTCAAGCAACAATCAACTGTACCTGCTGCTGCTGAAACGGTACCTCCACCATTACCTGTTA GAAATAATACTGGAGTTCACATCCCGTCATCCGATGAAGAAACAGAAAGTGAAGCTAATTTGGGAA GTTTGTTTGATTCAACATCAAACTTGCCGTTGCCTCCACCATCTACATATTCCGAATCAACAAAAC CTTCGAATGTAAACTCCCCTATGGAAAGTAACTTTGAAAGTTCATCAGCAGACTTGAATTCTGGTA

CAACATTGATATCGAAGGACACAGTTTTGTTATGTGATTGGGATAAGGAAATTTATCAAAAATGCT TTGGTGATAAAGAATTACAAGCATGGGAAAACATATCGAATTTACCGAATCCAGAATTGGAGAAAA ATAGAGCTCATTTTGAAAGACAAAGAAAAGCTAAAATTACATTATCTGATTGTCTTAAGAGTTTCA GTACCCCTGAAATTTTAGGTGAACATGATTTATGGTATTGTCCACGTTGTACTGAACATAAACGTG CCACAAAGACAATCCAACTTTGGTCAACGGGTGATATCCTCACTATTCATTTGAAAAGATTTCATA GTGCTCGTGCATTTAGTGATAAGATTGATGTTTTGGTTGATTTCCCAATTGAAGGTTTAGATATAA GTTCGTATGTTGCCAATACTGATTTGACACCTGAAGATTGTTTATACGACTTGATTGCCGTTGATA ATCATTATGGTGGGTTAGGAGGTGGTCATTACACTGCCTCGGTAAAGAATTTCAGAGATGATAAAT GGTATTATTTTAATGATAGTCGAGTCACTGAAATTAATAATCCTCAAGAAGTCGTAGCTAATTCTG CGTACCTTTTATTTTACCGTCGAAGAAGTTCGAAAGGAGCTGGTATTTTGGGAGGAGAAAACTTTA TCGACTTGCTTCAAAAAGGTCGAGAGGAATACTCTGAGAGTTTGCAAAAGAAAAGATTGGTTCTTC AAAATGTTGGCCAAATAGTCAATACGTATGCCAAAATTGAACAAGATATAATTGATAAAGAAACAG AGAAACAGAAAGAGGAACAGGAACAGGAACAGGAACAGGAACAGGAACAAGAGCAAGAGC AAGAGCCAGTTCAAGAGCCAGATCAAGAACAAGAGCCAGATCAAGAGCCAGATCAAGATCAAGATC AAGAGCCAGATCAAGACCAGATCAAGATCAAGAGCAGAATGAAACAATAAAAAAATCTAGACCAT TCGATGAACTCAAACCATCAACTAGTGAAACAAATAACCAACAACAACAACTCAGTTCAACTTTG ATGATGAAGATAATGATTACGATTATGAAGCAGAAGTAGAAGATTCCAATATTCGCAAACAAGAT TACTTTCAAAAGAAATAACAGCAATAAATTGGTGCATATTAAAAGCAATGGTCGCCAAGAAGTCA CTTCATCACCAGTACCAATTGAAACTGATGGTGACACTGATGTAACTGATTCCAATTCAACATAG

YJL197W_homolog 1372aa (SEQ ID NO 390) MPDNIEDRSEIPSDAKEIVTTNEIEATDSEHTTNVDNELPQGESNEQTGDDSNDNLASKRQLINDL LHNDHFEEGTERYIIPQNFLHEFLNLPIDNFSDLKDQLGPIDFHSLLNEQGNLYPENEEPVTFCHV SPEVFQHLGEWFGILGQPIIRAIIINPDTKEKQIERFPPLFWVHQLGKKTQPTYLRHRHNGSNHNH HHHGHHDSPIPVLLSKTSTFHRLMDVIRYNVLKAPRKSTKDFRIWFIVPQDKGLQYLISIQTFMFD ISKKTLVSPNMLEDALKDHGIVASSYNIMVEAKEKHQTEFPIDQFILSHSNAYEEVSQGGGHLGLS NMGNTCYMNSALQCLLHVPEINYYFFYNIYKKELNFDNPLGYHGDVANAFGSLLKQAFDHVKNSSS ISPREFKSTIGRYSSMFSGYLQQDSQELLSWLLDALHEDLNRIHQKPYCEKPELKDDEIDDPQAIT KLANTCWNQHKARNDSVIIDLFTGLYQSTLICPDCGKKSITFDPFNDLTLPLPISKKWYHTFTIVD LSNQGVIPERIMKLEVELNKTSNFDDLLSYLSNFLNVPSTELFAYEIFQNAIYSDFQLDYTKNKFL PISDIIRDTDDVIVYIVPHNPAVDIIVPVFNAVEDADSSYQMVNFFGIPLFVVMNKEVDVNSFGFI RKKLLETVSLLSKIDLVDEYEKIKRSNEDYVEKVFYKKSDFPALSQPLETSDCEKNNNNTSDNDDD EDADNDEGYDSEVSLANPYLGANFGFKIMYVHDYSPKLNSNLRSRYNHDQTTKFKQTERVINVPTH KPTFSDFKPLSDQLSESKRNYYFYPDYKKMDDEMDQLVEEVNQNLAEQXEARSSGSENSSRASEEQ DGFVLINKEDTLKQQSTVPAAAETVPPPLPVRNNTGVHIPSSDEETESEANLGSLFDSTSNLPLPP PSTYSESTKPSNVNSPMESNFESSSADLNSGTTLISKDTVLLCDWDKEIYQKCFGDKELQAWENIS NLPNPELEKNRAHFERQRKAKITLSDCLKSFSTPEILGEHDLWYCPRCTEHKRATKTIQLWSTGDI LTIHLKRFHSARAFSDKIDVLVDFPIEGLDISSYVANTDLTPEDCLYDLIAVDNHYGGLGGGHYTA SVKNFRDDKWYYFNDSRVTEINNPQEVVANSAYLLFYRRSSKGAGILGGENFIDLLOKGREEYSE SLQKKRLVLQNVGQIVNTYAKIEQDIIDKETEKQKEEQEQEQEQEQEQEQEQEQEPVQEPDQEQEP DQEPDQDQDQEPDQDQEQNETIKKSRPFDELKPSTSETNNQQQTTQFNFDDEDNDYDYEAEV **EDSNIRKORLLSKENNSNKLVHIKSNGRQEVTSSPVPIETDGDTDVTDSNST**

TTAATGTTAAACAACAATTAAAAATCACATTAAAACGTAAAGCCATTACATTATTATAAAATCTTT CTGAATTAAAATCATTTATTGAATTGAATAGAATTGGATTCACGAAAATTTGTAAAAAATTTGATA AAACTTGTGGTTATTCAATTAAACAAGATTTTATTAATGAATTTTTACCTCAATATTCTCGAGTAT TTGAAAATGATACCATTGAAGAATTAGATTATAAATTGAATCAAATTATTAAAATTTATGCCTTTT TATCAAATAAATTAACTACTCAATCAACAACTAAAGAAGATTTGGATAATATAAAATTTGAATTAA GATCTTATTTACGTGATCATATTGTATTTGAAAGAAATACCGTTTGGAAAGATTTATTATCATTAG AAAAGAAATCTTATAATATTGATTTAGATAATTCTGTGGTTCAAAATAATAAAATGGGTGATGAAG AATTGATTAAATATGATCATATTGATATTCCACAATTTTTATTAACTACTCAAATGCTTAAAATTA TTATTATTGTCATTGTTTTCATTATATTATTAGCAGTGAAAACTTTTAATGATCCAGTTCAAGGTC GTTGTTTAGCAGTATTAGTTGCTGCCGCCATGCTTTGGGCCTTCAGAAGCATTACCTTTATACACTA CAGCTTTATTAATCCCACTTTTGGTTGTTACTTGTAAAGTTTGTAAAACTCCGGGAACCGATGATC CAATGGATGCCACCAAGGCATCACAATATATTTTTGGGACAATGTGGAATTCCACAATTATGATAT TAATTGGTGGGTTTACATTAGCTGCTGCATTATCAAAATATAATCTTGCCAAAATATTATCATCAT ATATTTTAGCATTAGCAGGTACAAATCCAAGAAATGTATTATTGGCAATCATGTGTGTATCATTAT TTCTTTCCATGTGGATTTCTAATGTTGCTGCCCCCGTTTTATGTTTTTCATTAATTCAACCAGTTT TAAGAAGTATCCCCACAGATTCCCCCGTTGCTAAAGCATTAGTGTTAGGGGATCGCTTTGGCGTCTG ATGTTGCTGGTATGGCTTCACCAATTGCATCTCCACAAAATGTTATTGCTCTTGAATCAATGAATC CTAATCCAGGTTGGGGGAAATGGTTTGCTGTGGCATTACCTGTGGCAATCATTAGTTTAATTTTAA TTTGGGTGGAATTATTCATGACGTTTAAAATCAATAATGTTAAAATCAAACAATTCAAACCAATTA AAGAAAATTAACCATGAAACAATGGTTTGTATTTGCCGTCACTATAACTACTATTCTTTTATGGT GTGTTATGCAAAAATTGATGGAACATTTGGTGAATCAGGTATAATCACTTGTATCCCAATTGTAT TATTTTTCGGTACCGGTTTATTAAAAGTTGATGATTTAAATAATTATCCTTGGTCAATTGTTATGT TAGCCATGGGTGGTATTGCATTAGGGAAAGCCGTTACTTCTCAGGTTTATTGAAAACTATTGCTT TAGCATTACAAAAACGAATTATGCATTATGATGCCATTGTTGTATTAATCATTTTTGGAGCATTAA TTTTGGTGGTAGCTACATTTGTAAGTCATACTGTATCAGCACTTATTATTATCCCCCTTGGTTAAAG AAGTTGGAGATTCATTACCTAAACCTCATCCATTAATGCTTATTATGGGTGTAGCTTTAATTGCTT CAGGGGCAATGGGATTACCAACTTCAGGATTCCCTAATGTGACGGCAATTGGTATGAGAGATGAAG TTGGTAAACCTTATTTGACGGTTAATTTATTTATTACTAGAGGGGTTCCGGCAAGTATAATTGTTT ATGTTTGTATTATCACCATTGGTTATGGTATTATGTCATCATTGAACTTTTAA

YJL198W_homolog 896aa (SEQ ID NO 392)

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NYDLEKQNNTTVAIHDDDDSEDDEEEEEEETHSHDSVLLNHTHFNVKQQLKITLKRKAITLFINLS
ELKSFIELNRIGFTKICKKFDKTCGYSIKQDFINEFLPQYSRVFENDTIEELDYKLNQIIKIYAFL
SNKLTTQSTTKEDLDNIKFELRSYLRDHIVFERNTVWKDLLSLEKKSYNIDLDNSVVQNNKMGDEG
HIINSMMNLSMKRINLPQCLKKLIKYDHIDIPQFLLTTQMLKIIIIVIVFIILLAVKTFNDPVQGR
CLAVLVAAAMLWASEALPLYTTALLIPLLVVTCKVCKTPGTDDPMDATKASQYIFGTMWNSTIMIL
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RSIPTDSPVAKALVLGIALASDVAGMASPIASPQNVIALESMNPNPGWGKWFAVALPVAIISLILI
WVELFMTFKINNVKIKQFKPIKEKLTMKQWFVFAVTITTILLWCVMQKIDGTFGESGIITCIPIVL
FFGTGLLKVDDLNNYPWSIVMLAMGGIALGKAVTSSGLLKTIALALQKRIMHYDAIVVLIIFGALI
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ACAATTAAATCCAAAAAAAAAAAAAAGAATCGAATTCCATATGTCGCATAAGACTCAGAGCCAATTAT CTTCACAAATGAAAAACTTGAATACTCCACCAATAGACTTCAACTCAACTTCAAGTAACAATACCA TGCCTTCTGAACCAAATCTGCAACCGCAACAACAACAATCACAACCAGAAGCAAAAACGGAGCCAC AAACCATACGCCCTGCTACTTTTACAACTAGTGGCAATTCATCATCTTCGTCGATATCTACCTTAT CAGCGCCACAAAGCTCATCGTTTCAACGCCGAAACAATCCACAACGTTTCAATCGGAATCAACTCA ATGTATACACTGACTTCAATAGTACTACTTCATCTGCTTCAAGCATTAGTAGTTCACCAAAAGATT TCTTCACCAGAGAGCCACCACGGATCCATAGTAAATTGATATGTGAAGAGATTGCCTCTGCCAATA ATCGAGCTGCTAAAGAGGTTTTATCACGTTTATCTACTGATGAATTGCGTTCAGTTAAATCACATA CTGAATTAGCTGAAACTGCTAATGGAGTGAGAATGTTAGCCAAAAATTTATCCCGAGCAACCATTC AAGAAGTTGTTGAATGGATTTTGGATCAACATCCTCATATAACAATTTATGCTGATGAGAAATTAG CAAAGTCGAAAAGATTCAATCCGGAAAGTATTATTGCCAATTATCCAAATGGTTGTAAGAAATTAA AATATTGGAATAAAAATTAACTACGAAAAATCCAGAAATTTTCGATTTAGTACTTACATTAGGTG GTGATGGTACTGTATTATTTGCTTCAAACTTATTTCAAAAAATTGTTCCACCTATACTTTCATTTT CATTGGGCTCATTAGGTTTTTTAACCAATTTTGAATTCAGTGCATTTAGAACAGTATTGAGCAAAT GTTTTGATTCTGGAGTTAAAGCAAATTTGCGTATGCGATTCACTTGTCGAGTACACACTGATGAAG GGAAGTTGATTTGTGAACAACAAGTGTTGAATGAATTGGTAGTTGATAGAGGACCTAGCCCATATG TTACTCATTTGGAATTATACGGCGATGGATCATTGTTAACGGTTGCCCAAGCTGATGGGTTGATTA TTGCAACTCCAACTGGTTCGACTGCTTATTCATTATCTGCTGGTGGGTCTTTAGTTCACCCTGGTG TGAGTGCCATTAGTGTTACTCCAATTTGTCCTCACACCTTATCGTTCAGACCTATACTATTACCTG ATGGGATGTTTTTGAAGGTTAAAGTCCCACTGAGCAGTAGAGCCACTGCGTGGTGTTCATTCGATG GTAAAGTGCGTACTGAATTGAAGAAAGGTTATTATGTCACTATTCAAGCTTCACCATTCCCCTTAC CTACAGTAATGTCTTCCAAAACAGAATATATTGATTCTGTCAGTAGAAATTTACATTGGAACATCA GAGAGCAACAAAAACCATTTAGTTCATATTTGAAACCAGAAACGCGACAAAGTATTGCTGAAAGTG AAAGATTGGATAATTTACATATTTCAAGTGAACAAGATGAATCGAATCATGAGGAACCTGAAATAA CTGAAGATTTTGATATTAATTATACTGACAATGAACGTGATTCTTCTAGTTCCACTCCTAGTGAAG AAAGCAACGAAGAATGTGCTAATACCACGACATAA

YJR049C_homolog 592aa (SEQ ID NO 394)
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TVAQADGLIIATPTGSTAYSLSAGGSLVHPGVSAISVTPICPHTLSFRPILLPDGMFLKVKVPSSS
RATAWCSFDGKVRTELKKGYYVTIQASPFPLPTVMSSKTEYIDSVSRNLHWNIREQQKPFSSYLKP
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YLR048W_homolog EMBL_entry 1042bp public: 1..1042; CDS: 28..786 (SEQ ID NO 395)

YLR048W_homolog SWISS-PROT_entry 253aa (SEQ ID NO 396)
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IKESSYVNIPVIALTDMQSPSEYVDVAIPCNNKGKHCIGLIWWLLAREVLRLRGIIPDRTTEWSVM
PDLYFYRDPEEIEQNAVEEAKTEGVEGAPVAEAETEWTGETEDVDWADSGATPSC

YLR088W_homolog 1335bp public: 1..80/494..776/821..1335, PathoSeq: 81..493/777..820; CDS: <1..1332 (SEQ ID NO 397) TCGGGGCTACAAATTTCGTCCATGAAAATTGGGTTCGCCACCAATACTTTGTATGCGATTATGCAT TACAATGAAGGTGCTATGAGTTTGGCGGTGGCTTTGGCACGGTACTTTACAAAGATGTCGATCTGG TCGAAAAACATTATTTTGTATTTCCTGAGACGGCCACAGACCGTTGAGGTCGTGGGTTGAGGCA TACCATACGGTGTTGGACGATACTGCGGGGTCGATTGAGGCGGCGATTATTATGGAGTACGGCAAG AACGGTGATTATTTTGAGTATTACGATATGTTCTACGAAGGGTTGAATGGGCAGTTGCCGAATTTG GACTTGTTGAATACGGCCAATGTAATGACGTATCATGAACAGATCCCCTGTGCCATGCAAGGGATG TCGGATAGGGTTATCAATTATAGCACCCGGTTGCAGACTTTGTTTAGGGGGTATCCTCAAATTGACG CTTGTCGGGTTGACTGATGAAGTTCATGGGTGTGAAGCATTTTCGGGGTGGCAGATCCAGGCATTT ACGATCAAGGTAAGGGGACTGAAGGGAAAGATGTTACGCAGTTTGGCCGGATTGTCGATTCTACG TTTAGGTCGGTTAACAATTTGCTTGAAAAGTTTCACCAATCGTTTTTCTTTTACTTGATGTTGTCG CCAAAACACTTTGTGTCTATTGGGACGTACTTGCCGTCGGCGATTTTGTTGGCAGTATCGTATGCG TTGAGCTCTGTCAGTGCGGTGGTGGTTGCCGGGTTTGATTTTCGAAAGCTATATTTTGTGGTGGTG GTTGAAATTGCGTGTGCTATTTTGGCGTTTGTGCCGGTGAACCAGGTGATGCTTGTAGCGATTCTG GCGGTGGTGTTGCCGCCCCAAGCCATCTTTTCCAAGCAGGCGGCGTTTTCGCTAATTTCTATT GCGTTGTTGGCAGTGGCATTACTTATTACCGCCCTCTTGATTGTACATTTTGCATTGGCGTTTAGT ATTGGGATTTTAGCCCTTCCATTGACATTTGTCCCGACATTAATGAAGAACAAGTCTAGGCTAACA GCTTTTTGTTTGGCGGTGTCGAATCCGTTTTTTGTGATTTTCGTTGCTGGGAAAGTGCTTGGCCAC CCCGAGCTATTTGACCGGTTGGTCACTGCCTGGTCGGACATACAGTGTTGGACATGGTTTATCGTT GTTTTGGGGTGGTTCCCAGCGTGGGTGATTATCACACTAAGCTACTGTGGCTACAAGCCAGTTAAG GAAAAAAGTGAATAG

YLR088W_homolog 444aa (SEQ ID NO 398)
SGLQISSMKIGFATNTLYAIMHAPRGENTEAMALVVPWTNSDNEYNEGAMSLAVALARYFTKMSIW
SKNIIFVFPETGHRPLRSWVEAYHTVLDDTAGSIEAAIIMEYGKNGDYFEYYDMFYEGLNGQLPNL
DLLNTANVMTYHEQIPCAMQGMSDRVINYSTRLQTLFRGILKLTLVGLTDEVHGCEAFSGWQIQAF
TIKVRGTEGKDVTQFGRIVDSTFRSVNNLLEKFHQSFFFYLMLSPKHFVSIGTYLPSAILLAVSYA
LSSVSAVVVAGFDFRKLYFVVVVEIACAILAFVPVNQVMLVAISAVVLLPRQAIFSKQAAFSLISI
ALLAVALLITALLIVHFALAFSIGILALPLTFVPTLMKNKSRLTAFCLAVSNPFFVIFVAGKVLGH
PELFDRLVTAWSDIQCWTWFIVVLGWFPAWVIITLSYCGYKPVKEKSE

YLR167W_homolog 1190bp public: 1..1190; CDS: 501..1187 (SEQ ID NO 399)

WO 01/02550

138/161

CCATCGATAACGTCAAATCCAAGATCCAAGACAAAGAAGGTATTCCACCAGACCAACAAAGATTGA
TTTTCGCCGGTAAACAATTGGAAGACGGTAGAACCTTGTCTGACTACAACATCCAAAAAGAATCTA
CTTTACATTTGGTTTTAAGATTGAGAGGTGGTATGCAAATCTTTGTTAAAACTTTAACTGGTAAGA
CTATCACTTTGGAAGTCGAATCTTCTGACACCATCGATAACGTCAAATCCAAGATCCAAGACAAAG
AAGGTATTCCACCAGATCAACAAAGAATTGATTTTTTGCTGGTAAACAATTAGAAGATGGCAGAACCT
TGTCTGACTACAACAACATCCAAAAAAGAATCTACCTTGCACTTGGTCTTGAGATTGAGAGGTGGTTTCT
AA

YLR167W_homolog 229aa (SEQ ID NO 400)
MQIFVKTLTGKTITLEVESSDTIDNVKSKIQDKEGIPPDQQRLIFAGKQLEDGRTLSDYNIQKEST
LHLVLRLRGGMQIFVKTLTGKTITLEVESSDTIDNVKSKIQDKEGIPPDQQRLIFAGKQLEDGRTL
SDYNIQKESTLHLVLRLRGGMQIFVKTLTGKTITLEVESSDTIDNVKSKIQDKEGIPPDQQRLIFA
GKQLEDGRTLSDYNIQKESTLHLVLRLRGGF

YLR234W_homolog 2390bp public: 1..2390; CDS: 501..2387 (SEQ ID NO 401)

TCCAGAATAGTAATTAGGGACTTTAATTTATTAGGAGTGGATTGCATAGAATATGCTATCTAATA GATACATCTTATTATTCTTATTCATGGGAAAGCACCAGTATATGGAAATGCTGCCCAAGGTAGT GCACACAACAACTAGTTTACAAAGTAAAATTCGAAGTTACGTCAAAGCTTAGAATGGTTCTTATA GTAGTTGTCTACTCTATCAAAAAACCCATAATTTGTCTATATAACGTAAGGATCACTATATGCTGT TGAGTAAGAAATATGTTGCGAGCCGTACCGACAATGGATTGGCTGAAACTTGTTCTCATCAAACTT GCAAAACACTTGGAGACGCGCGCGCGTTTCAACACACAATAAACAACACGAAAAATAAGGTAGAAA ACAAAAAAAAAAAAGGAACTTTAAACAAGAAGTAATCCCCATTAAAACTTGATCAACACTTTT AGGGTTTCCGATTTCCCCATTTTCTTGACTAAAATAATATGAGAATACTATGTGTTGCCGAAAAAC AAAAATTCATCAAAAACTACGATTTCACCTTCACTTTCAACTCTGAAGATGGGCCATGTCAAGTAA CCATGACTTCGGTGGCTGGACATATCACAGGACTTGATTTTGGGTCTGCCTTTTCGTGGGGAAATT GTGTTCCCGGGCGACTATTTGAAGCAGACATCAAGACCATTATCACCAAGAAATCTATTTATGAAA ATATTGCAGAAGAGGCAAGAAACGCTGATAAGTTGATGATCTGGACAGATTGTGATAGAGAAGGAG AATACATTGGATTTGAAATTATGAATGCTGCAAGAAAATACAATAGGAACCTTGGGTTAAACAATA TTTGGCGAGCTAGGTTTTCACATCTTGAACGAAATCACATTATTCGAGCAGCAAAAAATCCCGTGA ATTTGGATATGAGTGCAGTTTCTGCAGTTTCTTGTCGTATGGAAATCGATCTTCGAGTGGGTACCA GTTTTACACGTTTGTTGACTGATCAATTGAGACAAAAGGGGATAATTGAAAAGAATGAACTAGCTT CTTATGGTACATGTCAATTCCCGACATTGGGGTTTGTTGTTGATCGATACAAACGAGTCAAGAGTT TTACACCGGAACCATTCTGGTATATTGAGATTGAAACTAGGAAAGAGAATAAAAAGACAATTTTCA ATTGGGTTCGAGGTCATTTTTTCGACAAGATGTATGTGGTTATGCTTTATGATCGATGCTGCAAAA GTGGAGAATTTGGAACCATATCAAAAATAGAATCAAAACGGAAACCAAATTTCCGTCCATTCCCAT TGACAACCGTGGAGTTACAAAAAGATTGTGCTAGATTTTTTAAGATGTCTGCTAAGACGGCGTTGG CAGCTGCTGAAAGACTTTATAACCTAGGGTATTTGTCGTATCCTAGAACTGAAACTGACAGGTTTG CAACAAAGCTTTTGAACGAAGGTTTCGAAACTCCTCGAAGCGGTTCTCATGATGATAAGGCGCATC ATGAATACGTTGTGCGACGCTTTATTGCCTGTTGCTCCAAAGATGCTGTTGGTACGCAAACCGTGG TGACTTTAAAATGGGGAGATGAATTCTTCACCGCAAGTGGATTAATGGTGCATGAAAAAAATTATT TGGAAGTGTATACTTACAAAAAATGGGAAAGCTCTAAACAACTACCGAAATTTACAGAGGGAGAAC AGGTCAAGTTGTCGAGTGGAATATTGAAAGACGGTAAAACAAGTCCACCCAATCATATGACCGAGC CCGAGCTAATTGCATTGATGGATGCCAACGGTATTGGAACCGATGCTACTATCGCTGAACATATTA ACAAAATAGAGACTAGGCACTATATTAATAAATTGAAAAAGGGGAAAAATGAATATATTCTTCCTA CTCCTTTAGGAATGGGGCTTATAGAAGGCCTTGAAAAAATGGAATTTGAAGATGTATCACTATCGA AACCATTTTTGCGGAAGTCGTTGGAACGATCACTTGAGGACATAGCAACCGGGTCCCGGCCAAAAG TTGTTTTGTGCAATGAATGTAGGAGAATTATACTTGGAAATAGCAGTAACAACAACAACAACAATA **ATAATAATACGTAA**

YLR234W_homolog 629aa (SEQ ID NO 402)

MRILCVAEKPSISKEVANILGGGRKKVRNSREKFIKNYDFTFTFNSEDGPCQVTMTSVAGHITGLD FGSAFSWGNCVPGRLFEADIKTIITKKSIYENIAEEARNADKLMIWTDCDREGEYIGFEIMNAARK YNRNLGLNNIWRARFSHLERNHIIRAAKNPVNLDMSAVSAVSCRMEIDLRVGTSFTRLLTDQLRQK GIIEKNELASYGTCQFPTLGFVVDRYKRVKSFTPEPFWYIEIETRKENKKTIFNWVRGHFFDKMYV VMLYDRCCKSGEFGTISKIESKRKPNFRPFPLTTVELQKDCARFFKMSAKTALAAAERLYNLGYLS YPRTETDRFAKETDFKSLLEVHKQDPRWGSYTTKLLNEGFETPRSGSHDDKAHPPIHPIKYVSLDT LNTLDEKKVYEYVVRRFIACCSKDAVGTQTVVTLKWGDEFFTASGLMVHEKNYLEVYTYKKWESSK QLPKFTEGEQVKLSSGILKDGKTSPPNHMTEPELIALMDANGIGTDATIAEHINKIETRHYINKLK KGKNEYILPTPLGMGLIEGLEKMEFEDVSLSKPFLRKSLERSLEDIATGSRPKVDVLNTTIGVYVD AYSVCSHQILVLCNECRRIILGNSSNNNNNNNNNT

YLR241W_homolog 3098bp public: 1..827/2190..3098, PathoSeq: 828..2189; CDS: 501..3095 (SEQ ID NO 403)
ATATATAGAATTATGGCTTAGTGCCCTTTATTAACTAAATTAGAGGTTACATTAATACAACTTAAC AAACAAGGAAACTAACATCCACGTATAGGGCTTCTTATATTAATATACCTAATTCAACCTGATTAT ATTGCCTTATATACAGCTTGTAAAAAAACACATAAGAAAGTTTACATCTCAAGATGAATTATCCCC CTATTGTAAAAAGTACATCGCCTAATGATAGACATCATAGAGTACTGGCGACTCCTTACATGATGG TAACGACAACAACAACAAAAAAAAAACATTATCTTGACGGTATAATTAGTAGTGTGCGAGAGG CACACGATAAGATTTATCAGTTTCCTTTTCTCGGTTGACCTTAATCTGTTTTTTGTATAGACTTTAT TTTTTTTGTTTTGACCACACCCACTTTTTAATATCACAAGATATTTAACTGATTATAGAAAACAA CAACAATAACCCAAATACGTTAACCACTTTTATTACATATGATAGACAATATAATCAATAATTTGC AAATCATACTACAGCAAAATGATGATAATTTTACATCCCCTCACGACGATGTGATATATCGACCAC ATTCTGCTCGTGTAGCACGATATCAAGTAATAATTGCATCTACATTGGGACTCACTGCCCTATTAC TATTTTCTATCTTACGATTAAAATATCCCAAAATATATGTGGCAAACTTTAATCATTTGAATTTCA CTACAGTTTACAAAATTACTGAGCAAGAAATTTTGGAACATGCTGGATTAGATGCAGTTGTGTTTT TGGAATTTTTTAAAATGTGCATTCGAATAATAAGCATATGTTTAGTATTTGCCATTATTATCATAT CTCCTATCAGATACAAGTTTACAGGGAGAGTAGATGAAGATTATCCCGACGATGATAGTGACAACG ATGACGATGATGGAAGTAATAATAATGGTACCACAATAATTAAGCATATAGTGTCAGCTGGAATTC TGGTGGCAAGTAAAAATAACGATGGAGAACAGTATCAACAATTTCTTTGGTTATACACTATTTTCA GTCAGAAGTATCTTGGATCGCAAAATTCAGTCACCGATAGAACGGTAAAAATATCTGGGATACCAG GATCATTACGAGATGAAGTGGCACTCGCACGGCACATTGACCGTTTGAATATTGGTGAAGTGGATT CTGTGTTGATTGTCAAGGAGTGGCAAAATCTAAACAAACTATTCAAAAGAAGGAGAAGAATAGTTC TATCGTTGCATCCCCAAGTTGGCGAACTGTATCGTTTTTCCAATAGGTATACTGATGATGCAGAAG **AATCACCAGACTGGGGATCTCAAAATTCGAACTCTGCACAAGCTTCAATAATAGATCAAGACTCAG** AATCTGTTGAAGGAGATTCTTCTGACACTTTGAATCGCTTGTTGAATGATGAACTGAGAACAAGAC CAAGTCTTCGGAAAGGTTGGTTCGGATTGTTTGGACCTAAAGTGGATTCAATAAACTACTACACCG ATAAATTGGAGGTCATAGATAAAGAGATTACCAGGGCCAGAACTAGAGAATATCCCGCCACTTCGA CTGCATTTCTCACTATGAAAACCGTGGCTGAAGCACAAATGTTGGCACAGGCAGTCTTGGATCCAA AAGTCAATCATCTTATCACCAACTTGGCCCCTGCTCCTCATGATATCCGATGGGATAATTTGTCAT TGTTGGTTTATCCAGTCAGATTTATGGCTAGTTTTTTAAACACTAAAAGCATTTCTAAAATATGGC CATCATTGGGGAAAGCTATTGAATCGCATAAATGGGCCGAAACTTTGATTACTGGATTATTGCCAA GTTATTTATCTCATAGTGATGAAGAGTTGTCATCGGTATCCAAGAACTTTTTCTATATATTTGTGA ACTTATTTTGGTTTTCACAACTTTTGGTACCGCCTCTTTTGTTGATACGACCAAAATTGCATTTG **ATTTAGCAAGATCACTCAGAGATTTGTCAATGTTCTATGTTGACTTAATAATTCTACAAGGATTGG** GGTGCAAGACCCCAAGAGATTACTTGAATTTGTACAAACCGCCAGTTTTCAATTTTGGTCTACAAT TACCACAACCAATATTGATATTTATTATTACGTTGGTATACTCGGTAATGTCTTCGAAGATATTAA CTGCAGGGTTACTATTTTATTATTGGTTATTTTGTGAGCAAATACCAATTGCTTTATGCTTGTG TTCATCCTCCACACTCAACGGGCAAAGTTTGGCCAATAATTTTCCGAAGAATCATATTAGGGTTAT TTCTTTTCAAATCACAATGGTTGGCACATTAGCATTACAAGATGCAATCACATGTGCTACTTTCT TGGCACCATTGCCGTTTTTGACACTTTACTTTTGGTGGAGTTTCCATAAACAATATATTCCCTTGT

CAACATTCATTGCCTTGAGAGCAATTGAAAGCAATGAAAATATCAACCCTACTGATTTGGAGCAAA TCATTGAAAACAACAATAATAAAACTCTTGACGAAAGAAGGGGAATTGAACACTAAATACGAATACC CCAATCTAGTTAATGATTTAGACGGGCCAATGATTGCATTGGATGGTGAAGATGTATTGATAGTTA ATCGAGATGGTACAACTGTACGGAAACCACCTCAATATTTCAGTTCAGAATGGGACTATTAA

YLR241W_homolog 865aa (SEQ ID NO 404)
MIDNIINNLQIILQQNDDNFTSPHDDVIYRPHSARVARYQVIIASTLGLTALLLFSILRLKYPKIY
VANFNHLNFSLHSTSRRNLPELPSNSLFGWIPTVYKITEQEILEHAGLDAVVFLEFFKMCIRIISI
CLVFAIIIISPIRYKFTGRVDEDYPDDDSDNDDDDGSNNNGTTIIKHIVSAGISVASKNNDGEQYQ
QFLWLYTIFTYVFTFVTVYFLFKQTNRIISMRQKYLGSQNSVTDRTVKISGIPGSLRDEVALARHI
DRLNIGEVDSVLIVKEWQNLNKLFKRRRRIVRKLEESWVEYFEKNGITNKSDLISLHPQVGESYRF
SNRYTDDAEESPDWGSQNSNSAQASIIDQDSESVEGDSSDTLNRLLNDESRTRPSLRKGWFGLFGP
KVDSINYYTDKLEVIDKEITRARTREYPATSTAFLTMKTVAEAQMLAQAVLDPKVNHLITNLAPAP
HDIRWDNLSLTRQDRNTKILAVTIFIGIMSLLLVYPVRFMASFLNTKSISKIWPSLGKAIESHKWA
ETLITGLLPTYLFTILNIVIPFFYVWISEKQGYLSHSDEELSSVSKNFFYIFVNLFLVFTTFGTAS
FVDTTKIAFDLARSLRDLSMFYVDLIILQGLGIFPFKLLLVGNLLRFLVNSLFRCKTPRDYLNLYK
PPVFNFGLQLPQPILIFIITLVYSVMSSKILTAGLLYFIIGYFVSKYQLLYACVHPPHSTGKVWPI
IFRRIILGLFLFQITMVGTLALQDAITCATFLAPLPFLTLYFWWSFHKQYIPLSTFIALRAIESNE
NINPTDLEQIIENNNNKTLDERRELNTKYEYPNLVNDLDGPMIALDGEDVLIVNRDGTTVRKPPQY
FSSEWDY

YLR321C_homolog 1559bp public: 1..947/1189..1559, PathoSeq: 948..1188; CDS: 501..1556 (SEQ ID NO 405)

TTCCAGAATTAGTAGATATTTCTGATATCAAGTTGGAGATAGGGATATCGAACTGGGATTCTATAT ATTCAATTGAAACATTTGAAGGAAATTCTTTCTTAAAAGCATCTAGTGACACATGATCTCTAATCT CCAGTCTTTTGATTAAATATTCTTTTAGAATATCAGGTGAAGAAGTGTTGGTAGTCATAGCTAGTA GATACTGTGTGGGTGTCTGGGATAATAATTATAATGTAAACAAAACAAAGTCGTGTCAGTGTATATT TGCTTGACAGAAAATACAGAACACTAAACAAACATTTTTTCATTCCTTTCTTGTTTTGTTCTGTT ATACCCCAAAAGTTTGAATAAGTCTTCAGATATCTAGCATGGCAACTTCTCAAGAATTGACAGCAG ACATACAAGCTCTTGCAACTAGTTTCCCCAAGCGATTAGCTAATGATAGTGACAATTCATTACTTA TTGGAGATGACCTTGATTTTGATGAATTCCCATCTTCGACACCCGGTACTAGAAGCTTAAATGAAA ATAAAGCTCAAATAGAAGCACAAAGATATTCTCTTGCGAAAAACACACCAACGCCCAAGAGAATCT TAGAAAAACCGGTGTTATCTGAGTTGGTTGAAAAACCAGTGGTGCTTATTCCTATCAAAATAATGA TTACACCAACTGAGTTTGCGGAAATTGTTTGCAGTGATTTAGATTTACCATTCAGTATGGCTGCAC AAATAGCAGACTCCATTAATCAACAGATTGAAGAGTATTCCTATGCATCTAATTTACAACTACCAA GATTTGAATGGGATATGAATCAAAATGAAGTTACACCAGAAATTTTTGCTGAAATAGTTGTTGCTG ATTTGGGGTTATCGTTAGAATTTAAGAATGCCATATCACATGCATTGCACGAAATAATTATCAGAG TGAAAAAAGAAGTAATAGATGGTACTTTTGACAATGAAATGCACAACTTGCATCTAGTAAAAGGTA TAATGTTTGAACAAGGAATTAGAATTTTCACTGAAAACAGTGTTCAAAATGGAAATGACCGTTGGG AACCTTTGGTCGAAGTATTGACTTCTAGTGAAATCGAAAGAAGAGAAAATGAAAGGGTTAGAAACT TGAGAAGATTAAAGAGAGAGAATATGAGAAGAGATTACGATGATCATAGTAGGAGAAGGCAAGCAG GAAAAAGAAGGTATGATGAGTTAGAAGGAGCCTGGGTATAG

YLR321C_homolog 352aa (SEQ ID NO 406)
MATSQELTADIQALATSFPKRLANDSDNSLLINVAPTGRQAKRHIQQINYSEEFGDDLDFDEFPSS
TPGTRSLNENKAQIEAQRYSLAKNTPTPKRILEKPVLSELVEKPVVLIPIKIMIENLNTNQKLIDS
FMWNLNESLITPTEFAEIVCSDLDLPFSMAAQIADSINQQIEEYSYASNLQLPNKGPYNVTIDLSV
NLNKQLYQDRFEWDMNQNEVTPEIFAEIVVADLGLSLEFKNAISHALHEIIIRVKKEVIDGTFDNE
MHNLHLVKGIMFEQGIRIFTENSVQNGNDRWEPLVEVLTSSEIERRENERVRNLRRLKRENMRRDY
DDHSRRQAGKRRYDELEGAWV

YLR325C_homolog 737bp PathoSeq: 1..737; CDS: 501..734 (SEQ ID NO 407)

YLR325C_homolog 78aa (SEQ ID NO 408) MAREIKDIKEFVELARRSDIKSAIVKVNAKVNANGKKFKQTKFKVRGSRYQYTLVVNDASKAKKLQ QSLPPTLKITNL

YLR344W_homolog 1348bp PathoSeq: 1..1348, exon 1: 501..515, intron 1: 516..979, exon 2: 980..1345 (SEQ ID NO 409) ATACCATGACAAGCAAGCTCAGGGTCGCGGGTTCGAGTCCCGCGGGGAGCTAATTATACCCTCATT CGTTTTATATTTTTTAAGAAATTTGATGTTGATTTGGTAAATGCCAAATTTTAAATGTGTGTTAG GGCTATAGCCCTAATGTACTGTATATGCAGTATCAGAAATACTTTTGTTACGCACAGTTTGTCTTA CCAAATACATTATATATATATTTTTTTTTTTTTTGAGTAGAGGAGCTACACTAGACCACAGTGCG CTTTTGGATCGATACTAGATAGCATATAATCATCAAAAATGGCCAAGATCAGTCAAGGTATGAAAT AGGAATATATACATTGAAAAGGAGATAGAACATCAAACAACCATTAAGAATTAAGTTTAATAC AGTTTCAATAAAGAGGGTTTTTTTCTCAGAACAAACCATTGACTGAAGTACTACACCAAGAAGGTA TAATGATTTCACGATTTACCTGAATATAAAGAACATCCTTAATATTGAATTTCAATATTAAAAATA CAATTTGGGGATATTGATGAAATTATGTATAGGAGATTCCATTTTTCAAACTTGTTGAATGGAAAA CTTGAAAAATCAAATCAAATCATAACCCTTCAATATATTCCTTCCTTATCTTACTTTTCCT ATTAAAACAAAGACTAAGAAACATTCAGTAAAATACTAACAAAAATTCCATTTATATAGACGTTTC TTCATCTCGTTCTAAAGCTAGAAAAGCTTATTTCACTGCTTCATCAGTTGAAAGAAGAGTTCTTTT ATCTGCTCCATTATCCAAAGAATTAAGACAACAATACAATGTCAAATCTTTGCCAATTAGACAAAA TGATGAAGTTTTAGTTGTTAGAGGTTCTAAAAAAGGTTCTGAAGGTAAAGTTAATTCTGTTTATAG ATTGAAATTTGCTATTCAAGTTGATAAATTACAAAAAGAAAAATCAAATGGTGCTTCTGTTCCAAT CAACATTCATCCATCTAAAGTTGTCATTACTAAATTACATTTGGACAAAGATAGAAAAGCTTTGAT TCAAAGAAAAGGTGGTAAAGCTGAATAA

YLR344W_homolog 127aa (SEQ ID NO 410) MAKISIDVSSSRSKARKAYFTASSVERRVLLSAPLSKELRQQYNVKSLPIRQNDEVLVVRGSKKGS EGKVNSVYRLKFAIQVDKLQKEKSNGASVPINIHPSKVVITKLHLDKDRKALIQRKGGKAE

TGAATATTCGTAATTAAAATTGATTCAAAATTGTATTGATGTTTGTATACTGGATAAACAACTTGT CTGAACCTTGTGGACTGGTAAACGCACGACATAGAGTAATATTTGGAGAAACCAAAAGAATTTTGA AAAACCGTGGTTTGAATTCGACCACAGATTGGTTGGACGACAAAATGCAAAGTGTATTCATCCGGA CTTTTGCTACCTCAAGAATAGAGTTCCAGCGGTACCAGCCGCGTTTTGTTAATACCATTAAAGAAA CGGTCAAATCGGCACAAGAAAAGTCGTACAGTATTACTAGACCATTGGGGTTGTCAAAACCAGTTT TGTTAAATCATAAATTGTCAGACACATACTCATTGTCCAATATATACGAGGAGTTGTTTGGTCAAA AATCCAAAGAAAGAAGACAGAAACAACTAGACTACGATTTGAAACACTCGCCAATTTATGAAGTCA AGTCATTTGAGAATACAAAGGGGAAAATATTTACTCCTCCTGTTTCGTACTTTCGACAAGACAAAT CTTTGTATTTCCCGGATTTTATAGCGAAAACATTGGCAGGTAATCAGAGAAGTTTGTACGACTCAT TAGACAATAGATTAAGCATAGTCAAATTGTTTTCTTCTGTTGCTGGTGAGCAGTGTACCCGTTCGT ACTTTAAGGTTGAAAACAAAGATTACTATTCCCAGGATTATGATACCTTTGTGGAGGAATATCCCC ATACCCAGATACTTGATGTGAATATGCCGCAAAGTTGGATCAAGGGGTTTGTGACAAACTTGAGCA CAGGAAATTTAAGAAAGACTTTGAAGCCAGCTCTGAGATACGAGAATTATTTCATCTTGCCTGGCC ACATAATGTCAGCGGAAATTAGAGAACAGTTGTACTGTGATAATCAATGTTCCGGGTATATTTATA TTGTTGATTCGATGGGGAAGATAAGATGGGCGACAAGTGGGTATGCAACTCCTGAGGATTTGAAAT TGATGTGGAAGGTTGTGAAAGGGGGTGCAAAGAGAAATGACCAAGTAA

YLR393W_homolog 376aa (SEQ ID NO 412)
MFVYWINNLCEIIQCICWRRRQGRTFFPSYFFFSLSLFFQSHCSSVKGWLFCAEPCGSVNARHRV
IFGETKRILKNRGLNSTTDWLDDKMQSVFIRTFATSRIEFQRYQPRFVNTIKETVKSAQEKSYSIT
RPLGLSKPVLLNHKLSDTYSLSNIYEELFGQKSKERRQKQLDYDLKHSPIYEVKSFENTKGKIFTP
PVSYFRQDKSLYFPDFIAKTLAGNQRSLYDSLDNRLSIVKLFSSVAGEQCTRSYFKVENKDYYSQD
YDTFVEEYPHTQILDVNMPQSWIKGFVTNLSTGNLRKTLKPASRYENYFILPGHIMSAEIREQLYC
DNQCSGYIYIVDSMGKIRWATSGYATPEDLKLMWKVVKGVOREMTK

YML063W_homolog 1271bp PathoSeq: 1..773, public: 774..1271; CDS: 501..1268 (SEQ ID NO 413) GAGACTTCAGGTACGACCCAGGGTTGCGACAAAGTTTAGGTAGTTTGTCGTCTGAATGTCGCAACA AAATAGGGCTGTAGCCCTAGTCATGTGATGTGAATTAACATAACAAGAAGAATTGCTGGTGCGCAA CATATTGGGCTGTATTTTTATTCTTGTTTTTCTGCTGTTCTCTCACTGTTAAGCTCTAAGTGAATT TTTCACTTGTTTCATATAATCACCAACTCAAGTACAACATGGCTGTCGGTAAAAACAAGAGATTGT CCAAAGGAAAGAAAGGATTAAAAAAAGAAGGTCGTTGACCCATTCACCAGAAAAGATTGGTTTGACA TCAAAGCTCCAACCACTTTTGAAAACAGAAATGTTGGTAAAACTTTGATCAACAGATCTACCGGTT CCGAAGACCACTCTTACAGAAAAATCAAATTGAGAGTTGATGAAGTTCAAGGTAAAAACTTGTTGA CCAACTTCCATGGTTTGGATTTCACTTCTGACAAATTAAGATCATTGGTCAGAAAATGGCAATCAT TAGTTGAAGCTAATGTCACTGTTAAAACTTCCGACGATTACGTTTTGAGAGTTTTTGCCATTGCTT TCACCAAAAGACAACCAAACCAAATCAAGAAAACTACTTACGCTCAATCCTCTAAATTGAGAGAAG TCAGAAAGAAGATGATTGAAATTATGCAAAGAGAAGTTTCCAACTGTACTTTAGCTCAATTAACTT CCAAATTGATTCCAGAAGTCATTGGCCGTGAAATTGAAAAATCCACCCAAACCATTTTCCCATTAC AAAATGTCCACATCAGAAAAGTCAAATTGTTGAAACAACCAAAATTCGACTTGGGTTCATTATTGG CTTTGCACGGTGAAGGTTCAACCGAAGAAAAGGTAAGAAGTTTCTTCTGGTTTCAAAGATGTTG TTTTAGAATCTGTTTAA

YML063W_homolog 256aa (SEQ ID NO 414)
MAVGKNKRLSKGKKGLKKKVVDPFTRKDWFDIKAPTTFENRNVGKTLINRSTGLKNAADGLKGRVF
EVCLADLQGSEDHSYRKIKLRVDEVQGKNLLTNFHGLDFTSDKLRSLVRKWQSLVEANVTVKTSDD
YVLRVFAIAFTKRQPNQIKKTTYAQSSKLREVRKKMIEIMQREVSNCTLAQLTSKLIPEVIGREIE
KSTQTIFPLQNVHIRKVKLLKQPKFDLGSLLALHGEGSTEEKGKKVSSGFKDVVLESV

YML128C_homolog 1517bp public: 1..1499, PathoSeq: 1500..1517; CDS: 501..1514 (SEO ID NO 415) TGATATGGATTTTTCAAAACTAAGAAACAATACCAACTACAACAACAAGAAACATAAGTGTTTGCT TAATTCAATGACCTCGAGTCATATTCCCACGTTTTAAGTATGAGTGTTTTACGAAGTTGTGGATCC TATTTTAAATAAACAATAATAGTAATAAAAAAAAAACCTTCTTTGCTTTTCGAGAATTTGTAAC GTTGCTCAATTATGTATAACAAGGGTAGAAACTCTGTGGGATTCCCTCCTTAAAAATATAGCAATC ATAATGTATTTCTCTTGTTCAGGATAATTATCACTATTTGTGACGTTTAATTTTTACATTTCTTCT TCTTCTTCTTCCTATTTCAACATTAAAGAACATTTAATATGTATTTCCCAATCATTGTATGGTTAT ATGTATCTATCACTTTTGTGGTTGCCAATTATGGTTTTGATCAATGGACAAATGATGATTTAAAAC CTAATGAAGAAGCTAAGAAATTAGAAAAAGGTTACAAGAAAGTTACTGAAGAATTAAATAACAATT AAAATTATTCAATTAAAGAATGGATTTTTGAAAGTTGGCCAGTAACCAGTTTGCAAACTTTTTTAA CTCAAAATAATATCCAATATAGTGCAAAGGATACCAAAGATGATTTAATCAATAAGGTTAAAGATC **AATTTGATTCTATTTCTAAGAAAAATCATGGGTCTAGTTTTTATCCTGGCAATTGGTTATATGAAT** CTTGGTCAGAAAATGATTTGAAAGATTGGTTGAAATCTTATGGCATTGAATTTAATCCTAGTTCAA CAAAGGATCAATTGGTTGAAAAATTAAAAGAATTTAGTTATCAAGCCACTCATTCAATTAGAGATT CCAAAGAATCTTTATTTGATTCATTGGATTTATTTGATAAAACCATTTTTGATAAAAAAGGTCAAA TTATTGACACTAAACCAGGAATTTACGTTGAAGATTTGGATAAGGAAAAATTAGTCAAGATTGCCC AACCTTGGATCACAAAGGGAGAACAAAAGTCTCAGAAAAAGGAGGGTAGTAATTTGATTAATGATA CATTCTTTGTTGGTATTAATAATTGGTCCAAGGATAAATTGCGTGAATTGGGCAATCTTGACTAA

YML128C_homolog 338aa (SEQ ID NO 416)
MYFPIIVWLYVSITFVVANYGFDQWTNDDLKQFLKERKVAFNDALENPKLISLANEEAKKLEKGYK
KVTEELNNNLNPPDDSLNDYLNFDYLFGKRKENYSIKEWIFESWPVTSLQTFLTQNNIQYSAKDTK
DDLINKVKDQFDSISKKNHGSSFYPGNWLYESWSENDLKDWLKSYGIEFNPSSTKDQLVEKLKEFS
YQATHSIRDSKESLFDSLDLFDKTIFDKKGQIEDEFFQTWSYSQLREWLYLHGFIDTKPGIYVEDL
DKEKLVKIAQSYKKCLLSDIHTWLANTEKKSQPWITKGEQKSQKKKGSNLINDTFFVGINNWSKDK
LRELGNLD

YML130C_homolog 2243bp public: 1..829, PathoSeq: 830..2243; CDS: 501..2240 (SEQ ID NO 417) ATGAGTTCATAGATGATCTGTTTCACTTTCAAATAACGTGTCAACAAAAATAAAGTTAGAGCATAG ATTTTGCCGCCACTTGTACAGATGGATAGAATTGAATGCAAATTCTGCATAAAGATTAAAGTGAAA TTCAAATTGTAGTTGCATGTATATAAAATAATATAAAAGATATATCACCAGCACAACTGATTACTT CTTTTCTTAGTTTGGTTTCTATAATCTTATTAAACATTCTTGCCTTTCATCCTTGATTATCATATT AGATCTTATCTTTAATTTGTTTGAAAAAATAATACCAATAATCTTCCCATTAGAACTTACAACACA ACAACAAAAAACCCATTCTAAATCACTATTCTCCATTATGAAAATTTTCAGATTATTTTCACTAC TAATCGTACAATTTATCATAAATACCACTGTTGCAGTATCACCTGTGTCAGCAGTTTTACCAAAAC TGAGTTTCAGTCCATTTGATTCACCAGAATTTTGTTCACAGATCATAACTCCCACTTGTAATACAA CTTTCACCTACATTGATGAATTGAATAAAGATATTCGTCCCTACTTGTCGGAATTAGTCAAGACCC TGTATTTCCGTTATTTTAAAGTCAATTTAGATAAACAATGTCGTTTTTGGAATGCTCAACATTTTT GTGCTAGTGAAAACTGTGCTGTTGAAATATTGGAAGATTTCAATTGGAGTCAAGTCACCAATGAAA GTTTGAAACCTTCAGGATTAGGTAAGATTTCATTACCTGACAAATCATCAATTGATAATTCCATTG AAACCGAAGAAGTTCAAACTTGTGAAGATTTAGATTATAGTGAAATAGATGATGACCATCATTGTG TTTATGTCAACTTGGTAAATAACCCAGAAAGATTTACTGGGTATGGTGGTAATCAAAGTTTTGATG TTTGGAAGGCTATTTACCTGGAAAATTGTTTCCCTAATACTAATCCAATGTCAGTGACAAATGATG CCGACAATGGTGGTGAACAATGTATCGAAAAGAACTTGTTTTATCGTGTTTAGTGGTATGCATG CTTCAATTGCAGTACATTTATCAAGAGAATATTTGAATTCTGAAACTGGTGAATTTTATCCTAATT

YML130C_homolog 580aa (SEQ ID NO 418)
MKIFRLFSLLIVQFIINTTVAVSPVSAVLPKSSFSPFDSPEFCSQIITPTCNTTFTYIDELNKDIR
PYLSELVKTSYFRYFKVNLDKQCRFWNAQHFCASENCAVEILEDFNWSQVTNESLKPSGLGKISLP
DKSSIDNSIETEEVQTCEDLDYSEIDDDHHCVYVNLVNNPERFTGYGGNQSFDVWKAIYSENCFPN
TNPMSVTNDADNGGEQCIEKNLFYRVVSGMHASIAVHLSREYLNSETGEFYPNLKVFMERVGMHND
RLSNIYFNYALVSQAIVKLSEILPLREFIQSGYDDITPAQKQHLLANNDVESVEVYDRLLLDDIIP
SLEANVVFNTSNLFDNSNLRDEFRSRFRNISAIMDCVGCDRCRMWGKIQTIGYGTALKILFEDDNY
DNHNLKFRRIEIVALINTFDRLSKSIESINMFKEMYLQHLKDIAEGLTQPGVYDKIQNNKPGNGFA
FPFVSPLPQKKPDQTNTPKNQQQKQPQETDKKRLTLEEIAHTKPEDRTFIEDFRLSFDEVWQALRF
VLTSYQRFPAVLSRFTLVQLNEWWNKLLGKPTVYDYQSSFDVDALQYSQVLG

YMR022W_homolog 1004bp public: 1..507/668..1004, PathoSeq: 508..667; CDS: 501..1001 (SEO ID NO 419) AACAATTTCAAAGTTGGGCTTGGAGATCGATTTTTTTTCCCGCGTCTGTGTGGCACGAGACAATTG AGTCGACCAGTACGTTTTAATTGAATACGAGAGTCGACGCAATTACATCCAACATTCCACTT ATTCTATATCAATGTAAAGTCATTTTTTGATAATATCGTAATTTACACATTTCGTATATCTCGGCA ATAGGGGGGATAAAAAATAGTATTGACTAATTAATATCTTGTTTATCAAATCAGGAGTATAGAA TTCCACCCAACAACTAGATTTTCCGAATGCGAAACGACGAGGACGACAACAACGACTAAAGAAG AAGAAGAAAAAAATATAAATTGATCACGCACACATTAGAAACACAATATTGGATCACTTTT TTCGATAATACTACCACCACACAGCTCATTCACCACTCATGCCCCGAAGTTCTACTGCTCAAAAGC GTTTACTAACAGAGTATCAACAATTATCGAGGGACCCACCACCTGGGATAATCGCAGGACCAGTGA GTGAAGATAATTTATACAAATGGGAATGTTTATTAGAAGGACCATCCGATACTCCATATGCAAATG GAGTATCCCCAGCAGTATTGACTTTCCCTAAAGATTACCCATTATCACCACCTACATTAAAGTTTG ATCCACCATTGTTACATCCAAATATTTATGCTGATGGAACCGTTTGTATTTCGATTTTACATCCTC CTGGTGAAGATCCAAATCAATATGAACGACCAGAGGAAAGATGGTCACCTGTGCAAAGTATTGAAA AGATCTTGTTGAGTGTCATGTCTATGCTTGCAGAACCTAATCCTGAAAGTGGGGCTAATATCGATG CTTGTAAATTATGGAGAGATAATCGTGCTGAATATGACCGACAAATTAGACAACATGTCAAGGAGT CATTAGGATTATGA

YMR022W_homolog 167aa (SEQ ID NO 420) MPRSSTAQKRLLTEYQQLSRDPPPGIIAGPVSEDNLYKWECLLEGPSDTPYANGVSPAVLTFPKDY PLSPPTLKFDPPLLHPNIYADGTVCISILHPPGEDPNQYERPEERWSPVQSIEKILLSVMSMLAEP NPESGANIDACKLWRDNRAEYDRQIRQHVKESLGL

YMR118C_homolog 1031bp PathoSeq: 1..1031; CDS: 501..1028 (SEQ ID NO 421)
CTACACAAAGCTTCGAGAGTTTTTTTTCGTTGCAGGGGTGGGACAGGTGAGTAACGAATAAAACGT
CGATTGTCTTTCCTTTATGATTGTTCTTTAACGGAATTGTGTTCCTTAAAACAAAATCAGTTCTGC

CGATTGTCTTTCCTTTATGATTGTTCTTTAACGGAATTGTGTTCCTTAAAACAAAATCAGTTCTGC ACGTGATATAATCTCCTATCGCTAGTAGTAAGTTTTAATTTTTTTGATCAAAAGTACACTCATCAG TCTATTGTCGTAGATTTCGCATACTTGTGATAATATCTGGTGTACACTACTTTTTTTGGTTTGTA

YMR118C_homolog 176aa (SEQ ID NO 422) MISRIGLLKRPTVSTLNNYVKLQSTLALKRYTSTVPATSNQEQEILVAQRKNRPTSPHLQIYEPQL TWIMSSFHRITGVAMAGAFYALTCGFAATSILNIPFDTTTLVSAFTTLPTFAQYGIKAICAYPFVY HIGNGIRHLVWDFGKELTIPGVYRTGYAVLAATAVIGSYLAFLW

YMR230W_homolog 1176bp public: 1..1176; exon 1: 501..551, intron 1: 552..870, exon 2: 871..1173 (SEQ ID NO 423) AAAAGCAAGAAGAAGAAGACTCGTTGGCCAATTTCTTCGGCAATTTCAAGAAGAAAAGAGTAGCTG TTTAGAACTATATATATATGTACTCGCGCTTTAATGTTTATAGCAATAATGAAATGTTTTAATAAT TATTTAATCAAACTTGGTTAACTTATGATTATGGTAGTGATCTAAGAACACAACTTGCAAAGCA TTTTTGCAGACATTAAACCTCAGGGCTATAGCCCTAATGGCAAAACATGCACGTGTATGTTTCTTG ATTTTTCTACACTACTAGTAAAAAAATTTTCTTTCCGCTCACTATTCACACATACACTCTTTTTCG CACAATTACAGTCTACCAACAGGAAAAGAAAAAAAAAGGAATCTGGTAATTGAAAAATTGAAGTT TGGTTCTTTTAATACTATCAATCAACTAGAGTCACAGCATGTTAATTCCAAAAGAAGACAGAAAGA AGATCCACCAATACCTCTTCCAAGGTATGTAAATATGAATTATAAACTGGAACAGAATATGGCATT TCAAGGGATGCACGATAAGTCAAGAGTTCATGAAAAAGCACAGATTATAACAGTCGTAAAGAAAAA TTTCACTACCAACAACAATAAGAAGATATCAAAGAGATTCAGTAATCACTACTTACAAGAAACATA TAACATCATGGAGAGTTTAATTTGAAATACGAATGAATATACAAATGAACTATACCCTTTTTATGG CCATATCACGTTTCAAGAAATATTTAAACAAAAATAAAATGAAGAATAAAACTTGGATATACTAAC GATACTAGAAACTTGTTCGTCATCAAAGCTTTACAATCTTTGACTTCTAAAGGTTACGTCAAGACT CAATTCTCATGGCAATACTACTACTACACCTTGACTGATGAAGGTGTTGAATTCTTGAGAACCGAA TTGAACATTCCAGAAGGTATCTTGCCATTGACCAGATTGAAGAATGCTCCAGCTGAAAGACCAAGA CCATCAAGAGGCGGTCCAAGAAGAGGTGGTTACAGAGGTAGAGCTAA

YMR230W_homolog 118aa (SEQ ID NO 424)
MLIPKEDRKKIHQYLFQEGVVVAKKDFNQPKHDEIDTRNLFVIKALQSLTSKGYVKTQFSWQYYYY
TLTDEGVEFLRTELNIPEGILPLTRLKNAPAERPRPSRGGPRRGGYRGRARD

ATGCTAGTAATATTAACAATAACAACAATAACAGCACCAATAACATTATCAATTTAGATAATGCTA GTGTTAACGGAAGTATGATTGCTTCATCCAATGCAATGGTGACTGGTCCTCCCGGAACATCGATAG CGTTAGGATCGGCCTTCGATCGCATCCATACTAGAGGGGGAACAGCTTCAATATTTTCATGACC CAGTGAGGCAACAACAGTTCAAACTTCCTTCTACCAAGGCTCCGTCAATTTCCAACTCCATCAGCA GTTCAAATAATATAGATTCAATACTTAAACGACCTGTACATCTACGTGAGGCATCAACGTATTCAG TGAATGATAATGACCACCGAAATCTTGTGCTACCAAACTCAACTGAAAGGTTTACTGCTTCACCTT CGAACAATATTGGTAATGAAAATATACCTCAATACCAGAAAACTAGTAGTGTTGCCCACTCAATCA ATGAAGGATACAATGATGATACATTTTCATATAATGAAGTTGAGGATAATTTAATTGATGAAGATT CCACGGACGATGGGGATTTGACAAAAAATACCATTACTAATAACAACAATCCACCAACCACGTCGA GCCAACAGCAACCACAACCACAGCCGCAACCACAGCAACCACAACTACATACTCTGTCTC CTCTAAATCAGATACAAGCAGCGACATCAGCAACACCTTCTGTGTCCACTAAAAACGCGTCTAAAA GAAATTACAAAACCTCATCCACTTCCTCAAAATTAAGATCAACTACATCAAAACTTTTCGATAAAA AAGGGTCACAACCAAGAAGATACAGTACCATTCCTGATGATATTGACATTGAAGATTTCGATGATG GTTATTTGTCAACTGGCCAACCTTTAGAGAGTTCTGATCGTGGCTCTAACAAGATGGTACTGATA ATGGAAACAACAGTGATCACAATATTAATTCTCCTTTGACTGCTAATAATAATAATAATAACGTCA ATCACAACGATCATGGTGATAACAAAAAGAGTAATACCAACAACAACAACATTGCTAATAATAGAG CATTTCCATTTCCTTATCAAGATCAACAACATCATTATTACTACGACTACGATGATTTTGACCAAG AATCACAAATCAATGGACCCAATTTTGATTTGCCAGACCTCCCTATAAACAGATCAGCTTCACGGA TGCTTACCATAGGGTTTGTATTGGGGTTTGTTTTGGCCACAACAAAGATTTAACTGATGTAGGTA ATCTACCTGATACAGATAATCTGAAAATATCTAACATGGGAGGGTCACAAAAAGTAGAGACGGTTA CGACAATTCAAAAGGGAGGAATCCGATTATTATATCCTGGCAAAAATGTTACTGCCGAGGCTAAAT GTAATGACACCAACGATAATGACAACTCCAAGAAGTGGGAAATCATATCAAGCAATCCATTTGATT TGATTATAACTGGAGTATTGAAGTATGATTTACCATTTTCAAGAACCTCAAGATCAGTCGTGGTTA GAAAAACTGGGTATATTGATCCTACCTTATTCGTAATACCACAAGGAGAATAATATTTCAATTT

YNL054W_homolog 779aa (SEQ ID NO 426)
MLHPNNSVVDMSSTGNMNENTDAPPKQQTKKKISKQNSTKTDFFAARLASAVDDIESSDSDETFIY
ENNDTELDDNASNINNNNNNSTNNIINLDNASVNGSMIASSNAMVTGPPGTSIALGSGLRSPSILE
GEQLQYFHDPVRQQQFKLPSTKAPSISNSISSSNNIDSILKRPVHLREASTYSVNDNDHRNLVLPN
STERFTASPSNNIGNENIPQYQKTSSVAHSINEGYNDDTFSYNEVEDNLIDEDSTDDGDLTKNTIT
NNNNPPTTSSQQQPQPQPQPQPQPQLHTSSPLNQIQAATSATPSVSTKNASKRNYKTSSTSSKLR
STTSKLFDKKGSQPRRYSTIPDDIDIEDFDDELIYYDNTARFPANESTSLLNQNQRIPHYRSLNLN
FPQVKRQSKRYLSTGQPLESSDRGSNKDGTDNGNNSDHNINSPLTANNNNNNVNHNDHGDNKKSNT
NNNNIANNRAFPFPYQDQQHHYYYDYDDFDQESQINGPNFDLPDLPINRSASRNFNNNNNPKRFGD
SHFFLPRKTDQYSQRTSFLKSCIYTFVCILIVLTIGFVLGFVLATTKDLTDVGITSIENPIVSKDE
LVFNVVIEAFNPGWFSVDINEVELDLFARSGYLPDTDNSKISNMGGSQKVETVKLGTILNFESVLN
FKGGFLSREPTIQKGGIRLLYPGKNVTAEAKLVVNMADIKIAASNSIAKESTTSNDTNDNDNSKKW
EIISSNPFDLIITGVLKYDLPFSRTSRSVVVRKTGYIDPTLFVIPOGENNISI

YNL075W_homolog 283aa (SEQ ID NO 428)
MIRKQARERREYLYRKALQLQESSLTEKRQQLKAALASGKSLSKELAEDEKLQRDFIYDESEQIEI
DDEYSRLSGISDPKVVITTSRDPSVKLLQFSKEIKLMFPNSLKLNRGNYIISDLVSTCNRVQVSDM
ILLHEHRGVPSSLTVSHFPHGPTAIFTLHNVKLRHDLPNLGNVSESYPHLIFENFQSDLGKRVVKI
LQHLFPPGVKKDSSRVITFVNNDDYISVRHHVYVKTKDSVELSEIGPRFEMRLYEIRLGLPDNKDA
DVEWQMRRFIRTANRKNYL

YNL096C_YOR096W_homolog 1061bp public: 1..1061; CDS: 501..1058 (SEO ID NO 429)

TCCTTTTGTTTTATTTTTGCTGTGTTACTCCAGAAATGTGCATAATAATGATAATAGTAATTTGT GACTAATATGAGATGATCGTATGTGGGTGGGTGGGGAGGAAGGGACCCGGAATTCTAGGAACAGGA TTTATTTTTGCCCACTTCTTTTGGATTAGGGCAATAGCCCTAAAGCTCGTGTTTTAGCCCCTTTATA TTGAAAAAAAAATCATTTTTACAGTTTACATTTCTCTAACCTGCAAAAAGCTCTCGTTTTTTTGTA GTGAGAGTTACTCGTTCACAATAGTATACTTTACAGGGGAGTTCTTTTCTTTTGGAATAGTCAACC AACAGCAAATAGCCAAGGATCAAGCTTCATCATTAATCATGTCCTCTAAGATCTTATCAGAAAACC CAACTGAATTAGAATTAAAAGTTGCTCAAGCTTTCGTTGATTTGGAATCTCAAGCTGATTTAAAAG CTGAATTGAGACCATTACAATTCAAATCTATCAAAGAAATTGATGTTAATGGAGGTAAAAAAGCTT TAGCTGTTTCGTTCCACCACCAAGTTTACAAGCTTACAGAAAAGTTCAAACTAGATTAACTAGAG AATTAGAAAAAAATTCCCAGATAGACATGTTGTCTTTTTAGCTGAAAGAAGAATCTTACCAAAAC CAGCTAGAAAAGCTAGAAAAACAACAAAAAAAGACCAAGATCAAGAACTTTGACTGCTGTTCATGATA GTAACAAAATCCAAAAAGTCTTGTTGGATTCTAAAGATTCAACTGCTGTTGATTACAAATTGGATT CTTTCCAACAATTGTACTCAAAATTGACTGGTAAACAAGTTGTTTTTGAAATCCCAGGTGAATCTC ATTAG

YNL096C_YOR096W_homolog 186aa (SEQ ID NO 430)
MSSKILSENPTELELKVAQAFVDLESQADLKAELRPLQFKSIKEIDVNGGKKALAVFVPPPSLQAY
RKVQTRLTRELEKKFPDRHVVFLAERRILPKPARKARKQQKRPRSRTLTAVHDKILEDLVFPTEII
GKRVRYLVGGNKIQKVLLDSKDSTAVDYKLDSFQQLYSKLTGKQVVFEIPGESH

YNL178W_homolog 251aa (SEQ ID NO 432) MVNAILSKKKKLVADGVFYAELNEFFTRELAEQGYAGVEVRKTPSKLEVIVKASNTQGVLGEQGRR IHELTSLIVKRFKLSPEGIAIYAERVEERGLSAAVQAEALKAKLLSGLPIRRAAYGVLRFAMGAGA KGVEVVISGKLRAARAKSQKYADGFMIHSGQPTRDFIDIAIRHVLMRQGVLGIKVKIMKDPAANRF GPRALPDAVKIAEAKDEDEVIPAPTVKSYKQTAEDETETDAPVEAEAEVEATA

YNL182C_homolog 2105bp public: 1..728, PathoSeq: 729..2105; CDS: 501..2102 (SEQ ID NO 433)

AAACTTTCTGATTGAATAAGTGAACTCAAATCACATTCTTCGGCATATATCAAACCATTATTAGT TAGTTGTGCTCCTCGTTGTCCCAATTCATATGCTATTTGAGCTCCAATACCACTGGTCCCACCAGT AATCATAAACACTTTCCCATGCATGTCTCGCTCCCACGTATTGGTGGCACCATGGAAATAATACTT GGCTCCAGCAAGAGTTAATAGAATGGGAAGAACGGTAGGTCCATATTCTTTAATTTGGTCCCAATA TGGAATCACCTCTGGCCCATCAAACACACACTAGTTAAAAAATTCACTGGCATAATTGGTATATC AAGAGTGAAGAAAATGCTGTATTGGAGGTTGGAATTTGTTCACAAATTGGTTGCCTTTTTATTCT TACAATTTCTTGTTCTTGTTCTCCCACTCATCTCATCGCTCTCTTATAAATTCACAAACATGGATG AAGTAGTATTTTACATAGCTCAAGGTGATCCAGCTGATAAACACAGTCAAGAATCATATGGATATG TTACATCAATCCATTCTTCCAAACAATATGCATCTTATCGACAAGCAGACTCGCATATAAACGGTA' CTGCCATAACTGGTATTGGCCCAGGAGAAAGAATTTTCACTGCTGTTCCTAACAAGGCATTAATCA ATGTATATTCATGGGGAAAAGAAGTGTTGATCAACGTATACCGATACCAGAAGCATTGACTTGTA TCACGTTGATAAACCATCCAAATGGCAGTAACAACAACAGCGACAATGATGACAACCAGTTATACA AATTACCAAATTACCGAGTTCCTTGGTTGTTAGCAGGTGGATCAAAGAGTGGGAAATTGTACATTT GGGAATTAAGTTCAGGCAATTTATTATGTGTCAGAGACGCCCATTATCAGGGGGATCACTACCATCA AGGGTTCAAGCTGTGGAACATTTTTAATTACTGGAGGAGGAGGATGCCAGATGTCTTGTATGGAATT TAGCAGAATTAATTAGTATTTATGACAAATCAGACCATCAAGTGAAACCATATTGGCAAATCACTG ATAACACATTACCACTCACTGATCTTTGTTTAAATGATACTCATAACATTAATGATCTAAAAATTAT ATACAACTTCAGAAGACAGCACGGTCAGGATTTATGATATAGTCACAAAGAGTTTGTTAACCACAT TTATTTTACCCAGTTCCGCTGAATGTATCACCAAGGATCCAGCTAATAGAGCGTTATATGTCGGGT TGAATAACGGTCTTGTAAGATCAATTCCTTTATATTCTATAAATAGCCATACATCAGTGTTGGAAA GTATTGGCGGCATGAATAAGATAATCACGGTTGATGCTGATCAAAATTTAAAAGAGACATTTGTTG CACATCAACAAAAGACGAAAACAGGAGACGATAAGCCTGTTGTTACGAAATTGACAATTTCTT TTGATGGTACAAGTATAATATCTGGTGATTCTGAAGGCAGAGTGTTTGTGTCTGACATTGTAACGA AACAAGTTGTGAAATCATTCACACCTTGTAACTCTCCAATAGCTTATATTGCTGTTGAAACTATCC CTGATGACTTTGTCAATAACTTAGCTACTAGTACTACCACTAATAAAGCTGACAAGAAACATAGAA TGATACCTCAATTTAAACGAGTACTAGCAAGCACCAATTCTGAAGAACATCAGATATTCTTGGACA TTCCTGGTAAAACCACCGCAACCACCAACGGCAACCGGCAATATTGACTTTGCAACTTGGTTACAAG GCAAACAATCTGAAGAATTACAATTCAAAAACCTTTCTGGAATAAACTCTATTGTCAAACAAGTTG GCAACGAGAATGTATCGGATCTCGAAGAGAGATTACAAAGAGTTTCTCAAGCATACACTGAATTAA GAAACAAACATGAAGAATTAATTAAAGAACATGCCAAATTATTAGATAAATTAGAATAG

WO 01/02550 PCT/BE00/00077

YNL182C_homolog 534aa (SEQ ID NO 434)
MYVLKKKNFVQFLVLVLPLISSLSYKFTNMDEVVFYIAQGDPADKHSQESYGYVTSIHSSKQYASY
RQADSHINGTAITGIGPGERIFTAVPNKALINVYSWGKESVDQRIPIPEALTCITLINHPNGSNNN
SDNDDNQLYKLPNYRVPWLLAGGSKSGKLYIWELSSGNLLCVRDAHYQGITTIKGSSCGTFLITGG
EDARCLVWNLAELISIYDKSDHQVKPYWQITDNTLPLTDLCLNDTHNINDLKLYTTSEDSTVRIYD
IVTKSLLTTFILPSSAECITKDPANRALYVGLNNGLVRSIPLYSINSHTSVLESIGGMNKIITVDA
DQNLKETFVAHQQKTKTGDDKPVVVTKLTISFDGTSIISGDSEGRVFVSDIVTKQVVKSFTPCNSP
IAYIAVETIPDDFVNNLATSTTTNKADKKHRMIPQFKRVLASTNSEEHQIFLDIPGKTTATTNATG
NIDFATWLQGKQSEELQFKNLSGINSIVKQVGNENVSDLEERLQRVSQAYTELRNKHEELIKEHAK
LLDKLE

YNL190W_homolog 896bp public: 1..896; CDS: 501..893 (SEQ ID NO 435)

YNL190W_homolog 131aa (SEQ ID NO 436) MKFTTVATVFAISSLAAAKGGEKDHGKASTVTKYVTETTHRYGRFDKTSRSKKPKETGTHRYGKFN KTPRPVTTTVLVKESDLPKKDAVVARDSKNASSNSTTSSGNNGVATGVSLGLAGVLAVGAALVI

YNL208W_homolog 1076bp PathoSeq: 1..1076; CDS: 501..1073 (SEQ ID NO 437)

TTTTTGATCAGGCCTTTTGTTTTTTTTTTTGGGTGGTGCTGTGGTTCGTTGGGTAGTTGGCTCTTG TTTCGGTTCTACTTGTTCCTTTTTTTTATTCTCCTCGTTAATCCTAATTTTGTGTAACAAATTAAT ATTACGTAAGTCACTATAACTTGCATAGAAATTTCAGGTTTTCAATTTAAGAAAGTATTAATCAAC TTTTACTCAATTGAATCAATATTAAAACAATAAAAGCCATGTCAGCTAACGATTTTTATTCATCTG AACAAGACAGAGGGTTATTATCTACTGTCGCCGGTGGTGTTGCTGGTGGTTATGGTGGTCACAAAT TAGGTGAAAAGGCACAACATGGTACTTTGGGTACTGTATTAGGTGCCATTGGGGGTGCCATTGGTG CCAATAAACTAGAAGATGCTTATGAAGACCGTAAAGAACATAAAAAAACACGAGCAACAATATGGTG GTAGTGGTAAACACGAAGGCGGAAGACATGAAGGTGGTTTTTGGTGGTGGTAGACCAGATGATCGTT ATGAAGGCGATAGAAGAAATGATAATTACGGTGGTGGTTACAATGATAGAAGAGATGACGGTTATG GTGGTGGTTACGGTGGCAGACCAGACGATAGAAGACACGAAGGTGGTTTCGGCGGTGGCAGAC CAGATGACCGTTTTGGTGGCGGTAGACCAGATGACCGTTTTGGAGGTGACAGAAGAGATGATAGAA GAGATGACCGTAGATGGTAA

YNL208W_homolog 191aa (SEQ ID NO 438)
MSANDFYSSGDQSNYDPKRSSNQGSSSSNDEQQDRGLLSTVAGGVAGGYGGHKLGEKAQHGTLGTV
LGAIGGAIGANKLEDAYEDRKEHKKHEQQYGGSGKHEGGRHEGGFGGGRPDDRYEGDRRNDNYGGG
YNDRRDDGYGGGYGGGRPDDRRHEGGFGGGRPDDRFGGDRRDDRRW

YOL031C_homolog 1745bp public: 1..1342, PathoSeq: 1343..1745; CDS: 501..1742 (SEQ ID NO 439)

TTGGTATTGAAGACACCGAAGACTTGTTGAAAGATATTGAACAAGCTTTACAAAAGGCTGCTTCTG AACCAGAAAAGTGGTTTATACAGGAATATTTTAATAGAAATATCGCTTATATTGTGATAAAAAATT TGAAAGACAATCCGAATGTAGTGCTTGTCTTATTCTGCTTGGGAATACTGTAGTATTAGCATCAAT TTGAAAAAGGATCATATCAAGTTCTTATTGTATATTATGTAGTAGTTTTCTGTTTTAGTATTACTTG CAGAAAACCCTTTAGATTGTTATCCAAAATTGTTTGTTCCAACAACGAGTGGCAAACCATTAAAC CAGGTCAAGATATACCACCTGGGTTACACGTTAGATTAAATATAGATACGTTGGAAAAAGAGGCCA AGCTAATGAGTGCTGACGAAAAAGACGAGCCAGTTCAAGAAGTAGTTGTTGGTGGCGAATTGCAGG ATCATTCGAGGGAAGCCATCACTGAGAATCTACAAAAGTTGCATGAGCTGAAACATCCTGAAGTAA AACAGGAGCACGCTCATCGTACAAAGGTTAGCCAGGGAGATTTGAGTAATTTTGACGCAGCTTGTC TGGAAATTGAGAGTTTCAAGCCACATGAGAGTGATGTGGAAAGGTTGCATTTGGCACTAGATACTT TAGAGGAATTAAGTCATGATATCGAATTTGGGGTGAAATTGACCTCAGACAAAGCCATATTTCAGA GTTTTGTCAACATTGCCAATGGTGCTTCTGATCCAAAAATAACCGAAAAGGTATATCGTGTAATGG GGTCTAGTTTGAGAAATAATCCTGAAGCGATTAGTAATATCTTGACCAACTTCGACAAGAGCTATG TGGATAATTTGTTTGAGCAATTAGCGAATGAAAATGATGTTCTACAAAAGAGGATTTTGGGTATAA TTCAAGCTTTAGTCCAAAATAGCCATTTTGCAAGACAATATTTTTCATTTGACCACAGTTCCGGGT TAAATGATTTAATAGCGATTTTTCCCAAACTTGGTCCAAACTCAAAGTCCAGGGCAAGTAACATTT TAGAGGATTTACAATTGTTCCCAGTAACAAACGATAGAAGATCACTTGAAGATCAAGATCCTGAAT CACAGGTTTCAAAATTTATTCAGAATTCCTTTGTTGGAAATAAACTTGACGAGAAGAATTTCAAGT CTTATTTTGATCAACTAGTAAATTTGCATCAGCTGAATAAGAGTTTGCGACCAAGTGGTGACTTTC TCAATTGGTTAGCTGAAGAAGTGGAGTCGCGTAAAGAGAATAAAAAAAGAGACGATTATTCACAAG AAGACAAAGACTTTGATGAGTACATGTTGCGAGCACGTCATGAAGTATTTGGCAATCCAATGGGAT TAAGAAAGGCAATTGCCGACGAGTTGTAG

YOL031C_homolog 414aa (SEQ ID NO 440)
MKFSVLVLLASYLVGVNSSIVDTSEELICPDPENPLDCYPKLFVPTNEWQTIKPGQDIPPGLHVRL
NIDTLEKEAKLMSADEKDEPVQEVVVGGELQDHSREAITENLQKLHESKHPEVKQEHAHRTKVSQG
DLSNFDAACSEIESFKPHESDVERLHLALDTLEELSHDIEFGVKLTSDKAIFQSFVNIANGASDPK
ITEKVYRVMGSSLRNNPEAISNILTNFDKSYVDNLFEQLANENDVLQKRILGIIQALVQNSHFARQ
YFSFDHSSGLNDLIAIFPKLGPNSKSRASNILEDLQLFPVTNDRRSLEDQDPESQVSKFIQNSFVG
NKLDEKNFKSYFDQLVNLHQSNKSLRPSGDFLNWLAEEVESRKENKKRDDYSQEDKDFDEYMLRAR
HEVFGNPMGLRKAIADEL

151/161

TTGTATTGTTTTTCCAATCTTCCAAGCGTGGACTAAAGGCACATGCAAGATACTTTAAGTTGAAAG
GGTTTCTGCGTAGTGACATAAGAACAATCCACAAGCTAAACAGACCAGCATATATGGGGTACGGAG
TGGTTGCGCTTTGGCCTCGAGCTGTTTCCATTTATCAATATGTTTTATGTTCACCAATACTTTGG
GAGCTGCTTTGTGGGCAGTTGATATTGAACAACAAGAGAAGGCCGTCACAGAGAATGTGGCCGCAG
CTACTACCACCGCCACAGATACGAATAGCGTCAATCAACAAGGTCTAGTTATACCCGTACACAATG
AACCAGCAACTAATATACCTGAGGCTACCCCAAAAACTGCTACAAATACCATCTAA

YOL048C_homolog 247aa (SEQ ID NO 442)
MFSLFFPPQAIVYTLLMGPLGVIGAWYSLISQASTLSIFVVTISLMPHIQRVAYDAILSRECANDV
VLMGKLRRYRKLPIRVRAREYLKAIPDFSIFPFSLLKLLVFFGIYFIPFVGPIIVLFFQSSKRGLK
AHARYFKLKGFSRSDIRTIHKLNRPAYMGYGVVALWLESFPFINMFFMFTNTLGAALWAVDIEQQE
KAVTENVAAATTTATDTNSVNQQGLVIPVHNEPATNIPEATPKTATNTI

YOR027W_homolog 2270bp PathoSeq: 1..947/1781..1828, public: 948..1780/1829..2270; CDS: 501..2267 (SEQ ID NO 443) TATTTAAATTATAGTAATCATCCTATAAATTTCAAAGTCAAAAGACAGATCTTAAGGTCTAATTAA TAACTCTCTATGGCCTTCTGTGTCAAATTGTTGTCGTTTGATAACAAGTTTGGAACGGTAATGGTT GAAATTAGAAAAGAAAAAATTACACATGGTAGCAGCTGATGTATAGAACTTTCTAGCAAAAAAA AAAGAAAGAATTTTTTTTTTCTTCCATTTTTCAAATTTGAGAGATCGAAATAATTTTCTTGAATTTA TTAAAAGGGAACCCCTTCCCGAAAAATCCAAAACCAAAACTTCCACCCAAATATCAAATAACTAAC TTATCATTCCAACAGATAATATTCCCACTTCAATAACAATGACAACAGCTGACGAATACAAAGCAG AAGGTAACAAATATTTTGCTGCTAAAGATTTTGAAAAGGCGATTGAAGCATTCACTAAAGCAATTG AAGCATCACCTGAACCAAACCATGTTCTTTATTCAAATCGTTCTGGATCTTATGCCTCTTTAAAAG ATTTTAACAACGCATTAAAAGATGCTCAAGAATGTCTCAAGATCAATCCTAGTTGGGCCAAAGGGT ATAATAGAATTGCTGGGGCTGAATTTGGTTTAGGTAATTTTGATCAAGCCAAATCCAATTATGAAA AATGTTTGGAGTTGGATCCAAATAATGCCATGGCTAAAGAAGGTTTAAAATCAGTTGAATCTGCTT TATCATCTGGTGGTGGTGATGACAAGGATTTAGGATTTGGTAAAATTTTAAATGATCCTAATCTTT TTGAACGTCTTAAAACTAATCCACAATTGGGTAATCCTGATATGTTTAGTGATCCAAGATTATTGA CGGCTTTTGCTGCTTTAATGGGTATTGACATGGATTTACCAAATATGGGATTCACTGCTCCAAACG AATCACAATCCAATGCATCAGAACCAAAACTGGAACCAAAATCAGTACCAGAATCTAAACCAGAAC CAAAAGCAGAACAAAAGGAAGAATCAACCTCAGCCAAAGATGAAGACACTCCAATGACTGATG CCCAAGACGACACTAATGATAATGATGCCAAAACCCAAGCTGACAATGCTAAAGCTGAAGGTAATG CCTTATACAAGAAACGTCAATTTGATGAAGCAATTGCCGCCTATAATAAGGCTTGGGAATTACATA AGGATATCACTTATTTAAACAATCGTGCTGCTGCCGAATATGAAAAAGGTGATTATGATGCTGCTA AATCATTTGCTAGATTAGGTAATATTTATTTGAAAAAAGATGAATTACCCGAAGCAGTGAAAAATT **AAATTAAAACTAGAGAATTAAATGCTTATATAGATCCAGAAAAGGCTGAAGAAGCAAGATTACAAG** GTAAAGAATATTTCACCAAAGGAGATTGGCCAAATGCCGTTAAGGCTTATACTGAAATGATTAAAA GAGCACCAGAAGATGCTAGAGGATATTCTAATCGTGCTGCTGCATTGGCAAAATTGTTATCATTTC CTGATGCTATACAAGATTGTAATAAAGCCATTGAAAAAGATCCAAATTTCATTAGAGCTTATATTA GAAAAGCTAATGCTCAATTGGCAATGAAAGAATATAGTCATGTCATGGATACTTTAACCGAGGCAA GAACTAAAGATGTTGAATTGGGTGGTAAATCAATTCATGAAATTGATGAATTAATGAATAAAGCTA CTTATCAAAGATTTCAAGCCATTGAAGGTGAAACTCCTGAACAAACTATGGAAAGAGTTTCTAAAG ATCCAGAAATTGTTCAAAATTTTACAAGATCCAGTAATGCAAGGAATTTTAGCTCAAGCTAGAGAAA ATCCTGCTGCTTTACAAGATCATATGAAAAATCCTGAAGTTTATAAAAAAATTAATATGTTGATTG CTGCTGGTGTTATTCGTACCAGATAA

YOR027W_homolog 589aa (SEQ ID NO 444)
MTTADEYKAEGNKYFAAKDFEKAIEAFTKAIEASPEPNHVLYSNRSGSYASLKDFNNALKDAQECV
KINPSWAKGYNRIAGAEFGLGNFDQAKSNYEKCLELDPNNAMAKEGLKSVESALSSGGGDDKDLGF
GKILNDPNLYTKLKNNPKTSEFMNDPQFVAKLERLKTNPQLGNPDMFSDPRLLTAFAALMGIDMDL
PNMGFTAPNESQSNASEPKSEPKSVPESKPEPKAEQKEEESTSAKDEDTPMTDAODDTNDNDAKTO

WO 01/02550 PCT/BE00/00077

ADNAKAEGNALYKKRQFDEAIAAYNKAWELHKDITYLNNRAAAEYEKGDYDAAIATCEKAIDEGRD MRADYKLIAKSFARLGNIYLKKDELPEAVKNFEKSLTEHRTPDVLNKLRSTQREIKTRELNAYIDP EKAEEARLQGKEYFTKGDWPNAVKAYTEMIKRAPEDARGYSNRAAALAKLLSFPDAIQDCNKAIEK DPNFIRAYIRKANAQLAMKEYSHVMDTLTEARTKDVELGGKSIHEIDELMNKATYQRFQAIEGETP EQTMERVSKDPEIVQILQDPVMQGILAQARENPAALQDHMKNPEVYKKINMLIAAGVIRTR

YOR312C_homolog 1019bp public: 1..1019; CDS: 501..1016 (SEQ ID NO 445)

TAAGAATTTCAGTTTAGAAGGTATTCAACAACAACCGAAGAGTATGTTCAACATCGTTATAATAGA ATAGAATAAGAGCATGACAAAGGGATACAAGCTTGAAAAAAGAAAAAGGGTGGGATATCTTAA **AATTATTAAAGAGTTTTTTTTTATAACATGTCATTGAGATTGAGATTGGGAATACTGAATTTCGATTT** TAAAGTCATTGGATGGGAGAGTTAATTATTCGTTTTTATTATTAGGATTACCAATGAATAGTAATGA AGTGATGGAGAGATAGAATGAAAGTATTCAGAAGAGCATCAAGTCCCTTATAAGTTTGTGAGACAT **AATATGTCTACCCCCTTGTCAACTTGTCATAAATTTTATTGCTCGTCCTTTAAAAAGAAATGAATAA** AAAGATTTACTAACTTAATTTCAATTATTATAGAAAGATGTCTAGATTAAACGAATATCAAGTTA TTGGTCGTAATTTACCAACTGAATCCGTTCCAGAACCAAAGTTGTTCAGAATGAGAATTTTTTGCTC CAAACACCGTTGTTGCCAAATCAAGATATTGGTATTTCTTGCAAAAATTGCATAAAGTTAAAAAAG CTTCTGGTGAAATTGTATCTGTCAACATTATTTCTGAAGCTAAACCAACTAAAGTTAAAACTTTTG GTATTTGGTTAAGATATGAATCCAGATCTGGTATTCATAACATGTACAAAGAATACAGAGATGTTA CTAGAGTTGGTGCTGTTGAAACCATGTACCAAGATTTAGCTGCTAGACACAGAGCTAGATTTAGAA GTATCCATATTTTGAAAGTTGTTGAATTAGAAAAAACTGATGATGTTAAAAGACAATACGTTAAAC AATTTTTGACTAAAGATTTGAAATTCCCATTACCACACAGAGTCCAAAAATCTAAGAAATTGTTCC AAGCTACTGCTCCAACCACTTTCTACTAA

YOR312C_homolog 172aa (SEQ ID NO 446)
MSRLNEYQVIGRNLPTESVPEPKLFRMRIFAPNTVVAKSRYWYFLQKLHKVKKASGEIVSVNIISE
AKPTKVKTFGIWLRYESRSGIHNMYKEYRDVTRVGAVETMYQDLAARHRARFRSIHILKVVELEKT
DDVKRQYVKQFLTKDLKFPLPHRVQKSKKLFQATAPTTFY

YOR369C_homolog 932bp PathoSeq: 1..228, public: 229..932; CDS: 501..929 (SEQ ID NO 447)
TGTTTACTTTTCTGTAGTTTTAAAGTTTCCTAATTTAACTTCCAAAAGTTTCATTAACAACAATA
TTAACATACCTTTGTCACAAGCAATTATATTGAAGTTTTTTTGTG
TACATGTGAGATATATAATTGTGTATATACAGTCACGTGAATAGAGCAGAAAAATTACGAAGTAGA

YOR369C_homolog 143aa (SEQ ID NO 448)
MSDVEQEQIVEEVVVEEQSGAITIEDALKVVLRTSLVHDGLARGLREASKALSKREAQLCVLCDSV
TEESIIKLVEALCNEPEEKIPLIKVSDAKLLGEWAGLCQLDRDGNARKVVGASCVVVKNWGADSDE
RNILLEHFSQQ

YPL047W_homolog 881bp public: 1..811, PathoSeq: 812..881; CDS: 501..878 (SEQ ID NO 449)

YPL047W_homolog 126aa (SEQ ID NO 450) MLFCFILTKICFFFFSKADSIFNDLINNIIKQHTLTSLTNIKDHSSLLNSSNSNTNSNTNGTIASN GGNGTTSDENNEIENSTIQDKSKLKQLETSRYFRCLNCGRNIAGGRFASHISKCLERKRK

YPL137C_homolog 5344bp public: 1..3342, PathoSeq: 3343..5344; CDS: 1250..5341 (SEQ ID NO 451)

CTCTAGAAGTAGGACATCGTATAGTGTATAAACACTCAATAAGTAATGAAGAAACACGTTTTGTTG TTTTCTCCTTATGGAAAACATTAGTACTAGTAGTGGTGGTAGTAGTTGCTGTTTGCACTTTGC ACGTAGTTGTTTTCCCCTCATTCTTTCATCTGATTATTCTGTCTTTGTTAACTGCATACAAAGGGA GGGGAAGAAGAACAACAAAAGGGGAATTTGAATATACGTCAATCTTTTAATCCTACTACCACGGG GGGGGGGGGGTCATACTTCTTGGTGTAAATAATGTATGGAGATTGAGGTTATTAGACTTTTAGAA AGAGGTCTTGGTTGAGTAAGGCGGGATAGCACAAATAATGCGTGTCTAATTGGTCAGAGAATAATA TGCTTTGGGGAACAATAGAAAGATGTAGCGAGAGAAATAGAATTNCAAGGGTAAGGATGATTAACT TTTTTTTTTTTAATGCTTGGAGTACTTTGTTGTTGGAAAGAGTATTGCAGAAGTAATAGTTTAAT AAAAGAAAGTATATAACTTTAGTAATCGGAGAACAATTGAAATCAATATTTTGAAAATATAGTTT TATAGAGTAACCTGGGTCGAGGTGAACCCGAATTCAATATTGGTTTTCGGTTGTTATATGCTACAT TGTTACTGTTGTATTCTGTTTTTTGGTCATTGCCATGGTAATTTCATATTTAGTAACAATTTAGTG TGTTAATTGTTGATTATTGATTGTTCCCCAATTAAAATTCCGATAAACTTGAACAATAA TTTATTTTCTTTTTGCTTCCTACTTCTCTTTTATTTTCTTAGTTTCATAATTTTTGACAGATAATA CTTGAAACTGGTTAATTTTAAATCAACTTCGTGATTTTTTTCCGGAAATCTAATAATATCAATGAC CAGTAATCTGCCACCACTTGGTTCTACAACTAACGATCAGAGACTACCCCAAAGCGGAGTTTCATC CATACCCACAAATAAATTGCCTTTACCTAATGCCAATGAAGATTTTGCCACGGGTGTGTCGAATGG AGATGTTGACTGGCTATTTCGAGGTAAATCAAAGAATTGGGGAAAAAGATGGCTAACAACAATGC CAATAAGGATGAACGAAAGAATAGTCATGGTAACATCAAAAACTCGGAAAAAACTACCGCAAAACC CAATGAAACTAAACATGAGTCTAATGGTGAGAAGTTAGAATTCAATGTTCCAAAATCTGTAATGCC AACAAAGCATACATCGTCTGGGAACCCAAAAGCACCTACCAATGGACAAATCTCAAATGTAACACC AAGTCAACCAAGTCCGAAACAGACCACTTCTGGGTCAACAAATGCAAATGATATACCTCCAATTTC TCCTAAACAACCAGAAAAGGCATCAAAGTTGAATAAACTAAAAATTGGGCGTTCAAGATCGTCTTC TGCATCAACAGTCGTACCTTCATCTACAACAGCTTCAACTACTACTAATCCTGGAGATCCTAAAAG TGACGATCCTGCATTGGTATCTCAATTATCAAACAATTCAAATTCTCTGAACTCATCCTCGCCTAA TGTTTCTCGTTCAAATAGCAAAAAAGGTGGGTTATTCAGTTCACTTTCATCAAAATTTAGATCAAG CTCGGCTTCATCTAAACAACCACAACTGCATTCATCGTCTACACCATCAACCACAACGACAAATGG TGGCGGTAACTCGTCCGCTGCTCCAAAATCATCCCATCACTCCCCCAAATTTAATCCTTCACTTGT TGGTCCAGTATCAAAGCACAATCGAGAAGCTGAAGATTTGGTGTCTCTTACCAATACTTTGCCTGC TGGGAGTGGAATACCAATTAAACGTAAACCATCAATATCGGGAAATTCAATTTTCAAAGATTCATT

TCTCGATGATGCAAGTTCTTCACCGTCATCTTCATTAAACTCTGATGGGGGGGCTTAAGTTTTTCAG GAGACGTTCCTCTGTGGCATCTACACCATCAACACACGCGTCAACACCTCGAGTGATTTTGAACAA AAACCCCAATAGGAGAAAAGTACCCATTGAAGAAATATCTGAAGTTCGATTGCGTCGGGTTACCTT TTCTGTTGATAAACTCGAGCACGATCCGCAACAGCAGATTCCTTCAAGAAGACCTAAACGAGGTAA TGTTTTAATTCCACAGGACATCAATGCACCACCTCCAAGACTATGTCTTGGGATTTCAGTTAATGA ACCAAATAATAAAGATGACGGTAAATCACACAACCATTCCAAATATAGTGATCATGAAATTGCATT AGCTGAAGATGCTCAACGCCGAGCAATTATTGAAGCAGAAAAACATGCTCAAGAAGCTCATCGACA AGCCAAAAAGATTGCTCAAGAAGTTTCTGGGTATAGATCACATAGATTCATATCCATTAAAGAAGG TGGTAGTGTTGGTAATTCTAACACCAACGGCAACGACAATGACGAAGATGATGATGAGGTTGAAGA TTTCGAAGAAGAAATTGAAAGCAAAACAGGTGAAAAGACCATTTCATTGGAAACAATCTATACAAG ATGTTGTCATTTACGAGAAATTTTACCAATCCCAGCAACATTGAAAACAATTGAAAAATAAGACAGC ACCGTTGGAAGTGTTAAAGATGCTCAACCCAAAACCAACTTTAATTGATGTGTTATCTTTTTCAGA TTTTATTGCCATTACACCTATTAACACGGTCATTTTTGATAACGTGACTATGACAACAGAGATGTT GAAAAACTTTCTTGGATCGTTGACATATAATAAACAATTGGAAAAGTTATCGTTGAGAAATGTTTC CATTGATGAGTTGGGAAGTATTTGTGTGAATTTTTGGCAACAAATAAAACAGTTAAGAAATT GGATATATCACAACAACGTATCAAGCCAGATACCCCAGACACAAGCATTCGTGGTAATATGAACTG GGACTTATTTATTCGATCATTAATTTTGCGTGGTGGAATAGAAGAATTGGTTATCAATGGATGTAA ACTATCCGATGCAATATTTGAAAAGTTCATCAATCAAGCGGTTAAGAAGTCAACCTATCGATTAGG TATTGCTGGTATTGATTTGAATGTTAAAAAATCAGAAATGGTCACATCGTGGTTAACTGATGGTAA TTCTCAATGTGTTGGTGTTGATATTGCTTTTAATGATTTGAGCAAGGGACAATTACGTCCATTCAT TTTAAGTTCCATACCTAATATCTTCCCGAAAATAATTACCCATTTGGACAAATACTTGCCCAGATA TCCTAATCTTCGAAGAATACATTTTGATCTTAATGAATTAACCGCACAAGCTATTGGGTCATTGGC GGGGTGTTTACTGAAAATGCCCCAATTAGTTCATGTCTCGTTATTGGGTAATAGAAATTTGTCAAC TACGTCAGCAGCTACATTATACGGAGCAGTTAAACAATCCAAGACCTTGTTTGCTCTTGATTTGGA CTACGATTAATACCTGATCAATTATCACAACGTATTGCCTTTTATTTGATGAGAAACTTGGAATA CACTTTGAAGCCATCTCATGGCGGCAATATTGAAAGCAATCCAGAAAAACCAGAGGATTTGATGTA GGATATCAAAATGCAAAGAATTATATCCGATTCAGTATTGGAAAGAACAAGATCGATTCGTAAGGA TATTCACAAAACCATTGATACATTATTCGAACAAAGAAATTTAGGTAAATTATCATTTGAAGGTAA AGAGAATTTAGTTCGATTTTGTTTATTAGATTCGTCTTTAGAAAAATTGGTTGTTATGGTTGAGGA ACATGCCAACGGATTATTATTAACACCAACGACCTCCACGGACGATCTCAGAAGTAGAGCCATGTC GCCATCGGTCACTGTTGATACAATCCATGAAAGTGCAAATGAGTTGATTACTGCTGGACCAATTTT ATCACCACATGTCAATAGGAAAGCAGAACAAAGCTCGTATTTCCCAGTGTTTGCCAATAATGATAA TTTGACCCCTCATCAAGTTGTCGTTGAGTCAAATGATGAAGGTAGAGATGTTCCAATAGATAAAAT TGAAGAAGGGGAGCTTCATAAATTTGGATTCTTTATTCAACAAAAAGAGAGACAAAAAACAACAACA ACAACAACAACAACAGAACTCACACCACCAGCACCAACCGGCCCAGCTGATCCAACAAGAAAA CCAGCTGCCGCTGCCACAACAAGGAAAATATGAAGATTTACCGATATTAAATACATTACCGTCAGG AATTAATAATCATCGTGTTAAAATCGATGCACCATCGACAAAACACCATCATGAATTGAACAAACC AAATTCTGACAAAGTAGTTGAGGATGAAGTTGAAGTTTCTGATAATGCCTCTATTGATTCTACTAA TGGTGACGATTTACATCAACTTGGTGACGGTAAACATAATGGTAATGGTACGGTTGATCCCATGGT TAGTGAAGTTTATGACAAGTTGTTAAATGATGCTGAACGAGTCAGACTGAATAGAGATATATAA

YPL137C_homolog 1364aa (SEQ ID NO 452)
MTSNSPPLGSTTNDQRLPQSGVSSIPTNKLPLPNANEDFATGVSNGDVDWLFRGKSKKLGKKMANN
NANKDERKNSHGNIKNSEKTTAKPNETKHESNGEKLEFNVPKSVMPTKHTSSGNPKAPTNGQISNV
TPSQPSPKQTTSGSTNANDIPPISPKQPEKASKLNKLKIGRSRSSSASTVVPSSTTASTTTNPGDP
KSQPKRRSSSFNFVTPSLTSDLAYDDPALVSQLSNNSNSSNSSSPNVSRSNSKKGGLFSSLSSKFR
SSSASSKQPQSHSSSTPSTTTTNGGGNSSAAPKSSHHSPKFNPSLVGPVSKHNREAEDLVSLTNTL
PAGSGIPIKRKPSISGNSIFKDSFLDDASSSPSSSLNSDGGLKFFRRSSVASTPSTHASTPRVIL
NKNPNRRKVPIEEISEVRLRRVTFSVDKLEHDPQQQIPSRRPKRGNVLIPODINAPPPRLCLGISV

NEPNNKDDGKSHNHSKYSDHEIALAEDAQRRAIIEAEKHAQEAHRQAKKIAQEVSGYRSHRFISIK EGGSVGNSNTNGNDNDEDDDEVEEAVDKKLANDVSVDGPLHVHEQHFEEEIESKTGEKTISLETIY TRCCHLREILPIPATLKQLKNKTAPLEVLKMLNPKPTLIDVLSFSDFIAITPINTVIFDNVTMTTE MLKNFLGSLTYNKQLEKLSLRNVSIDELGWKYLCEFLATNKTVKKLDISQQRIKPDTPDTSIRGNM NWDLFIRSLILRGGIEELVINGCKLSDAIFEKFINQAVKKSTYRLGIAGIDLNVKKSEMVTSWLTD GNSQCVGVDIAFNDLSKGQLRPFINAFNTGKVNNLVFFSLNSTNLSNIEETSDLIKSLINVKTLRFLDLSSIPNIFPKIITHLDKYLPRYPNLRRIHFDLNELTAQAIGSLAGCLSKMPQLVHVSLLGNRNL STTSAATLYGAVKQSKTLFALDLDYDLIPDQLSQRIAFYLMRNLEYTLKPSHGGNIESNPEKPEDL MYDGSLLMETAEKLLVEIEKGKKEDIKMQRIISDSVLERTRSIRKDIHKTIDTLFEQRNLGKLSFEGKENLVRFCLLDSSLEKLVVMVEEHANGLLLTPTTSTDDLRSRAMSPSVTVDTIHESANELITAGPILSPHVNRKAEQSSYFPVFANNDNLTPHQVVVESNDEGRDVPIDKMTGRPVLIRSISQTSVHAKEQEIEEGELHKFGFFIQQKERQKQQQQQQQQNSHHQHQPAQSIQQENQSPSPQQGKYEDLPILNTLPSGPELRDAIMAAKGVANVTELIDRINNHRVKIDAPSTKHHHELNKPNSDKVVEDEVEVSDNASIDSTNGDDLHQLGDGKHNGNGTVDPMVSEVYDKLLNDAERVRSNRDI

YPL175W_homolog 1859bp public: 1..393/395..1859, PathoSeq: 394;CDS: 501..1856 (SEQ ID NO 453)

ACGGAATAATGTTATGCGAACAGAGTAACTGGGATTATCAACAAGCATCAGTCAATTTCAAAAACT AATTCAATGTAGGTGATATCACTTTCTGAGAGTTCTTATTACGATATATAAAATACATAGCCAAAA TTATAATGAAGTAAAAACATGTAACTGTGTAATTTTATTCAAGTCCAAAGGTATTGATTAATATTG TAGAGTGTTGAGCATTTAAAATATGAAGGAAGACCGATAACCTAAAGTTTTCCTCAGGGTGTCGAA GGCTAGGAGGAATAAAATCTGAGTAGAGAACTTTCGTTTATATCAGTTTTTTGCAAGAAAAAAAGG AAAACAAAACAAAATAACACCACAAACGAATTACACAAGCACATCCTAAACACCACTCTGTTGGAG CACCAATCAACCTGAGAAATGCAAACTTGTAATAAAATATGGGATACAATATAGCAATGGTAACAG ATTTTTTTTACCCTCAACCTGGAGGAGTAGAGTTTCATGTGTATCATTTATCACAAAAACTCATTG AACTAGGACACTCAGTGGTTATCATAACTCATAATTATTCATCAAGAAATGGTGTACGAGTATTAA CGAATGGTTTGAAAGTGTATTATGTACCACTTTGGGTGATCTATAGAAGCTCAGTTTTCCCAACTG TATTTCTGTGCTTCCCAATATTGAGGAATATCTTCATACGAGAAAACATTGAGATTATTCACGGAC ATGGTTCCTTCAGCACATTATGCCACGAAGCTATATTACATGGCCGAACAATGGGATTAAAAACAG TCTTCACTGATCATTCACTTTTTGGATTTGCCGAGATTGGATCAATTATGGGGGAATAAAGCATTAA TAAGAGGATCAATAGACCCCATAAAAGTGAGTGTGATACCGAATGCAGTTATTCTGAAAGATTTCA AGCCCAAATCGCATTGTGTTAACAAGAACTATACTAAAGAGATCACCATTGTGGTGATCACGAGAT TGTTTCCAAATAAAGGAGCCGATCTATTAACGGCTGTTATCCCCAAAATTTGCCAGTTGAAACCAA AAGTGAAATTTCTAATTGCTGGTGACGGCCCCAAGTTTTTAGATTTAGAACAAATGAGAAAAAGT ACTTTCTTCAGGAAAGGGTTACATTAGTAGGCGCTATAAAACACGAAGAAGTAAGAGATGTAATGG TCCAAGGTGACATATACTTACATCCTTCATTAACAGAGGCGTTTGGTACAGTTATTGTGGAAGCTG CATCATGTGGGTTATATGTTGTCACTACAAAAGTTGGAGGCATACCCGAAGTCTTACCAAACGAAA TTGAAAGTAATGAAATCGATACCTCAAAATTTCACGATGCGGTTGCAAAGATGTACAGTTGGAATG ATATTGCAAGAAGAACAGAAAATGTTTATAATTCACTTGATTTAGACAAACTAAACGAGTCTTTAC TTCACCGATTACAAAGATACTATTGTTGTGGTATAATAGCAGGCAAACTTTATGCTTTATGTGTAA TAGTGGATATTTTTATTTTCGTGATACTAGAATGGTTGTATCCCGCTGATCATATCGATAAAGCAA **AAGTAAATTAG**

YPL175W_homolog 452aa (SEQ ID NO 454)
MGYNIAMVTDFFYPQPGGVEFHVYHLSQKLIELGHSVVIITHNYSSRNGVRVLTNGLKVYYVPLWV
IYRSSVFPTVFSCFPILRNIFIRENIEIIHGHGSFSTLCHEAILHGRTMGLKTVFTDHSLFGFAEI
GSIMGNKALKFTFSDVGHVICVSHTCKENTVLRGSIDPIKVSVIPNAVISKDFKPKSHCVNKNYTK
EITIVVITRLFPNKGADLLTAVIPKICQLKPKVKFLIAGDGPKFLDLEQMREKYFLQERVTLVGAI
KHEEVRDVMVQGDIYLHPSLTEAFGTVIVEAASCGLYVVTTKVGGIPEVLPNEMTSFAEPEENSLI
DAAIDAINKIESNEIDTSKFHDAVAKMYSWNDIARRTENVYNSLDLDKLNESLLHRLQRYYCCGII
AGKLYALCVIVDIFIFVILEWLYPADHIDKATKWPSAIKEEDESEEETFIFPNKVN

YPL218W_homolog 1231bp PathoSeq: 1..407, public: 408..1231; exon 1: 501..518, intron 1: 519..676, exon 2: 677-1228 (SEQ ID NO 455) GATACAATTCACGACCTCTAATTTCCTTAGTGATAGGTTAATCATGAAATATATAAAATGTCTAGA AATAATTGAATAATAATATAATGTTGTGAAACTTGTGGAAAAATTTGACAGCCTAGTAAC TCAAGTGTTGTTACACTCTTGTTATTATTATTATTATATCGTTTACAAGTAGATTTCTCATTTTGA ACAACTTGTAGATTAACAGAATTTGAACATTTCTAGAGTTTCTTATATTCCCCCCAAGGTGGACAA TTTATTCTATTAACCAAGTTTGATCTAATTACTGATCTGTATATACTAACCAAATATTTACCTTAT CACTTAATTATTACAGTTCAAGATATATTATCATCATTAGGATTATGGAATAAACATGCCAAATT ATTATTTTAGGGTTAGATAATGCTGGTAAAACTACTCTTTTACATATGTTAAAGAATGATAGATT GGCCACTTTACAACCAACATTACATCCAACTTCAGAAGAATTGGCCATTGGATCAGTTAGATTTAC TACTTTTGATTTAGGTGGACATCAACAAGCTAGAAGATTATGGAAAGATTATTTCCCTGAAGTCAA TGGTATTGTCTTTTTAGTCGATGCTGCTGATACCGAAAGATTTGCTGAATCCAAAGCTGAATTGGA AAGTTTATTTAGAATTGAAGAATTGAGTCAAGTTCCATTTGTTATTTTGGGTAATAAGATTGATGT TCCTACTGCAGTAGGGGAAATGGAATTGAAAAATGCCCTTGGATTATATAATACTACTGGTAAAGA TACTGGTAAATTGCCTGAAGGTACTAGACCAATTGAAGTGTTTATGGTTTCCGTTGTTATGAGATC TGGATATGGTGAAGCCTTCAAATGGTTATCACAATACATTTAA

YPL218W_homolog 190aa (SEQ ID NO 456)
MWIFDWVQDILSSLGLWNKHAKLLFLGLDNAGKTTLLHMLKNDRLATLQPTLHPTSEELAIGSVRF
TTFDLGGHQQARRLWKDYFPEVNGIVFLVDAADTERFAESKAELESLFRIEELSQVPFVILGNKID
VPTAVGEMELKNALGLYNTTGKDTGKLPEGTRPIEVFMVSVVMRSGYGEAFKWLSQYI

YOL127W_homolog 429 bp, public: 1..429, CDS: <1..429 (SEQ ID NO 475)

YOL127W_homolog 142 aa (SEQ ID NO 476) LIATTKASAAKKAALKGVNGKKALKVRTSTTFRLPKTLKLTRSPKYQRKSVPHYNRLDAHKIIVAP IATETAMKKVEDGNTLVFQVDIKSNKHQIKSAVKELYDVDALYVNTLIRPNGTKKAYIRLTSDYDA LDIANRIGYI

YJL188C_homolog 117 bp public: 1..117, CDS: <1..>117 (SEQ ID NO 477)

TTAGATACCCAACTTAGTTCTCTCCAGTGTCTTCTTTTAGCATTGTATCTGATTTTGTTGTCAGT TCTCAATCTGATCCATTGTGGCAATGGTCTGTTTTGCTTTTTGAGCCTTTAGC

YJL188C_homolog 39 aa (SEQ ID NO 478) LDTQLSSSPVSSFSIVSDFVVSSQSDPLWQWSVLLLSLS

YGR183C_homolog 198 bp public: 1..198, CDS: 1..198 (SEQ ID NO 479)

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YGR183C_homolog 65 aa (SEQ ID NO 480) MLTVLGRLLERNSIYVATIFGGAFAFQGFFDVAVNKWWEEHNKAKLWKNVKGKFLEGEGEEEDDE*

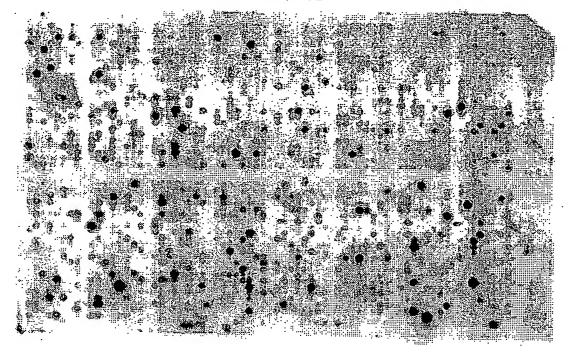
YDR529C_homolog 457 bp Pathoseq: 1..457, CDS: 1..457 (SEQ ID NO 481)

YDR529C_homolog 151 aa (SEQ ID NO 482) MVQSMTSVVKAANFILARPTLSKIITPLAQKFTAYAGYREMGLKFNDLLLEETPIMQTAIKRLPSE LNYSRNFRILTAHQLALSHQLLPAEKAVKPEEDDNYLIPYILEAEKEAFEKAVLGNIDASAIVINT TNKKRTRKKKMRRSNIEI

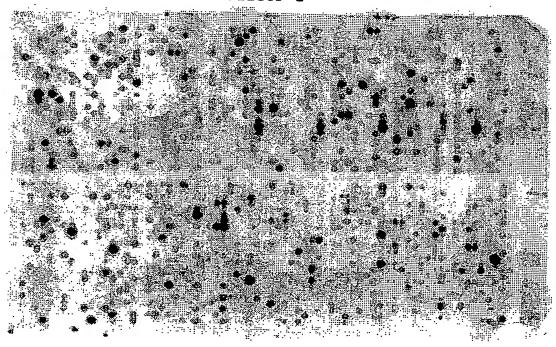
YBL003C_YDR225W_homolog 399 bp public: 1..399, CDS: 1..399 (SEQ ID NO 483)

YBL003C_YDR225W_homolog 132 aa (SEQ ID NO 484) MSGGKGKAGTSEKASTSRSAKAGLTFPVGRVHRLLRKGNYAQRIGSGAPVYLTSVLEYLAAEILEL AGNAARDNKKSRIIPRHLQLAIRNDEELNKLLGDVTIAQGGVLPNIHQNLLPKKSGKGGVKASQEL

158/161



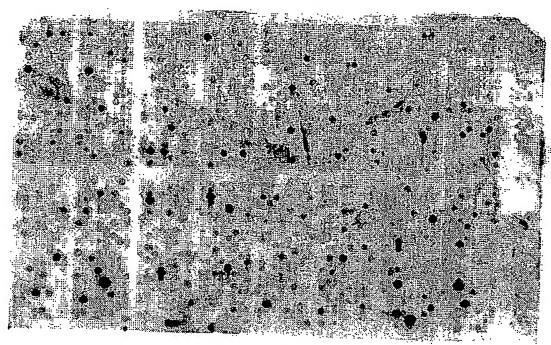
Filter I



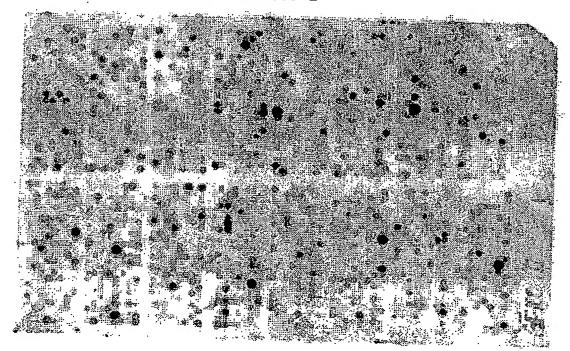
Filter II

FIG. 3A

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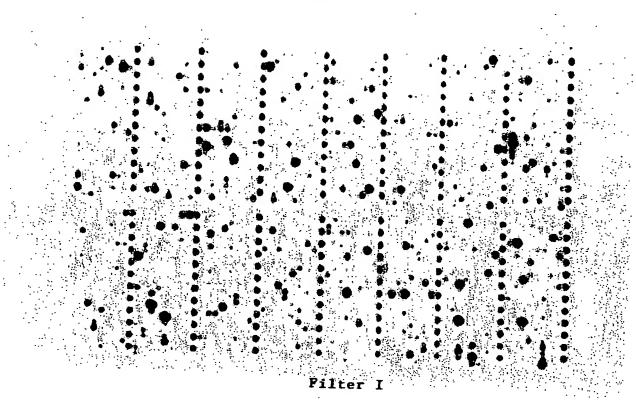
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Filter II

FIG. 3B





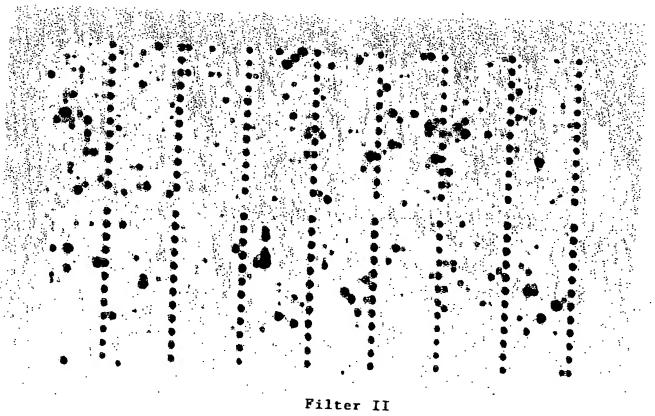
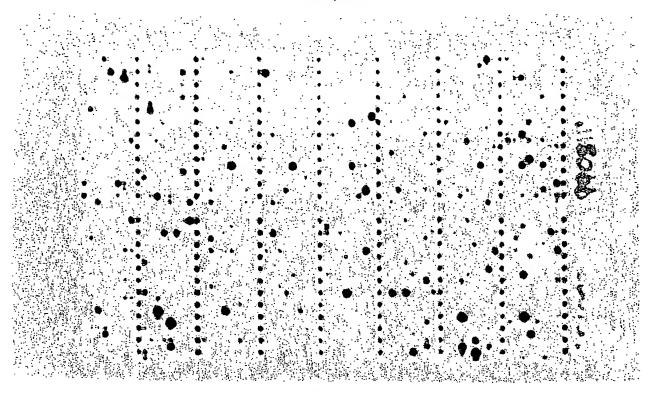


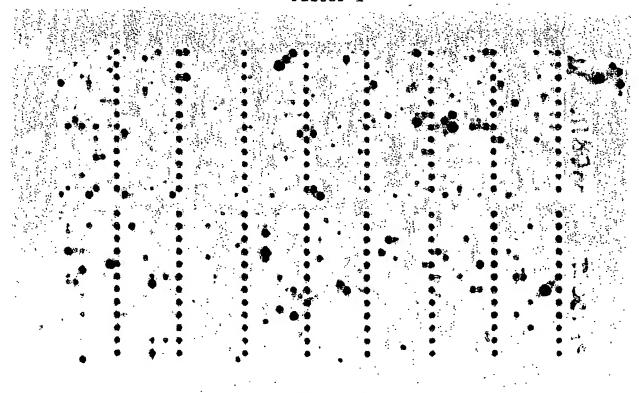
FIG. 4A



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Filter I



Filter II